SEARCH REQUEST FORM

Scientific and Technical Information Center

| Requester's Full Name: _ | | Examiner # : | Date: |
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| Art Unit: | Phone Number 30 | Serial Number: | |
| Mail Box and Bldg/Roon | n Location: | Examiner # : Serial Number: Results Format Preferred (circle): | PAPER DISK E-MAII |
| f more than one searcl | h is submitted, please | prioritize searches in order of ne | ed. |
| include the elected species or atility of the invention. Defin known. Please attach a copy of | structures, keywords, synony e any terms that may have a s if the cover sheet, pertinent cl | | ombine with the concept or |
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| Inventors (please provide fu | ıll names): | | |
| Inventors (please provide fu | all names): | | |
| Inventors (please provide functions) Earliest Priority Filing D *For Sequence Searches Only* | all names): | | stent numbers) along with the |
| Inventors (please provide functions) Earliest Priority Filing D *For Sequence Searches Only* | all names): | | itent numbers) along with the |
| Inventors (please provide fu | all names): | | stent numbers) along with the |

Point of Contact:
Jan Delaval
Librarian-Physical Sciences
CM1 1E01 Tel: 308-4498

| STAFF USE ONLY | Type of Search | Vendors and cost where applicable |
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| Searcher: | NA Sequence (#) | STN |
| Searcher Phone #: | AA Sequence (#) 26 | Dialog |
| Searcher Location: | Structure (#) | Questel/Orbit |
| Date Searcher Picked Up: 1/14 | Bibliographic | Dr.Link |
| Date Completed: | Litigation | Lexis/Nexis |
| Searcher Prep & Review Time: | Fulltext | Sequence Systems |
| Clerical Prep Time: | Patent Family | WWW/Internet |
| Online Time: | Other | Other (specify) |
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| A46160 | A56047 | T05821 | A84232 | T32755 | T05518 | S01066 | T50195 | T18912 | F83354 | T33084 | T21576 | T26696 | S77572 | A48457 | T04107 | T02011 | T18230 | DEBYA2 | DEBYA | E85798 |
| interferon alpha-i | gamma-interferon a | hypothetical prote | spore cortex synth | hypothetical prote | hypothetical prote | regulatory protein | hypothetical prote | hypothetical prote | probable sulfatase | hypothetical prote | hypothetical prote | hypothetical prote | oligopeptide trans | hexokinase (EC 2.7 | calmodulin-binding | probable cathepsin | alcohol dehydrogen | alcohol dehydrogen | alcohol dehydrogen | hypothetical prote |

ALIGNMENTS

light-harvesting protein alpha chain - Ectothiorhodospira halochloris
N,Alternate names: antenna pigment protein alpha chain
C;Species: Ectothiorhodospira halochloris
C;Date: 19-Mar-1997 *sequence_revision 19-Mar-1997 *text_change 21-Aug-1998
C;Accession: S23164
R;Magner-Huber, R.; Brunisholz, R.A.; Bissig, I.; Frank, G.; Suter, F.; Zuber, H.
Eur. J. Biochem. 205, 917-925, 1992
A;Title: The primary structure of the antenna polypeptides of Ectothiorhodospira halo A;Reference number: S23164; MUID:92249336
A;Accession: S23164
A;Molecule type: protein
A;Residues: 1-65 <WAG>
C;Superfamily: light-harvesting protein alpha chain
C;Keywords: antenna complex: bacteriochlorophyll; blocked amino end; light-harvesting
F;1/Modified site: N-formylmethionine *status experimental aphid transmission protein - cauliflower mosaic virus N;Alternate names: ORF II; ORF2 protein C;Species: cauliflower mosaic virus C;Species: cauliflower mosaic virus C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 23-Jul-1999 C;Accession: A90799; JA0010; A93799; A94613; JN0494; A04157 R;Franck, A.; Guilley, H.; Jonard, G.; Richards, K.; Hirth, L. Cell 21, 285-294, 1980 A;Title: Nucleotide sequence of cauliflower mosaic virus DNA. A;Accession: A90799; MUID:81001865 A:Molecule type: DNA
A:Residues: 1-159 <FRA>
A:Residues: 1-159 <FRA>
A:Cross-references: GB:V00141; GB:J02048; NID:g58821; PIDN:CAA23457.
A:Experimental source: strain Strasbourg
A:Modjtahedi, N.; Volovitch, M.; Mazzolini, L.; Yot, P.
FEBS Lett. 181, 223-228, 1985
FEBS Lett. 181, 223-228, 1986 FEBS Lett. A; Title: Co δÃ Matches Query Match Best Local 58 1 wkxxsyxg 8 Comparison of the predicted secondary structure of aphid transmission factor WKRTSYDG 65 Similarity Conservative 86.1%; 0; Score 31; DB pred. No. 2.9; 0; Mismatches DB 2.9; <u>ب</u> Length 65 Indels 0; <u>.</u>. Gaps PID:958823 0

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A; Reference numbe
A; Accession: JA00
A; Molecule type:
A; Residues: 1-159
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A,Title: The complete nucleotide sequence of cauliflower mosaic virus isolate A; Reference number: JN0493; MUID:93154593

A,Accession: JN0494

A;Molecule type: DNA

A;Residues: 1, R',3-117,'N',119-126,'D',128-137,'K',139-159 <CHE>
A;Cross-references: GB:M90542; NID:9678542; PIDN:AAA62372.1; PID:9293182

A;Experimental source: isolate BBC
C;Superfamily: cauliflower mosaic virus aphid transmission protein
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A;Accession: A94613
A;Molecule type: DNA
A;Residues: 1-50,'K',52-101,'P',103-126,'DE',129-159
A;Experimental source: strain D/H
A;Chenault, K.D.; Melcher, U.
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A; Introns: 73/3
C; Superfamily:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type; DNA
A;Molecule type; DNA
A;Residues: 1-246 <TIN>
A;Residues: 1-246 <TIN>
A;Cross-references: EMBL:AF036692; PIDN:AAB88326.1; GSPDB:GN00022; CESP:C44B12.3
A;Experimental source: strain Bristol N2; clone C44B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, December 1997 A; Description: The sequence of C. elegans cosmid C44B12 A; Reference number: Z21183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C44B12.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000 C;Accession: T32510 R;Tin-Wollam, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-88, 'N', 90-93,'R', 95-104,'V',106-117,'N',119-120,'N',123-126,'D',128-159
A; Experimental source: strain CM1841
R; Guilley, H.
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R;Gardner, R.C.; Howarth, A.J.; Hahn, P.; Brown-Luedi, M.; Shepherd, R.J.; Messing, J.
Nucleic Acids Res. 9, 2871-2888, 1981
A;Title: The complete nucleotide sequence of an infectious clone of cauliflower mosaic A;Reference number: A93729; MUID:82014878
A;Accession: A93729
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A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1180 <STO>
A; Cross-references: GB: AE005174; NID: g12517302; PIDN: AAG57931.1; GSPDB: GN00145; UWGP:
A; Cross-references: GB: AE005174; NID: g12517302; PIDN: AAG57931.1; GSPDB: GN00145; UWGP:
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A; Residues: 1-1180 <FNI>A; Residues: 1-1180 <FNI>A; C.A.; PIDN:CAA28250.1; PID
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E
R; Blattner, E.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
A; Accession: E65064
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: recB
C;Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                               R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: exodeoxyribonuclease V 135K chain C;Keywords: ATP; DNA repair; hydrolase; nucleotide F;23-30/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000365; GB:U00096; NID:g2367163; PIDN:AAC75859.1; PID:g17891 A;Experimental source: strain K-12, substrain MG1655 C;Comment: This enzyme is required for efficient DNA repair; it catalyzes the unwindill of these activities require concomitant hydrolysis of ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1180 <BLAT>
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A; Title: Complete nucleotide sequence of the Escherichia coli recB gene A; Reference number: A25532; MUID:87066729
A; Accession: A25532
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C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988
C:Accession: A25332: B65064
R:Finch, P.W.: Storey, A.: Chapman, K.E.: Brown, K.
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                                                                                                                                                                                                                                                                                                                                                    A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A; Reference number: A85480; MUID:21074935; PMID:11206551
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                        DB 2;
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| wkxxsyxg

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A:Status: proliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA A:Rosidues: 1-278 <KAM>
A:Rosidues: 1-278 <KAM>
A:Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29818.1; PID:d1030761; PID:g3257: A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank C:Genetics: C:Genetics: A:Gene: PH0727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein PH0727 - Pyrococcus horikoshii C;Specles: Pyrococcus horikoshii C;Specles: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999 C;Accession: H71119
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamo, M.; Ohiuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushid
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A;Rosidues: 1-1208 <HEI>
A;Cross-references: GB:AE004303; GB:AE003852; NID:g9656890; PIDN:AAF95464.1; GSPDB:GN001
acetylpolyamine aminohydrolase [validated] - Mycoplana ramosa C;Specics: Mycoplana ramosa C;Decics: Mycoplana ramosa C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_chancC;Accession: T48858
                                                                                                  RESULT
T48858
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A:Title: Complete sequence and gene organization of the genome of a A:Reference number: A71000; MUID:98344137
A:Accession: H71119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Heldelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mckalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
A;Accession: B82091
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C; Superfamily: exodeoxyribonuclease V 135K chain
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C;Accession: B82091
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                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
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99 WRVSSYMG
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                                                                                                                                                                                                                                                                                                 Conservative
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50.0%;
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Pred. No. 59;
1; Mismatches
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Pred. No. 1.5e+02
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endoplasmic reticulum insertion protein F13P17.9 - Arabidopsis thaliana N;Alternate names: hypothetical protein At234250 C:Species: Arabidopsis thaliana (mouse-ear cress) c:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001 C:Accession: T02313; C84754 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K submitted to the EMBL Data Library, July 1998 h;Description: Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
""" Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable beta-lactamase - Deinococcus radiodurans (strain C;Species: Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: aphA
C; Function:
A; Description: involved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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A;Title: Acetylpolyamine amidohydrolase from Mycoplana ramosa:
                                                              A; Accession: T02313
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A; Residues: 1-424 <WHI>
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A;Experimental source: ATCC 49678; strain FERM
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A; Molecule type: DNA
A; Residues: 1-475 <R
                                             A;Status: translated from
                                                                                  A; Reference number: 214657
                                                                                                                                                                                                                                                                                     T02313
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Best Local S
Matches 4
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1-475 <ROU>
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4; Conservative
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50.0%;
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50.0%;
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Pred. No.
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T.; Zalewski, C.;
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EMBL: AC004481; NID: g3337347; PIDN: AAC27401.1;

PID: 93337356

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A;Status: preliminary
A;Molecule type: DAA
A;Residues: 1-475 <STO>
A;Cross references: GB:A:
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ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial R.Zzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

R.Zzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: F86415
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
NA;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: C84754
A;Status: preliminary
A;Status: preliminary
     R; Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.;
                                                          hypothetical protein F9K20.24 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date + 00-Mar - 2001 #sequence_revision 02-Mar - 2001 #text_change 23-Mar - 2001 C;Accession: B96816
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C;Superfamily: yeast SSH1 protein
C;Keywords: endoplasmic reticulum; protein transport; transmembrane
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A; Map position: 2
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A; Cross-references: GB:AE002093;
C; Genetics:
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A; Residues: 1-475 <STO>
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                                                                                                                                                                                                                                                                                       WKESEYSG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yeast SSH1 protein
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:AE005172; NID:g9502410; PIDN:AAF88109.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                            77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28; DB 2;
Pred. No. 1e+02;
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Pred. No. 1e+02;
     C.J.; Federspiel, N.A.; Kaul, S.; White, Conway, A.B.; Conway, A.R.; Creasy, T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 475;
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                                   0.;
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        Dewar
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        Alonso,
war, K.;
C;Accession: $45345

R;Halford, S:, Wadey, R:, Roberts, C:; Daw, S:C.M.; Whiting, J:A
J:, Cross, I:, Burn, J:, Scambler, P.J.

Hum. Mol. Genet. 2, 2099-2107, 1993

A;Title: Isolation of a putative transcriptional regulator from A;Reference number: $45344; MUID:94154685

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                  RESULT
S45345
                                                                                                                                                                                                                         TUP1-like enhancer - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 26-May-2000
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166 WKSAEYLG 173

S.C.M.; Whiting, J.A.; O'Donnell,

the region of

1 wkxxsyxg

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C: Accession: B69415

R: Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
R: Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L.
Nature 390, 364-370, 1997

A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A; Reference number: A69250; MUID:98049343
A; Accession: B69415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group II decarboxylase homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
Rer, Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A; Reference number; A86141; MUID; 21016719
A; Accession: B96816
                                                                                                                                   A;Cross-references: GB:AE001012; GB:AE000782; NID:g2689335; PIDN:AAB89922.1; PID:g264 C;Superfamily: Escherichia coli glutamate decarboxylase
                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-488 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 1
C; Superfamily: yeast
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C; Genetics:
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A;Molecule type: DNA
A;Residues: 1-475 <STO>
                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation
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Query Match
Best Local Similarity
Matches 4; Conser
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Best Local
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  Conservative
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                             77.8%;
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Score 28; DB
Pred. No. 1e+0
0; Mismatches
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  0;
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Pred. No. 1e+02;
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                             DB 2;
1e+02;
     4
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                                                       Length 488
     Indels
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  0;
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probable serA protein - Mycobacterium tuberculosis (strain H37RV)

C; Species: Mycobacterium tuberculosis

C; Species: Mycobacterium tuberculosis

C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C; Accession: G70854

R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;

Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A; Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987

A; Accession: G70854
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A:Residues: 1-519 <HAL>
A;Residues: 1-519 <HAL>
A;Residues: 1-519 <HAL>
A;Cross-references: EMBL:X75295; NID:g434992; PIDN:CAA53043.1; PID:g434993
A;Cross-references: EMBL:X75295; NID:g434992; PIDN:CAA53043.1; PID:g434993
C:Superfamily: unassigned WD repeat proteins; WD repeat homology <WD1>
F;22-55/Domain: WD repeat homology <WD1>
F;126-159/Domain: WD repeat homology <WD2>
                                                                                                                                                                                                                                                                    phosphoglycerate dehydrogenase [imported] - Mycobacterium leprae C:Species: Mycobacterium leprae C:Species: Mycobacterium leprae C:pate: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000 C:Accession: 745418 R:Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, September 1997 A:Accession: 745418 A:Accession: 745418 A:Accession: 745418 A:Status: prelimnary: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Rcs1dues: 1-528 <COL>
A;Cross-references: GB:AL021287; GB:AL123456; NID:g3261508;
A;Experimental source: strain H37Rv
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C; Super!
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T45418
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C;Superfamily: Bacillus phosphoglycerate dehydrogenase
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A; Residues: 1-528 <PAR>
A; Cross-references: EMBL: Z99263; PIDN: CAB16440.1
A; Experimental source: cosmid B637
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Best Local S
Matches 4
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Matches 4
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  Similarity 50.0
4; Conservative
                                                                                                                    Bacillus
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                                                                                                                  phosphoglycerate dehydrogenase
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50.0%;
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Pred. No. 1.1e+02;
1; Mismatches
  Score 28; DB 2; Li
Pred. No. 1.1e+02;
1; Mismatches 3;
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Pred. No. 1.1e+02;
1; Mismatches 3
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probable D-3-phosphoglycerate dehydrogenase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000 C;Accession: T35831 R;Murphy, L; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajanc submitted to the EMBL Data Library, February 1999 A;Reference number: Z21589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein K04E7.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change C;Accession: T16557 R;Nhan, M.
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL035569;
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-529 <MUR>
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RESULT 19
$45344

$45344

TUPL like enhancer - human

C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 26-May-2000
C.Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 26-May-2000
C.Accession: $45344
R.Halford, S.; Wadey, R.; Roberts, C.; Daw, S.C.M.; Whiting, J.A.; O'Donnel:
R.Halford, S.; Wadey, R.; Roberts, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Description: The sequence
A:Reference number: Z18535
A:Accession: T16557
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U39666; NID:g1049408; PID:g1049411; PIDN:AAA80412.1; A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, October 1995 A; Description: The sequence of C. elegans cosmid
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A:Introns: 43/3; 81/3;
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A; Residues: 1-551 <NHA>
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C;Genetics:
A;Gene: HIRA
A;Gene: HIRA
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
F;66-99/Domain: WD repeat homology <WD1>
F;127-160/Domain: WD repeat homology <WD2>
F;170-203/Domain: WD repeat homology <WD3>
Search completed: January 14, 2002, 07:37:25 Job time: 895 sec
                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nuclear protein HIRA - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-May-2000
C;Accession: S68141
R;Scamps, C.; Lorain, S.; Lamour, V.; Lipinski, M.
Blochim. Blophys. Acta 1306, 5-8, 1996
A;Title: The HIR protein family: isolation and characterization of a complete murine cDN A;Reference number: S68141; MUID:96201697
A;Accession: S68141
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A;Title: Isolation of a putative transcriptional regulator from the region of 22q11 delg
A;Reference number: $45344; MUID:94154685
A;Accession: $45344
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1756 < HALL
A;Cross-references: EMBL:X75296; NID:9434982; PIDN:CAA53044.1; PID:9434983
A;Cross-references: EMBL:X75296; NID:9434982; PIDN:CAA53044.1; PID:9434983
A;Note: the authors did not translate the codon for residue 201
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
F;22-55/Domain: WD repeat homology <WD1>
F;33-116/Domain: WD repeat homology <WD3>
F;126-159/Domain: WD repeat homology <WD3>
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Pred. No. 1.6e+02;
1; Mismatches 3
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| 17340; AAF98151.1; 77340; AAG17984.1; 178001832; Claudin, 19R000729; PMP22_Claudin, PS01346; CLAUDIN; 1. oction; Transmembrane. 8 | ween the Swiss Instit European Bioinformat Buropean Bioinformat by non-profit ins lified and this statem lified are this statem statem and the lice | FROM N.A. Wan D.F., , Huang Y., an L.H.; an L.H.; d (AUG-1999 TION: COMPO ELLULAR LOC LARITY: BELLULAR | N. N. R-2 | STAN (Rel. 4 (Rel. 4 (Rel. 4 | |
| AF98151.1 3.G17984.1 3.G17924.1 3.G17922.1 2.G1aud 29; PMP22 2-C1aud 20; PMP22 102 102 137 183 183 183 184548 | entry is copyr iss Institute o oinformatics In ofit instituti is statement is es a license ag to license@is | Zhao X Qiu X lone w lone w lone t NENT O ATION: | Chord Prima Prima (aguch | ANDARD; 40, Crea 40, Last 40, Last | 749 1 450 1 140 1 140 1 391 1 411 1 420 1 420 1 446 1 456 1 475 1 |
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| OD CRC64; | duced through a collaboratio s and the EMBL outstation are no restrictions on it its content is in no was Usage by and for commerciate;//www.isb-sib.ch/announce | yg H.Q., Zhang P.P., L.P., Li H.N., Yu Y., biting cancer cell f databases.) STRANDS. ROTEIN. | Hominidae; Homo. ; ; ; ; ; ; ; ; ; ; | | p42228 mus musculu p52630 homo sapien Q02173 gallus gall p00107 pavlova lut Q9uxa sulfolobus Q57954 methanococc p48618 brassica na p76056 escherichia Q00749 streptococc p27933 oryza sativ p27932 oryza sativ p27932 oryza sativ p46310 arabidopsis Q53320 mycobacteri p48590 drosophila p45320 haemophilus p26153 gallus gall p06858 homo sapien |

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01-FEB-1994
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PROSITE; PS00968; ANTENNA_COMP_ALPHA; 1.

Antenna complex; Light-harvesting polypeptide; Transmembrane;

Magnesium; Bacteriochlorophyll; Inner membrane.

Magnesium; Bacteriochlorophyll; Orner membrane.

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           "The primary structure of the antenna polypeptides of Ectothiorhodospira halochloris and Ectothiorhodospira halochloris and Ectothiorhodospira halophila. Fou core-type antenna polypeptides in E. halochloris and E. halophila."; Eur. J. Biochem. 205:917-925(1992).

-I- FUNCTION: ANTENNA COMPLEXES ARE LIGHT-HARVESTING SYSTEMS, WHICH TRANSFER THE EXCITATION ENERGY TO THE REACTION CENTERS.

-I- SUBUNIT: THE CORE COMPLEX IS FORMED BY DIFFERENT ALPHA AND BETA CHAINS, BINDING BACTERIOCHLOROPHYLL MOLECULES, AND ARRANGED MOST PROBABLY IN TETRAMERIC STRUCTURES DISPOSED AROUND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Last annotation update)
LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (EHS-ALPHA-2)
(ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN).
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                                                                                                                                                                                                                                           SEQUENCE
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-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. INNER MEMBRANE.

PIR; $23164; $23164.

InterPro; IPR002361; Antenna_comp_alpha.

InterPro; IPR000066; LHC.
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P80103;
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                                                              STANDARD;
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Brunisholz R.A., Bissig I.,
      39, Created)39, Last sequence update)39, Last annotation updat
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28, Last sequence update)
28, Last annotation updat
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62.5%;
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                                                                                                                                                                           Score 31; DB Pred. No. 1.8; 0; Mismatches
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AXIAL LIGAND TO THE BAC
MAGNESIUM (POTENTIAL)
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Pred. No.
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ed. No. 3.5;
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P56745;
30-MAY-2000
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SEQUENCE
                                                                                                                                                      Rattus norvegicus (Rat).
Rattus norvegicus (Chordata;
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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TRANSMEM
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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Mammalia; Eutheria;
NCBI_TaxID=10116;
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30-MAY-2000
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-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                           STRAIN-SPRAGUE - DAWLEY;
                                                                                                                     SEQUENCE FROM N.A
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                                                                                                                                                                                                           CLAUDIN-1.
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Mammalia; Eutheria;
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InterPro; IPR000729; PMP22_Claudin.
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184
22881
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Rodentia;
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62.5%;
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Institute.
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POTENTIAL.
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Pred. No. 5.4;
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                                                                                                                                                         Sciurognathi; Muridae;
                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; | Sciurognathi; Muridae;
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on update)
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Q01087;
01-APR-1993 (Rel. 25, C
01-APR-1993 (Rel. 25, L
15-JUL-1999 (Rel. 38, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE:92391.094; Pubmed:1519358;
Q1u S.G., Schoelz J.E.;
Q1u S.G., Schoelz J.E.;
"Three regions of cauliflower mosaic virus strain W260 are involved in systemic infection of solanaceous hosts.";
Virology 190:773-782(1992).
-1- FUNCTION: THIS PROTEIN IS INVOLVED IN VIRUS TRANSMISSION.
-1- SIMILARITY: BELONGS TO THE CAULIMOVIRUSES ORF II FAMILY.
                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF195500; AAF04850.1; -. InterPro; IPR001832; Claudin. InterPro; IPR000729; PMP22_Claudin.
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NCBI_TaxID=31558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cauliflower mosaic virus (strain W260) (CaMV). Viruses; Retroid viruses; Caulimovirus.
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WKINSYFG
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RESULT

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ID VAT_CAMVC
AC PO3549;
AC PO3549;
DT 21-JUL-1988
DT 21-JUL-1989;
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GN II.
GN II.
GN Cauliflowe
OC Viruses; R.
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GA GATONER R.
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21-JUL-1986 (Rel. 0)
15-JUL-1999 (Rel. 3)
APHID TRANSMISSION (
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MEDLINE-82014878; PubMed-6269062;
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21-JUL-1986
15-JUL-1999
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P03550;
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Nucleic Acids Res. 9:2871-2888(1981).
-i- FUNCTION: THIS PROTEIN IS INVOLVED IN VIRUS TRANSMISSION.
-i- SIMILARITY: BELONGS TO THE CAULIMOVIRUSES ORF II FAMILY.
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDILINE-831064(8); PubMed=7152260;

Balazs E., Guilley H., Jonard G., Richards K.;

Balazs E., Guilley H., Jonard G., Richards K.;

"Nucleotide sequence of DNA from an altered-virulence isolate
the cauliflower mosaic virus.";
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                                                                                                                                                                                                                             Gene 19:239-249(1982).
-!- FUNCTION: THIS PROTEIN IS INVOLVED IN VIRUS TRANSMISSION
-!- SIMILARITY: BELONGS TO THE CAULIMOVIRUSES ORF II FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cauliflower mosaic virus
Viruses; Retroid viruses;
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MISSION PROTEIN (PROTEIN 2).
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SEQUENCE
                                               Cauliflower mosaic virus (strain NY8153) (CaMV) 
Viruses; Retroid viruses; Caulimovirus.
NCBI_TaxID=31557;
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01-APR-1993 (Rel. 25, Last seq
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APHID TRANSMISSION PROTEIN (PR
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MEDLINE-93154593; PubMed-8428667;
Chennault K.D., Melcher U.K.;
"The complete nucleotide sequence of cauliflower mosaic virus isolate
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01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
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APHID TRANSMISSION PROTEIN (PROTEIN 2).
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                                                                                                                                                                                                                                                                                                                                                                                                         Franck A., Guilley H., Jonard G., Richards K., Hirth L.; "Nucleotide sequence of cauliflower mosaic virus DNA."; Cell 21:285-294(1980).
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"Nucleotide sequence of cauliflower mosaic virus isolate NY8153.";
Plant Physiol. 100:542-545(1992).
-!- FUNCTION: THIS PROTEIN IS INVOLVED IN VIRUS TRANSMISSION.
-!- SIMILARITY: BELONGS TO THE CAULIMOVIRUSES ORF II FAMILY.
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30-MAY-2000
30-MAY-2000
30-MAY-2000
                                                                                                                                   EXSB_ECOLI STANDARD; PRT; 1180 AA P08394; 01-AUG-1988 (Rel. 08, Created) 01-AUG-1988 (Rel. 08, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update EXODEOXYRIBONUCLEASE V BETA CHAIN (EC 3.1.1 V 135 KDA POLYPEPTIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98311639; PubMed-9647647;
Furuse M., Fujita K., Hiiragi T., Fujimoto K., Tsukita S.;
"Claudin-1 and -2: novel integral membrane proteins localizing tight junctions with no sequence similarity to occludin.";
J. Ccll Biol. 141:1539-1550(1998).
I- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
I- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Tight jur
TRANSMEM
TRANSMEM
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                     SEQUENCE FROM N.A. MEDLINE-87066729; PubMed-3537960; Finch P.W., Storey A., Chapman K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00822; PMP22_Claudin; PRINTS; PR01077; CLAUDIN. PROSITE; PS01346; CLAUDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR001832; Claudin.
InterPro: IPR000729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLAUDIN-2
                                                                                                     Bacteria; Proteobacteria;
                                                                                                                 Escherichia col
                                                                                                                              RECB OR RORA OR B2820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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            Emmerson P.T.
                                                                           NCBI_TaxID-562;
                                                                                           Escherichia
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  "Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        junction; Transmembrane
                                                                                                                                                                                                                                                                                                                                        4; Conservative
nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                          230
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50.0%;
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Pred. No. 16;
1; Mismatches
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POTENTIAL.
38A7C074A1E0D5D2 CRC64;
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                                                                                                      subdivision;
                                                                                                                                                                                                                      1180 AA
Escherichia coli recB gene.";
                         Brown K., Hickson
                                                                                                                                                    update)
3.1.11.5) (EXODEOXYRIBONUCLEASE
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16;
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                                                                                                      Enterobacteriaceae;
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Matches 4; Conser
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STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                   NP_BIND
SEQUENCE
                                                                                                                                                       EcoGene; EG10824; recB.
InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease;
DNA repair; Complete proteome.
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Arnold D.A., Kowalczykowski S.C.;
"Facilitated loading of RecA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic [2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding protease III.";
Nucleic Acids Res. 14:7695-7703(1986).
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MEDLINE=87040734; PubMed=3534791;

Finch P.W., Wilson R.E., Brown K., Hickson I.D.,

"Complete nucleotide sequence of the Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RecBCD enzyme.";
J. Biol. Chem. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHOOLIGONUCLEOTIDES.
SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECISIMILARITY: BELONGS TO THE UVRD SUBFAMILY OF HELICASES
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1180 AA;
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                         50.0%;
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  Score 29; DB Pred. No. 76; 1; Mismatches
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                                             Length 1180;
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Q9Z1L1;

30-MAY-2000 (Rel. 3

30-MAY-2000 (Rel. 3

30-MAY-2000 (Rel. 3
                                                                                 CLD1_HUMAN STANDARD; PRT; 211 AA.
095832;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CLAUDIN-1 (SENESCENCE-ASSOCIATED EPITHELIAL MEMBRANE PROTEIN).
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SEQUENCE
                                                                                                                                                                                                                                                                                                   Tight ju
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keen T.J., Inglehearn C.F.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                               Homo sapiens (Human)
                                                                        CLDN1 OR CLD1 OR SEMP1.
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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  Swisshelm
       SEQUENCE FROM N.A. MEDLINE=99132301; PubMed=9931503;
                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1077; CLAUDIN. 1. PROSITE; PSO1346; CLAUDIN; 1.
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[1]
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191 AA;
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                                              Primates;
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Pred. No.
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83B445908DFFF41A CRC64;
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; Mismatches
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                                             Catarrhini;
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                                                       Craniata; Vertebrata; Euteleostomi;
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22;
 Robertson
                                              Hominidae;
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R.,
                                               Homo
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7_HUMAN
CLD7_HUMAN
095471;
30-MAY-2000
30-MAY-2000
30-MAY-2000
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CONFLICT
CONFLICT
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                                                       CLDN7
                                                                CLAUDIN-7.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            SEQUENCE
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Assignment(1) of claudin-1 (CLDN1) to human chromos with somatic cell hybrids"; Cytogenet. Cell Genet. 88:217-217(2000).
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRAN-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF101051; AAD16433.1; -. EMBL; AF115546; AAD22962.1; -. EMBL; AF134160; AAF61393.1; -.
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MEDLINE=20290992; PubMed=10828592;
Halford S., Spencer P., Greenwood J.,
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1077; CLAUDIN.
PROSITE; PSO1346; CLAUDIN; 1.
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MEM 82
MEM 116
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ced (DEC-1998) to the
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IPR000729; PMP22_Claudin.
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(Rel.
(Rel.
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                                                                                                                                                                                                       STANDARD;
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                                                                                                                     39, Created)
39, Last sequence update)
39, Last annotation update)
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102
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB.
Pred. No. 25;
1; Mismatches
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I -> V (IN )
V -> A (IN )
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                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> V (IN REF. 2).
-> A (IN REF. 2).
07269000E6C214F0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
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Query Match
Best Local Similarity
Tarches 4; Conserv
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TRANSMEM
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ011497; CAA09626.1; -.
Interpro; IPRO01832; Claudin.
Interpro; IPRO00729; pwP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                           Morita K., Furuse M., Fujimoto K., Tsukita S.; "Claudin multigene family encoding four-transmembrane components of tight junction strands."; Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).
-I- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
                                                                                                                                                                                                                                                                                                                                                                                                           Q9Z261;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF087825; AAD0 MGD; MGI:1859285; Cl Interpro; IPR001832;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-99110921; PubMed-9892664;
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                          CLDN7
                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000
20-AUG-2001
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                                                                                                                                                                                                                                                                                                NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                     CLAUDIN-7.
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SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                              SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMEM 82
SMEM 118
SMEM 161
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                           AF087825; AAD09760.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 39, 20) (Rel. 39, 20) (Rel. 39, 20)
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                                                                                                                                                                                                                                                                                                                                          (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                 Cldn7
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102
138
181
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  Claudin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.8%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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7F3CC1B963D912E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA
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25;
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RESULT 17
CLDX_BRARE
ID CLIDX_B
AC Q9YH92
DT 30-MAY
OC Cuthon
RA Keen T
RN [2]
RP SEQUEN
RA Chin A
RT "Heart
RT heart
RT heart
RT heart
RT Dev. B
CC -!- SI
CC -!- SI
CC -!- SI
CC -!- SI
CC This S
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Best Local
Query Match
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PROSTTE; PSO1346; CLAUDIN; 1.
Tight junction; Transmembrane.
TRANSMEM 8 29 PO;
TRANSMEM 82 102 PO;
TRANSMEM 120 140 PO;
TRANSMEM 161 181 PO;
SEQUENCE 211 AA; 22359 MW;
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G9YH92;

30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

CLAUDIN-LIKE PROTEIN ZF4A22 (CLAUSIN 7).

Brachydanio rerio (Zebrafish) (Zebra danio).

Brachydanio rerio, Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi

Cypriniformes; Cyprinidae; Rasborinae; Danio.

WCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                   TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20525589; PubMed=11071763; Chin A.J., Tsang M., Weinberg E.S.; Chin A.J., Tsang M., Weinberg E.S.; "Heart and gut chiralities are controlled independently from heart position in the developing zebrafish."; Dev. Biol. 227:403-421(2000).

-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                          PRINTS; PRO1077; CLAUDIN.
PROSITE; PSO1346; CLAUDIN; 1.
Tight junction; Transmembrane.
                                                                                                                                                                                                                                                                    InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
                                                                                                                                                                                                                                                                                                                                             EMBL; AJ011788; CAA09776.1; -. EMBL; AF260240; AAG24512.1; -.
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Pfam; PF00822; PMP22_Claudin; 1.
                                                                         SEQUENCE
                                                                                                 TRANSMEM
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163
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50.0%;
77.8%;
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Pred. No.
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  Score
                                                                      POTENTIAL.
POTENTIAL.
BC04870B75B8CB9D CRC64;
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4FE87F3A57AC9F29 CRC64;
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28;
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25;
  В
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Length 215;
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RESULT 19
SERA_MYCLE
ID SERA MY
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APHA_MYCRA
ID APHA_M
AC 048935
DT 15-JUL
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GN APHA 0
OS MYCOPL
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Matches 4; Conservative
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STRAN-ATCC 49678 / NCIB 9440 / FERM BP-1845;
MEDLINE-96422009; PubMed-8824626;
Sakurada K., Ohta T., Fujishiro K., Hasegawa M., Aisaka K.;
"Acetylpolyamine amidohydrolase from Mycoplana ramosa: gene cloning and characterization of the metal-substituted enzyme.";
J. Bacteriol. 178:5781-5786(1996).
  SERA_MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89087434; PubMed-3207420;
Fujishiro K., Ando M., Uwajima T.;
*Crystallization and some properties of acetylpolyamine
amidohydrolase from Mycoplana bullata.";
Biochem. Biophys. Res. Commun. 157:1169-1174(1988).
-i- FUNCTION: ACTS ON MANY TYPES OF ACETYLPOLYAMINES HAS HIGH AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01270; HDASUPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000286; His_deacetylse
Pfam; PF00850; Hist_deacetyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D10463; BAA01256.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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STRAIN-ATCC 49678
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last segu
15-JUL-1999 (Rel. 38, Last anno
ACETYLPOLYAMINE AMINOHYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplana ramosa (Mycoplana bullata).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Brucellaceae; Mycoplana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=40837;
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nes 4; Conserv
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COFACTOR: BINDS ONE ZINC ION PER MOLECULE.
SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
                                                                                                                                                                                                                                                                                                                                                                               Zinc.
341 /
                                                                                                                                                                                                                                              Conservative
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / NCIB 9440 / FERM BP-1845;
PubMed=3207420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36, Created)
36, Last sequence up
38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                             36332 MW;
                                                                                                                                                                                                                                                                  77.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%;
                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                         Score 28; DB Pred. No. 39; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                       950583DF79059F4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
528
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                                                                                                                                                                                                                                                                  DB 1;
39;
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                                                                                                                                                                                                                                                                                        Length 341;
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RESULT 20
SERA_MYCTU
ID SERA_M
AC 053243
DT 15-JUL
                                                                                                       DЪ
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Best Local
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ACT_SITE
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SEQUENCE
                SERA_MYCTU 053243;
15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                            Pfam; PF01842; ACT; 1.

PROSITE; PS00065; D_2_HYDROXYACID_DH_2; 1.

PROSITE; PS00670; D_2_HYDROXYACID_DH_3; 1.

PROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.

Serine biosynthesis; Oxidoreductase; NAD; CACT_SITE 232 232

ACT_SITE 261 BY SIMILARITY, ACT_SITE 279 279 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21128732; PubMed-11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                Pfam; PF00389; 2-Hacid_DH; 1. Pfam; PF01842; ACT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restiuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an extitution of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL583923; CAC
HSSP; P01542; 1CCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 299263; CAB16440.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      Leproma; ML1692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Squares S., S. Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.
SERA OR ML1692 OR MLCB637.25.
                                                                                                       129 WKRSSFSG
                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             033116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AL583923;
                                                                                                                                                            Similarity 50.4; Conservative
                                                                                                                                                                                                                                                                                                                                                                     IPR002912; ACT.
IPR002162; D_2_hydroxyacid_DH.
IPR000205; NAD_binding.
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261
279
528 7
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                               STANDARD;
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                                                                                                                                                                                                                                  54469 MW;
                                                                                                                                                                          77.8%;
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                                                                                                                                                                        Score 28; DB
Pred. No. 59;
                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                         luctase; NAD; Complete SUBSTRATE-BINDING (BY
                               PRT;
                                                                                                                                                                                                                                1A6DC60F9FB71222 CRC64;
                                                                                                                                                            Mismatches
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                              528
                                                                                                                                                                                      1;
                                                                                                                                                                                      Length 528;
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SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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Tuberculist; Rvzyyu.,

R InterPro; IPR002912; ACT.

R InterPro; IPR002162; D_2_hydroxyacid_DH.

R InterPro; IPR002165; NAD_binding.

Pfam; PF00389; 2-Hacid_DH; 1.

DR Pfam; PF01842; ACT; 1.

DR PROSTTE; PS00670; D_2_HYDROXYACID_DH_2; 1.

DR PROSTTE; PS00671; D_2_HYDROXYACID_DH_3; 1.

DR PROSTTE; PS00671; D_2_HYDROXYACID_DH_3; 1.

CR PROSTTE; PS00671; D_2_HYDROXYACID_DH_3; 1.

RW Scrinc blosynthesis; Oxidoreductase; NAD; Complete proteome.

KW Scrinc blosynthesis; Oxidoreductase; NAD; Complete proteome.

ACT_SITE 232 232 SUBSTRATE-BINDING (BY SIMILARITY).

ETT ACT_SITE 261 261 BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

PROSTER 279 BY SIMILARITY.
                                                                     Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

-I- CATALYTIC ACTIVITY: 3-PHOSPHOGLYCERATE + NAD(+) = 3-PHOSPHOHYDROXYPYRUVATE + NADH.

-I- PATHWAY: FIRST COMMITTED STEP IN THE "PHOSPHORYLATED" PATHW OF LASRING BIOSYNTHESIS.

-I- SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98295987; pubMed-9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Holroyd Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Ouall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-CDC 1551 / Oshkosh;
Flelschmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Flelschmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.;
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20-AUG-2001 (Rel. 40, Last annotation update)
D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PGDH).
SERA OR RV2996C OR MT3074 OR MTV012.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL021287; CAA16081.1; -. EMBL; AE007127; AAK47403.1; -. TIGR; MT3074; -.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; MCBI_TaxID-1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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1 wkxxsyxg 8
                                                                          Similarity
4; Conserv
                                                                          Conservative
                                                                                                          77.8%;
                                                                 Score 28; DB 1; Length 528; Pred. No. 59; 1; Mismatches 3; Indels
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Search completed: January 14, Job time: 503 sec 2002, 07:40:37

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Perfect score:
Sequence:
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Maximum DB
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pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length:
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1: sp_archea:*
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36
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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10.366 Million cell updates/sec
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O9et38 mus musculu
O9rph6 mycobacteri
O9nfp2 plasmodium
O83157 cauliflower
O83157 cauliflower
O83162 cauliflower
O83165 cauliflower
O83166 cauliflower
O94186 cauliflower
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|-------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|------|--------|------|------|--------------------|----------|------|------|------|--------------------|--------|--------|--------------------|-------------------|------|--------|--------|--------------------|--------|------|------|-------|------|---------|------|
| |) i |) ! | 27 | 27 | 27 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 29 | 29 | 29 | 29 | 29 | 29 | 29 | 29 |
| 70.0 | 7 | 75 0 | 75.0 | 75.0 | 75.0 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 80.6 | 80.6 | 80.6 | 80.6 | 80.6 | 80.6 | 80.6 | 80.6 |
| 14.7 | 1 1 0 | ا د د د | 121 | 117 | 109 | 4919 | 4152 | 1038 | 529 | 490 | 490 | 488 | 475 | 475 | 475 | 475 | 429 | 424 | 308 | 278 | 243 | 211 | 197 | 1208 | 635 | 174 | 149 | 149 | 134 | 125 | 102 |
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| K S N O D O | , | | 0 | | Q9PB67 | _ | | Q45780 | _ | _ | | | | | | | Q9RDP7 | Q9RSY4 | | 0 | | Q9BVN0 | Q9ЛНG0 | Q9KPP6 | Q9NKKO | _ | | | | O | |
| | Ognuba homo sapien | Q9c9g0 arabidopsis | Q9nub9 homo sapien | P89081 human adeno | Q9pb67 xylella las | | | | | | Q9nvc5 homo sapien | _ | 4 | | | Q9zv90 arabidopsis | 8 | | Q91r22 dianthoviru | 058458 pyrococcus | | | С | Q9kpp6 vibrio choi | | | U | numan | | Leishma | |

ALIGNMENTS

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Matches 5
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O9ET38;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence up
O1-JUN-2001 (TrEMBLrel. 17, Last annotation
CLAUDIN-19 (FRAGMENT).
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SEQUENCE
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Kiuchi Y., Morita K., Furuse M., Tsukita S.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ

EMBL; AF249889; AAF98323.1; -

InterPro; IPR001832; Claudin.

InterPro; IPR000729; PMP22_Claudin.

Pfam; PF00822; PMP22_Claudin 1.

PRINTS; PR01077; CLAUDIN.

PROSITE; PS01346; CLAUDIN; UNKNOWN_1.
                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
20
                1 wkxxsyxg 8
WKQSSYAG
                                        l Similarity
5; Conserv
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193 AA;
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27
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20299 MW;
                                                      88.9%;
62.5%;
                                          Score 32; DB
Pred. No. 11;
0; Mismatches
                                             0;
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mutagenesis.

Nucleic Acids Res. 2/:300,

R EMBL; AF157643; AAD46808.1; -.

R EMBL; AF157643; AAD46808.1; -.

R HSSP, P56355; 2PpN

HRSP, P56355; 2PpN

InterPro; IPR001993; Mitoch_carrier.

DR InterPro; IPR001912; UvrD-helicase.

DR Pfam: PF00880; UvrD-helicase.

DR Pfam: PF00800; UvrD-helicase; 1.

DR Pfam: PF0081TE; PS00215; MITOCH_CARRIER; UNKNOWN 1.

PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN 1.
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Q9RPH6
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                                                                                                                                                 parasite Plasmodium falciparum.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
-i- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES
EMBL; AJ276023; CAB76949.1; --
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0002290; Ser_thr_kin_actsite.
                                         Pfam; PF00069; pkinase; 1.

SMART; SM00220; S.TKC; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-property of the property of th
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
      SEQUENCE
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01-MAY-2000
01-MAY-2000
01-JUN-2001
                              NON_TER
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Mycobacterium smegmatis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Corvnebacterineae; Mycobacteriaceae; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Corynebacterineae; NCBI_TaxID=1772;
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    432 AA;
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(TrEMBLrel. 13,
(TrEMBLrel. 17,
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49698 MW;
                                         Serine/threonine-protein kinase;
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62.5%;
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Q83157;
Q83157;
Q1-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-NOV-1998 (TrEMBLrel. 08, L
APHID ACQUISITION FACTOR 5' E
Cauliflower mosaic virus.
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Q83162;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 01, Last annotation update)
                                                                                                        "Characterization of a virus-specific proteolytic activity processing the grecursor of the simian sarcoma-associated virus."; Virology 160:246-251(1987).
EMBL; M17415; AAA66604.1; -.
                                                                                                                                                          STRAIN-APHID NONTRANSMISSIBLE CAMPBELL ISOLATE; MEDLINE-87122167; PubMed-3027976; Moolston C.J., Czapłewski L.G., Markham P.G., G
                                                                                                                                                                                                                            HYPOTHETICAL PROTEIN (FRAGMENT).
Cauliflower mosaic virus.
Viruses; Retroid viruses; Caulimovirus
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                                                                             SEQUENCE
                                                                                       Hypothetical protein.
                                                                                                                                                     Davies J.W.;
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                                                                                                                                                                                                                     NCBI_TaxID=10641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for mechanisms of recombination."; Virology 177:717-726(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Recombination sites in cauliflower mosaic virus
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                      Conservative
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Modjtahedi N., Volovitch M., Mazzolini L., Yot P.;
Modjtahedi N., Volovitch M., Mazzolini L., Yot P.;
Molecular mechanisms regulating the synthesis of transferrin receptors and ferritin human erythroleukemic cell lines.";
FEBS Lett. 181:223-228(1985).
EMBL; M37582; AAA96696.1; -.
SEQUENCE 159 AA; 17941 MW; FF7D27C67CB38D41 CRC64;
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Cauliflower mosaic virus.
Viruses; Retroid viruses;
NCBI_TaxID~10641;
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Q83166 PRELIMINARY Q83166; 01-NOV-1996 (TremBLrel.
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; X79465; CAA55971.1;
ENCE 159 AA; 17759
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01-JUN-1998 (TrEMBLrel. 06
01-JUN-1998 (TrEMBLrel. 06
E 04412.3 PROTEIN.
N C44B12.3 PROTEIN.
S Caenorhabditis elegans.
PEukaryota; Metazoa; Nema'
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Best Local Similarity 62.:
Matches 5; Conservative
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'Caulliflower mosaic virus isolate CP
Plant Physiol. 101:1395-1396(1993).
EMBL; M90543; AAA21733.1; -.
SEQUENCE 159 AA; 17815 MW; 753AV
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Cauliflower mosaic virus.
Viruses; Retroid viruses; C:
NCBI_TaxID=10641;
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O9WI33;
O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
APHID TRANSMISSION HELPER FACTOR.
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Fang R., Wu X., Bu M., Tian Y., C
"Complete nucleotide sequence of
isolate) genomic DNA.";
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NCBI_TaxID=10641;
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           Nematoda;
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62.5%;
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           Chromadorea;
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STRAIN=BRISTOL N2; MEDLINE=94150718; PubMed=7906398;

SEQUENCE FROM N.A.

Rhabditidae; Peloderinae; NCBI_TaxID=6239;

Caenorhabditis.

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 6.9 KDA PROTEIN.
SC4A7.10.
MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D., Eichner A Kinashi H., Hopwood D.A.; Aset of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Memurray A., Morthnore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                    Cerdeno A.M., Parkhill J., E Submitted (DEC-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=A3(2);
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NCBI_TaxID=1902;
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STRAIN=BRISTOL N2;
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Q9RDI7;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
            Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                                  SCC57A.10C.
                                           HYPOTHETICAL
                                                                                                                                                                                                                                                 Hypothetical page 55
                                                                                                                                                                                                                                                                    "A set of ordered cosmids and a detailed genetic and the 8 mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL, AL136519; CAB66277.1; -.
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01-MAY-2000 (TrEMBLrel. 13, I
HYPOTHETICAL 7.0 KDA PROTEIN.
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EMBL; AL133423; CAB62714.1; -.
Hypothetical proteein.
SEQUENCE 65 AA; 6944 MW; F2
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Seeger K.J.,
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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            Firmicutes; Actinobacteria;
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SEQUENCE 94 AA;
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MEDLING-9700/351; PubMed-8843436;
MEDLING-9700/351; PubMed-8843436;
Kinashi H., Kieser H.M., Denapaite D., Eichner A.,
Kinashi H., Hopwood D.A.;
Rinashi H., Hopwood D.A.;
The set of ordered cosmids and a detailed genetic and
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL136519; CAB66278.1; -.
Hypothetical protein.
SEQUENCE 65 AA; 7127 MW; 4C9A4476C44B727A CRC64;
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Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
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Seeger K.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-PATIENT PA FROM FRANCE;
MEDLINE-98285741; PubMed-9621043;
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01-JUN-2001 (TrEMBLrcl. 17, Last annotation
ENVELOPE GLYCOPROTEIN (FRAGMENT).
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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NCBI_TaxID-11676;
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DT 01-NOV-1998 (TrEMBLrel. 08, Created)

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DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retrovirid

OX NCELTAXID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-PATIENT PA FROM FRANCE;

RX MEDLINE-98285741; PubMed-9621043;

RA SEQUENCE FROM N.A.

Sequetically related human immunodef

RT Genetically related human immunodef

RT adults of a family with no identifie

RT transmission.";

RL J. Virol. 72:831-5839(1998).

DR EMBL; U87183; AAC32943.1; -.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

KW ENYELOPE PYOTEEIN.

KW ENYELOPE PYOTEEIN.

SEQUENCE 94 AA; 10550 MW; B4BEII
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Safar M., Barre-Sinoussi F., Kazatchkine M.D.;
"Genetically related human immunodeficiency virus
adults of a family with no identified risk factor
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01-NOV-1998 (TrEMBLrel. 08, Create 01-NOV-1998 (TrEMBLrel. 08, Last 01-JUN-2001 (TrEMBLrel. 17, Last ENVELOPE GLYCOPROTEIN (FRAGMENT).
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Viruses; Retroid viruses; Retroviridae;
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MEDLINE-98285741; PubMed-9621043;
Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann Bafar M., Barre-Sinoussi F., Kezatchkine M.D.;
"Genetically related human immunodeficiency virus type 1 in three adults of a family with no identified risk factor for intrafamilia transmission.";
                                                                                                 J. Virol. 72:5831-5839(1998).

EMBL; U87184; AAC32944.1; -.

Interpro; IPR000777; GP120.

Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                         Viruses; Retroid
NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                091297
                                           SEQUENCE
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
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RESULT
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Best Local
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01-MAY-1999 (TrEMBLrel. 10, Create 01-MAY-1999 (TrEMBLrel. 10, Last: 01-JUN-2001 (TrEMBLrel. 17, Last: ENVELOPE GLYCOPROTEIN (FRAGMENT).
      transmission.";
J.\virol. 72:5831-5839(1998).
EMBL; U87186; AAC32946.1; -.
InterPro; IPR000777; GP120.
                                                     Belec L., Si Mohamed A., Mueller-Trutwin M.C., Gilquin J., Gutmann Safar M., Barre-Sinoussi F., Kazatchkine M.D.; Safar M., Barre-Sinoussi F., Kazatchkine W.D.; "Genetically related human immunodeficiency virus type 1 in three adults of a family with no identified risk factor for intrafamilial
                                                                                                    STRAIN=PATIENT PA FROM FRANCE;
MEDLINE=98285741; PubMed=9621043;
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=11676;
                                                                                                                                                                          Human immunodeficiency
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EMBL; U87182;
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STRAIN-PATIENT PA FROM FRANCE;
MEDLINE-98285741; PubMed-9621043;
Belec L., Si Mohamed A., Muller-Trutwin M.C.,
Safar M., Barre-Sinoussi F., Kazatchkine M.D.;
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IPR000777; GP120.
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es; Retroviridae;
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Best Local
Belec L.,
Safar M.,
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O91299; O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-UN-2001 (TrEMBLrel. 17, Last annotation update)
               SEQUENCE FROM N.A.
STRAIN-PATIENT PA FROM FRANCE;
MEDLINE=98285741; PubMed-9621043;
Belec L., Si Mohamed A., Muller-T
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091298;
01-NOV-1998
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J. virol. 72:5831-5839(1998).
EMBL; U87187; AAC32947.1; -.
InterPro; IPR000777; GP120.
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STRAIN=PATIENT PA FROM FRANCE;
MEDLINE=98285741; PubMed=9621043;
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Safar M., Barre-Sinoussi F., Kazatchkine M.D.
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Viruses; Retroid viruses; Retroviridae;
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01-JUN-2001
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(TrEMBLrel. 08, Last sequence update)
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50.0%;
Muller-Trutwin M.C., F., Kazatchkine M.D.
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Pred. No.
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Compugen Ltd
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5.725 Million cell updates/sec
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 3322 | 3333 | 332 | 32 | Score |
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| AAB54052 AAY36134 AAY36181 | AAM25829 AAM42193 AAE04228 | AAM40407 AAE04281 AAY12226 | AAY12227 AAE04286 | ID |
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ALIGNMENTS

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AAY12227;
                                                          Human 5' EST secreted protein SEQ ID NO: 540.
                                                                    18-JUN-1999
                                                                                AAY12227 standard; Protein;
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                                                                   (first entry)
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forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition. Human; secreted protein; EST; expressed sequence tag; diagnosis;

Homo sapiens

W09906554-A2

11-FEB-1999

31-JUL-1998; 98WO-IB01238

01-AUG-1997; 97US-0905134.

(GEST) GENSET.

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RESULT
AAE04286
ID AAE0
XX AAE0
XX AAE0
XX O9-A
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XX Huma
XX Huma
XX Huma
XX Foct
KW immu
KW infl
KW card
KW skin
KW gast
KW endc
KW edl
KW edl
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Best Local Similarity
"~+ches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY01602 and AAY11294 to AAY12260, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, respectively. The proteins of the protein activity, and thromone regulating activity, chemotactic/chemokinetic activity, haemastatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter
                                                                                                                                                                                                                                                 Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; skin disorder; angiogenic disorder; kidney disorder; cardiovascular disorder; angiogenic disorder; kidney disorder;
                  15-NOV-2000; 2000WO-US31162.
                                                          25-MAY-2001.
                                                                                               WO200136432-A2
                                                                                                                                                                                              endocrine disorder; infection; wound healing;
cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                            Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acids encoding human secreted proteins - obtained cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue
                                                                                                                                                                                                                                     gastrointestinal disorder; pregnancy-related disorder; gene
                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE04286 standard; peptide; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                   peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      skin disorders (e.g., poriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, properties can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the discolosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, asthma, and allergies (disease), cognitive disorders, schizophrenia, asthma, and developmental abnormalities (disease).
                                                                                                                                                                               Human polypeptide
                                                                                                                                                                                                                                                                               AAM40407;
                                                                                                                                                                                                                                                                                                                     AAM40407 standard; Protein;
                                                                                                                                                                                                                               22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or genetherapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AADO8488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
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30-JUN-2000;
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2000US-0215136
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Best Local :
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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-05598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-06539036.

19-CCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT,
Wang J,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotractic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-442253/47.
N-PSDB; AAI59563.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -       
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic diimmune system disorder; AIDS; autoimmune disease; rheumatoid art
                                                                                                                                                                                                                                                                                                                                                                                         C.N.S disorders.
Note: The sequence data
                                                                                                                                                AAE04281 standard;
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                         Human gene
                                                                                                                                                                                                                                                                            Local Similarity
nes 5; Conser
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Wang 2
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; SEQ ID NO 3552; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                   83
                                                           10 encoded secreted protein fragment, SEQ
                                                                                                                                                                                                                                                                               Conservative
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                                                                                      (first entry)
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodrich
                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                           88.9%;
                                                                                                                                                                                                                                                                                                                                                                                              for this patent did not form part of the printed
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Xu C, Xue AJ,
R, Drmanac RT;
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Pred. No. 12;
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Yang Y,
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                                                              ID NO:145
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pmatopoietic disorder; rheumatoid arthritis;

Best Local Similarity Matches 5; Conserv

Conservative

88.9%;

Score 32; DB Pred. No. 17; 0; Mismatches

Length 113; Indels

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CC AADD8488-AADD8529 represent cDNAs corresponding to 18 human secreted CC protein genes, and AAED419-AAED4239 represent the proteins they encode. CC AAED4240-AAED4297 represent human secreted protein fragments or variants. CC The secreted proteins and their genes are useful for preventing. CC treating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Pathological conditions can be diagnosed by determining the CC amount of the new genes. Specific uses are described for each of the CC and include developing products for the diagnosis or treatment of CC and include developing products for the diagnosis or treatment of CC and include developing products for the diagnosis or treatment of CC allers, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, CC parkinson's diseases (e.g., rheumatoid arthritis), inflammation, CC parkinson's diseases, cognitive disorders, schizophrenia, asthma, CC parkinson's diseases), cognitive disorders, schizophrenia, asthma, CC cardiovascular disorders, angiogenic disorders, kidney disorders, can also be used to aid wound disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and cinmunosorbent assay (ELISA). The present sequence represents a human cc secreted protein fragment referred to in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation; allergy; neurological disorder; Alzhelmer's dise
parkinson's disease; cognitive disorder; schizophrenia; asthma
skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
cardiovascular disorder; angiogenic disorder; kidney disorder;
gastrointestinal disorder; pregnancy-related disorder; gene the
endocrine disorder; infection; wound healing; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endocrine disorder; infection; wound hea cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 502; 509pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
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30-JUN-2000; 2000US-0215136.
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Sequence
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L-amino acids"
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                                                                                                                                                                                                                                                                                                                                                                                                 AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY01602 and AAY11294 to AAY12260, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell products. The proteins obtained may have cytokine activity by cell proliferation/differentiation activity, heemstopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activity. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into
                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-153784/13.
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                                                                                                                                                                                                                                                                                     114 AA
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Gaps

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CC AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; cantiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cc central nervous system; virucide; anti-HIV; fungicide; antimutagen; cc cardiovascular; antianemic; antiaggregant; haemostatic; vulnerary; cc cardiovascular; antianemic; antiaggregant; haemostatic; vulnerary; cc antidiabetic; cytostatic; neuroprotective; antidapressant; nootropic; cc antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; cc encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides concoding them can be used in gene therapy, antisense therapy and vaccine cc encoding them can be used in gene therapy.

CC anotiparkinsonian; and immunostimulant. The proteins and polynucleotides concoding them can be used in gene therapy.

CC anotiparkinsonian; and polynucleotides are useful for screening for caponists or antagonists of a protein and for the treatment and diagnosis confidency, cardiac with the activity of a protein e.g. inflammation, cc inflammation, caponists of an anabylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, thrombocytopaenia, wounds, burns, ulcers, cardiac anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
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AAM25829
ID AAM2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiavascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; inmunostimulant; gene therapy; antisense therapy; vaccine; inflammation; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
         osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-457603/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2001.
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elet disorders, thrombocytopaenia, wounds, severe combined immunodeficiency, eczema,
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                                                                                                                                                                                                                                                                                                                                                                                                                         1217pp;
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Matches 5
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
13-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; cNS; peripheral nervous system; cNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and neurological disorders.
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypoptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypoptide or polypucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang
Wang
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                                                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                          Novel nucleic acids and such as central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
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29-NOV-2000;
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DB; AAI61349.
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5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
Wang 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhou
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                                                                                                                                                                                                                                             SEQ ID NO 7124; 10078pp; English.
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2000US-0552317
2000US-0559802
2000US-0620312
2000US-0653450
2000US-0652191
2000US-0693036
2000US-0727344
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Wehrman T, Xu
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                                                                                                                                                                                                                                                                                          polypeptides, useful for treating disorders system injuries -
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Yang Y,
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Zhang v
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RESULT
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C.N.S d
                                                                                                                                                                                                                                                                                                                                                                                                      parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene the endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, drug screening, and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent \operatorname{did} not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; partitions disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
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                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                          binding
          Claim
                                  Isolated nucleic acid molecule e used in preventing, treating or
                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                       19-NOV-1999;
30-JUN-2000;
                                                                                                                                                                                           15-NOV-2000;
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                                                                   2001-343793/36
DB; AAD08518.
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          11;
                                 in preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene 10 encoded secreted protein HTPIH83,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           partner identification
          Page 459; 509pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
                                                                                                          Komatsoulis
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                                                                                                                                                       99US-0166415.
2000US-0215136.
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136
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62.5%;
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                                                                                                                                                                                                                                                                                            "Mature secreted
                                                                                                          GA,
                                                                                                                                                                                                                                                                                                                   signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32;
Pred. No.
                                                                                                          Baker
                                  encoding a human secreted protein r ameliorating a medical condition
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                                                                                                                                                                                                                                                                   by GNT"
                                                                                                          ΚP,
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19;
                                                                                                                                                                                                                                                                                            protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy;
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AADO8488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants miss

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RESULT
AAB54052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC allergies, hemotoping products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental CC abnormalities, haematopoietic disorders, foetal and developmental CC abnormalities, haematopoietic disorders, diseases of the immune system, CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC Parkinson's disease), cognitive disorders, schizophrenia, asthma, CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC cardiovascular disorders, angiogenic disorders, kidney disorders, CC cardiovascular disorders, pregnancy related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound CC healing and epithelial cell proliferation, to prevent skin ageing due to Sunburn, to maintain organs before transplantation, for supporting cell CC cognate ligands or binding partners, and in chemotaxis, and can be used cognate ligands or binding partners, and in chemotaxis, and can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
KHUMA-) HUMAN GENOME SCI INC
                                                                        12-MAR-1999;
                                                                                                                                                         08-MAR-2000; 2000WO-US05989
                                                                                                                                                                                                                                                                                                              WO200055320-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nootropic; immunomodulatory; relaxant; contraceptive; gynaecoantiinflammatory; cardiant; gene therapy; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pancreatic cancer antigen protein sequence SEQ ID NO:504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pulmonary; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
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linkage analysis; tissue identification; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB54052 standard;
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nes 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pancreas; pancreatic cancer; pancreatic cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the new protein in a sample or by determining the presence of in the new genes. Specific uses are described for each of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; identification; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
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                                                                            99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        system; muscular;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gynaecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        forensic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect treat or prevent approach affectors.
                                                                                                                                                                                                                                                                                                                          27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins can be used to treat or prevent neural,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
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N-PSDB; AAC98817.
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55 wktssyvg 62
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97US-0069957.
                              98US-0074121.
98US-0081563.
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Pred. No.
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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY36129-Y36222 represent novel human secreted proteins encoded by the extended cDNA sequences represented in AAX97813-X97906. The proteins of the invention have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Uses also include design of expression vectors and secretion vectors.
                                                                                                                                                             04-SEP-1998;
13-NOV-1997;
17-DEC-1997;
09-FEB-1998;
13-APR-1998;
10-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extended cDNAs encoding secreted proteins
                                                                                                                                                                                                                                                                                                                                                 Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic;
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                                                                                                                                                                                                                                                                                                                                       diagnostic; gene therapy; chromosome mapping; secretion vector
                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein #53
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                                                                                                                                                                                                                                                                    27-MAY-1999
AAY36129-Y36222 represent novel human secreted proteins encoded by the extended cDNA sequences represented in AAX97813-X97906. The proteins
                                  Claim 7; Page 289; 307pp; English.
                                                                                                                 Bougueleret L,
                                                        Extended cDNAs encoding secreted proteins
                                                                                N-PSDB;
                                                                                                                                        (GEST ) GENSET
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DB; AAX97818.
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DB; AAX97865.
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62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-SEP-1998;
09-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; PRO polypeptide; membrane bound protein; receptor;
transmembrane; secretion; immunoadhesion; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY99378;
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98US-010038B

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98US-0100627

98US-0100661

98US-0100662

98US-0100664

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                                                           Human; membrane associated organizational protein; HJNCT; cell proliferative disorder; cancer; autoimmune disorder; inflammatory disorder; neurological disorder; developmental disorder; vesicle trafficking; reproductive disorder; gastrointestinal disorder; renal disorder; therosoclerosis; leukaemia; rheumatoid arthritis; Alzheimer's disease; anxiety; diabetes: ovulatory Anfordational disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                    A human membrane associated organizational protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide o small molecule inhibitors of the relevant receptor/ligand interactions
                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Fig 78; 773pp; English.
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                                                   bowel
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98US-01088001.
98US-0108806.
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98US-0108807.
98US-0108848.
98US-0108853.
98US-0108853.
98US-0108853.
98US-0108853.
98US-0108853.
                                                   syndrome;
 Location/Qualifiers
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                                                   allergy.
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Pred. No.
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34;
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                                                                  renal failure;
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13-OCT-1998;
04-MAY-1999;
                                                                                             renal failure and irritable bowel syndrome. A vector expressing HJNCT, and an agonist of HJNCT can be used to treat or prevent a disorder associated with decreased expression or activity of HJNCT. An antagonist of HJNCT or a vector expressing the complement of a polynucleotide encoding HJNCT can be used to treat or prevent a disorder associated with increased expression or activity of HJNCT. Antibodies which bind HJNCT can be used for diagnosis of disorders associated with HJNCT expression or to monitor patients being treated with HJNCT, agonists, antagonists or inhibitors of HJNCT, Assays are preferably carried out on body fluids from a patient using radioimmunoassay, enzyme linked immunosorbent assays or fluorescent activated cell sorting assays. Polynucleotides encoding HJNCT are also used in hybridisation assays to determine absence, presence or excess expression of HJNCT and to monitor regulation of HJNCT levels during disease therapy.
                                                                                                                                                                                                                                                                                                        The present sequence represents a membrane associated organizational protein (HJNCT). HJNCT is used for the diagnosis, treatment and prevention of cell proliferative disorders including cancer and autoimmune/inflammatory, neurological, developmental, vesicle trafficking, reproductive, gastrointestinal and renal disorders. These disorders may include atherosalerosis, leukaemia, allergies, rheumatoid arthritis, alzheimer's disease, anxiety, diabetes, ovulatory defects,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human membrane associated organizational protein and nucleic acid sequences useful in the diagnosis, treatment and prevention of cell proliferative associated disorders e.g. cancer, rheumatoid arthritis and Alzheimer's disease -
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98US-0155251.
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187
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155
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62
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208
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224
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               88.9%;
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Pred. No.
   Mismatches
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RESULT 14
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21-JAN-2000;
25-APR-2000;
09-JUL-2000;
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03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c. N s discorders
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N-PSDB; AAI58013.
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                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-)
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29-NOV-2000;
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Sequence
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                                                     disorders.
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Wang Z,
                                          sequence
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; 2000US-0552317.
; 2000US-0598042.
; 2000US-0620312.
; 2000US-0653450.
; 2000US-0652191.
; 2000US-0693036.
; 2000US-0727344.
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קי
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Wehrman T, X
, Goodrich R,
                                          data
                                        for this patent did
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                                                                                                                                                                                                                                                                                                                                                                                           Chen R,
                                                                                                                                                                                                                                                                                                                                                                                Xu C,
                                                                                                                                                                                                                                                                                                                                                                  hen R, Ma
(u C, Xue
Drmanac R
                                                                                                                                                                                                                                                                                                                                                               Y,
aJ,
RT;
                                          not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                             Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                 for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                             Wang D;
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RESULT 15
AAU12417
AC AAU12417
AC AAU12417
AC AAU12417
AC AAU1241
AC AAU124
AC AAU1241
AC AAU1241
AC AAU124
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18-FEB-2000
22-FEB-2000
24-FEB-2000
01-MAR-2000
20-MAR-2000
21-MAR-2000
30-MAR-2000
30-MAR-2000
17-MAY-2000
17-MAY-2000
                                  Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
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01-DEC-1999;
02-DEC-1999;
                         lung, breast, prostate, cervical
                                                                                                                                      N-PSDB; AAS21489
                                                                                                                                                                                                                          Gerritsen ME,
                                                                                                                                                                                                                                                                                                                                            02-JUN-2000;
10-NOV-2000;
                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000;
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16-DEC-1999;
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02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cartilage; ear; proliferation; glucose;
adipocyte; A-peptide; factor VIIA; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breast; prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secretory and transmembrane; PRO; mammalian; cancer; lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU12417 standard; Protein; 230 AA
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                                                                                                                                                                                                                                                    Beresini M,
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2000WO-US07532.
2000WO-US08439.
2000WO-US13705.
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2000WO-US04341.
2000WO-US04342.
2000WO-US04414.
2000WO-US044914.
2000WO-US05004.
2000WO-US05601.
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2000WO-US14941.
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2000WO-US00376.
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                                                                                                                                                                                                                            Goddard
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99US-0170262
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99WO-US28634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cervical; tumour necrosis factor-alpha; TNF-alpha; rolliferation; glucose; free fatty acid; skeletal muscle; ide; factor VIIA; gene therapy.
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                                                                                                                                                                                                     Tumas D,
                                                                                                                                                                                                                          P
                                                                                                                                                                                              Deforge L, Desnoyers L, Filvaroff E,
A, Godowski PJ, Gurney AL, Sherwood S;
Funas D, Watanabe CK, Wood WI, Zhang Z
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                                                                                                                                                                                                                                             Gao W;
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Query Match
Best Local Similarity
Watches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
19-NOV-1999; 99US-0166415
30-JUN-2000; 2000US-0215136
                                                        15-NOV-2000; 2000WO-US31162
                                                                                                                                                                                              Protein
                                                                                                                                     WO200136432-A2
                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                    binding partner identification
                                                                                                                                                                                                                                                                                                                                                  endocrine disorder; infection; wound hea cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene 10 encoded secreted protein HTPIH83,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE04207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE04207 standard; Protein; 230 AA.
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                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                     Location/Qualifiers
1..24
                                                                                                                                                                                            /label= signal_peptide
25..230
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62.5%;
                                                                                                                                                                        "Mature secreted protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 230;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 439; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                           Human; PRO protein; mapping
                                                                                                Human PRO1356.
                                                                                                                                            AAB87565;
                                                                                                                                                                 AAB87565 standard; Protein;
                                                                                                                                                                                                                                                                                                                           Sequence
                               WO200116318-A2
                                                     Homo sapiens
                                                                                                                     15-MAY-2001 (first
                                                                                                                                                                                                                                                                              Local
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5; Conser
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Pred. No. 34;
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                                                                                                                                                                                                                                                                                         Length 230;
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Query Match
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RESULT 18
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18-FEB-2000;
18-FEB-2000;
22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and chromosome and gene mapping. 
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Grimaldi CJ,
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15-SEP-1999;
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N-PSDB; AAF92097.
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22-MAY-2000;
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                                                                                                             Human; secretory protein; membrane protein; vaccine; gene therapy;
rheumatoid arthritis; diabetes.
                                                                                                                                               Human membrane or secretory protein clone PSEC0059.
                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                     07-JUL-2000;
                                           10-JAN-2001
                                                                                         Homo
                                                                                                                                                                       23-MAY-2001
                                                                                                                                                                                              AAB88342;
                                                                                                                                                                                                                    AAB88342 standard; Protein;
                                                                  EP1067182-A2
                                                                                                                                                                                                                                                                             30 wktssyvg 37
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                                                                                         sapiens
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J, Gurney
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2000WO-US04341.
2000WO-US04342.
2000WO-US04414.
2000WO-US05601.
2000US-0187202.
2000US-019397.
2000US-019393.
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                       (first entry)
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                      2000EP-0114090
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99US-0169495.
99US-0170262.
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                                                                                                                                                                                                                                                                                                                                   88.9%;
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Watanabe
                                                                                                                                                                                                                                                                                                                          Score 32; DB; Pred. No. 34; 0; Mismatches
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Wood WI;
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08-JUL-1999;

99JP-0194179

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                                18-FEB-2000; 2000WO-US04342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diseases which may be treated include rheumatoid
23-JUN-1999;
                                                                   28-DEC-2000
                                                                                                     WO200078961-A1
                                                                                                                                       Unidentified
                                                                                                                                                                   Secreted; transmembrane; gene therapy.
                                                                                                                                                                                                         Protein of the invention #39.
                                                                                                                                                                                                                                           02-APR-2001
                                                                                                                                                                                                                                                                                                         AAB66127 standard; protein; 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0ta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding secretory proteins/membrane proteins, useful gene therapy or as candidate target molecules in drug development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-093989/11.
N-PSDB; AAF93769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JAN-2000;
02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                              30 wktssyvg 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to nucleic acid sequences AAF93744 - AAF93916
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2000JP-0183766.
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 99US-0141037.
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Pred. No.
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34;
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21-JAN-2000;
25-APR-2000;
09-JUL-2000;
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26-JUL-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
02-DEC-1999;
16-DEC-1999;
                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzhaimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents.
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Pan J,
                                                26-DEC-2000;
                                                                                                WO200153312-A1
                                                                                                                                                                                                                                                                                                             AAM40643 standard; Protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization
                                                                                                                        Homo sapiens
                                                                                                                                                          chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                             22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The nucleic acids may also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-071395/08
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06-JAN-2000;
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30 wktssyvg 37
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, Paoni NF, Roy J
abe CK, Williams
                                                                                                                                                                                                                                   polypeptide SEQ
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2000US-0488725.
2000US-0552317.
2000US-0598042.
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99WO-US30095.
2000WO-US00219.
2000WO-US00376.
                                                2000WO-US34263
                                                                                                                                                                                                                                                            (first entry)
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99US-0145698.
99WO-US20111.
99US-0162506.
99US-0162506.
99WO-US28313.
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62.5%;
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owski PJ, Grimaldi CJ,
MA, Smith V, Stewart TA
PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No.
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34;
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Search completed: January 14, 2002, 07:35:58 Job time: 809 sec
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                                                                                                                                                                                                                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) and ct the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful CC in gene therapy. A composition containing a polypeptide or polynuclectide CC of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system diseases, such as CC Alzhelmer's, parkinson's disease, Huntington's disease, amyotrophic CC alteral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activities such as: Immune system suppression, CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC c.N.S disorders.

CNote: The sequence data for this patent did not form part of the printed or specification.
                                                                                                                      Query Match
Best Local Similarity 52.-
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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N-PSDB; AAI59799.
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                                                                                  60 wktssyvg 67
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2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Yang Y,
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Zhang J;
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Perfect score:
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  No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
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36
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Copyright (c) 1993 - 2000 Com
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US-07-857-2248-93
US-09-222-817-12
US-09-222-817-12
US-09-222-817-14
US-09-222-816-14
US-09-222-86-14
US-09-222-786-14
US-08-369-796-10
US-08-852-754-10
US-08-956-852-10
US-08-956-859-10
US-08-956-859-10
US-08-956-859-10
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US-08-956-859-10
US-08-956-859-10
US-08-956-859-10
US-08-956-652-2
US-08-956-952-2
US-08-956-852-2
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US-07-857-224B-92
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   AUTHORS:
AUTHORS:
TITLE: A
                                AUTHORS:
                                                                                                             TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                            STATE:
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| | | | | | | | | 72.2 | | | | | | | | | | | | | | |
| 41 | 971 | 971 | 971 | 497 | 497 | 497 | 483 | 446 | 446 | 446 | 435 | 404 | 404 | 378 | 378 | 852 | 852 | 851 | 851 | 851 | 851 | 851 |
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| US-08-706-344C-23 | US-09-177-431-8 | US-09-270-984A-22 | US-08-724-354D-22 | US-08-471-961-5 | US-08-464-258B-5 | US-08-278-635B-5 | US-08-770-544-8 | PCT-US94-01321-10 | PCT-US92-10284-5 | US-08-244-205-5 | US-09-072-917A-9 | PCT-US92-10284-9 | US-08-244-205-9 | PCT-US92-10284-7 | US-08-244-205-7 | US-08-781-890-13 | US-08-276-099A-13 | PCT-US95-17025-2 | US-09-364-970-2 | US-09-087-465-4 | US-08-948-547-2 | US-09-012-710-2 |
| Sequence 23, Appl | Sequence 8, Appli | Sequence 22, Appl | Sequence 22, Appl | Sequence 5, Appli | Sequence 5, Appli | Sequence 5, Appli | Sequence 8, Appli | Sequence 10, Appl | Sequence 5, Appli | Sequence 5, Appli | Sequence 9, Appli | Sequence 9, Appli | Sequence 9, Appli | Sequence 7, Appli | Sequence 7, Appli | Sequence 13, Appl | Sequence 13, Appl | Sequence 2, Appli | Sequence 2, Appli | Sequence 4, Appli | Sequence 2, Appli | Sequence 2, Appli |

ALIGNMENTS

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Sequence 92, Application US/07857224B Patent No. 5958784
                                                                                                                                                                                                                                                                                                              TELEX: none INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                        MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Scizosaccharomyces pombe
FEATURE: Alcohol dehydrogenase, Table
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MACINTOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 633
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ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
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                Persson, M. Jeffery, J.
dehydrogenases
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                 Query Match
Best Local Similarity
Tatches 4; Conserv
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; DATE: 1981
US-07-857-224B-92
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US-07-857-224B-93
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Matches 4; Conservative
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                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Aspergillus
ORGANISM: Alcohol dehydrogenase, Table 3 Column 16
                                                                                                                                                                                                                                                     FEATURE: Alcohol dehydropublication information:
                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION: TELEPHONE: (International)
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APPLICATION NUMBER: US,
FILING DATE: 03/25/92
CLASSIFICATION: 436
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MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
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CORRESPONDENCE ADDRESS:
                                                                                                                                               TITLE: Alco
JOURNAL: Pr
VOLUME: 78
                                                                                                                      PAGES: 4226-4230
DATE: 1981
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CITY: Zurich
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VOLUME:
                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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1 wkxxsyxg 8
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                                Conservative
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50.0%;
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                            Score 27; DB:
Pred. No. 1.7e-
0; Mismatches
                               0;
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                       DB 2; L.
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RESULT 5
US-09-22-817-12
; Sequence 12, Application US/09222817
; Patent No. 6037154
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; SOFTMARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum US-09-222-786-2
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US-09-222-817-2
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LENGTH: 345
TYPE: PRT
GENERAL INFORMATION:
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APPLICANT: MIKIKO SUGA, MASAKAZU SUGIMOTO, TSUYOShi OSUMI, TSU'
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION
FILE REFERENCE: OP812
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Best Local Similarity
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Best Local Similarity
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TİTLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION
EILE REFERENCE: 08813
CURRENT APPLICATION NUMBER: US/09/222,817
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: UP 10-3751
EARLIER FILING DATE: 1998-01-12
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EARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.7e+02;
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Pred. No. 1.7e+02;
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US-09-22-786-12

; Sequence 12, Application US/09222786A
; Sequence 12, Application US/09222786A
; Patcnt NO. 6258573
; GENERAL INFORMATION:
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY
FILE REFERENCE: OP812
; CURRENT APPLICATION NUMBER: US/09/222,786A
; CURRENT FILING DATE: 1998-12-30
; EARLIER APPLICATION NUMBER: JP 10-3751
; EARLIER APPLICATION NUMBER: JP 10-353513
; EARLIER APPLICATION NUMBER: JP 10-353513
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CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER FILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: JP 10-353521
EARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
LENGTH: 530
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US-09-222-817-14
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EARLIER FILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: JP 10-353521
EARLIER FILING DATE: 1998-12-11
EARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 12
LENGTH: 530
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Best Local Similarity
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APPLICANT: MIKIKO SUGA, MASAKAZU SUGIMOTO, TSUYOShi OSUMI, TSUYOShi NAKAMATSU
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION
FILE REFERENCE: OP813
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Best Local Similarity 50.0%;
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CURRENT FILING DATE: 1998-12-30
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Pred. No. 2.5e+02;
1; Mismatches 3
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Pred. No. 2.5e+02;
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US-08-408-318-2
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SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 12
LENGTH: 530
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CURRENT APPLICATION NUMBER: US/09/222,786A
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-12-11
NUMBER OF SEO ID NOS: 14
NUMBER OF SEO ID NOS: 14
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Hoey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 530
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/408,318
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: flehr, Hohbach, To
STREET: 850 Hansen Way, #200
                                                                                                                                                                                                                                                                         APPLICANT: Hoey, Timothy
TITLE OF INVENTION: Human Signal Transducers and Binding
TITLE OF INVENTION: Assays
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 WKRSSFNG 139
                                                                                                                                                         STREET: 850 Hans
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 WKRSSFNG 139
                                                                                                                                ZIP: 94304
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                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 wkxxsyxg 8
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                                                                                                                                              USA
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50.0%;
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Pred. No. 2.5e+02;
1; Mismatches 3
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Pred. No. 2.5e+02;
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FILING DATE:

CLASSIFICATION:

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; MOLECULE TYPE: US-08-%69-796-10
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-494-8771
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: FÜNCTIONALLY ACTITLE OF INVENTION: TRANSDUCER AND NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              500 WQFSSYVG 507
                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                        NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watch 75.0%;
Local Similarity 50.0%;
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                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 wkxxsyxg 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07603
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DGY: linear
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Osman, WIMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 Hackensack Avenue
                                                                                                                   748 amino acids
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                                                                   protein
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FÜNCTIONALLY ACTIVE REGIONS OF SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A-60845
Score 27;
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Pred. No.
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Length 748;

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RESULT 12
US-08-852-091-10
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                                                                                                                              Patent No. 5883228 GENERAL INFORMATION:
                                                                                                                                                 Sequence 10, Application US/08852091 Patent No. 5883228
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                Matches
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Patent No. 5756700
GENERAL IMPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
APPLICANT: James E. Darnell, Jr.

APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: OSMAN, RICHARD A
REGISTARION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-44-8700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 23-APR-1
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                         500 WQFSSYVG 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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STATE: CA
                                                                                                                                                                                                                                                                                          1 wkxxsyxg
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amino acid
oGY: linear
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50.0%;
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                                                                                                                                                                                                                                                                                                                                             Score 27; DB 1;
Pred. No. 3.5e+02;
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                                                                                                                                                                                                                                                                                                                                                             Length 748;
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                                                                                                                                                                                                                                                                                                                            0;
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CORRESPONDENCE ADDRESS:

ADDRESSEE: STREET: 4

411 Hackensack Avenue

Klauber & Jackson

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-820-754-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEO ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Appli
Patent No. 5976835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5976835
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/852,091 FILING DATE: 05-MAY-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-116 TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                   STREET: 411 ...
STREET: 411 ...
CITY: Hackensack
STATE: New Jersey
IIGA
                                                                                                                                                                                                                                                                  TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: Klauber & Jackson Addresses: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
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STATE: New Jerse
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APPLICATION NUMBER: US/0 FILING DATE: 19-MAR-1997
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                   US/08/820,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 2;
Pred. No. 3.5e+02;
1; Mismatches 3
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RESULT 14
US-08-956-652-10
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Patent No. 6013475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0
"Catches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,652
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                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/854,296
                                                                                                                                                                                                                                              CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                 STREET: 411 Hackensack Avenue
                                                                      FILING DATE
                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                     CLASSIFICATION:
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50.0%;
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Pred. No. 3.
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3.5e+02;
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US-08-956-869-10
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Best Local
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                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                  APPLICATION NUMBER: US/08/956,869
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 25
                                                  PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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LENGTH: 748 amino acid
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NAME: Jackson Esq., David
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APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
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APPLICATION NUMBER:
FILING DATE: 19-MAR-
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TELEFAX: 133521
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APPLICATION NUMBER: US 0: FILING DATE: 19-MAR-1992 RIOR APPLICATION DATA:
                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
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                                   US 07/854,296
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Pred. No. 3.5e+02;
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US-08-948-547-10
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                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/948,547
FILING DATE:
FILING DATE:
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Best Local Similarity
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                                 APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
                                                                                                                                                                                              CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/212,185
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                             APPLICATION NUMBER: US/08
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acids
TYPE: amino acid
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ATTORNEY/AGENT INFORMATION:
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CITY: Hackensack
STATE: New Jersey
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TELEX: 133521
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Zhong, Zhong
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50.0%;
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US 08/126,588
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; Pred. No. 3.5e
1; Mismatches
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3.5e+02
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US-09-087-465-8
                                                                                                                                                                    PCT-US95-17025-10; Sequence 10, Application PC/TUS9517025; GENERAL INFORMATION:
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                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/087,465A
CURRENT FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 748
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Best Local Similarity 50.0
Matches 4; Conservative
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APPLICANT: Chen, Xiaomin
APPLICANT: Chen, Xiaomin
APPLICANT: Darnell Jr., James E
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS
TITLE OF INVENTION: USE
FILE REFERENCE: 500-1-229
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acid
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TYPOLOGY: line
YOLECHT
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ATTORNEY/AGENT INFORMATION:
                                                APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIP
NUMBER OF SEQUENCES: 39
                                 CORRESPONDENCE ADDRESS:
                                                                                                                                        APPLICANT:
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Local Similarity 50.0%;
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
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                  ADDRESSEE:
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E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                         James E. Darnell, Jr.
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Curt M. Horvath
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Pred. No. 3.
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Pred. No. 3.5e+02;
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3.5e+02;
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                                                                      TRANSCRIPTION (STAT) PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Applia Patent No. 5591825
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Best Local Similarity
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acids
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REGISTRATION NUMBER: 26.742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Floppy disk
COMPUTER: PA COMPATIBLE
COMPUTER: PA COMPATIBLE
COMPUTER: PA COMPATIBLE
COMPUTER: PA COMPATIBLE
COMPATIBLE
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION 165/08/276,099A
FILING DATE: 15-UUL-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: INTITLE OF INVENTION: BINUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD AFON
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59451-1/RAO
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: McKnight, Steven L
APPLICANT: Hou, Jinzhao
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STATE: California
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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1; Mismatches
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-276-099A-15
                                                                                                                                                                                               APPLICATION NUMBER: US/08/781,890
FILING DATE: 05-JAN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,099
FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59451-1/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELERX: 910 277299
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 749 amino acids
TVER: amino acids
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US-08-781-890-15
Query Match 75.0%;
Best Local Similarity 50.0%;
Matches 4; Conservative
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Best Local Similarity 50...
Thes 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MCKNIght, Steven L
APPLICANT: MCKNIght, Steven L
APPLICANT: HOU, Jinzhao
TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND
TITLE OF INVENTION: BINDING ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAFING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 749 amino acid
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                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
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Score 27; DB 1; Length 749
Pred. No. 3.5e+02;
1; Mismatches 3; Indels
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Search completed: January 14, 2002, 07:23:41 Job time: 72 sec

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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Compugen Ltd
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9.586 Million cell updates/sec
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| 50 | 49 | 48 | 47 | 46 | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ω 51 | 34 | ω ω | 32 | 31 | 30 |
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| 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 |
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| 488 | 475 | 475 | 475 | 455 | 424 | 396 | 386 | 381 | 381 | 381 | 379 | 379 | 378 | 378 | 378 | 376 | 376 | 375 | 375 | 375 |
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| в69415 | в96816 | F86415 | T02313 | C84133 | D75330 | S31959 | S31140 | T04164 | T03289 | JN0447 | S71244 | S51357 | F81097 | H64052 | A49662 | S51187 | JC4967 | A33909 | DEHUAB | I55359 |
| group | hypoti | hypoti | endop. | glutar | probal | acyl- | alcoho | forma | forma | alcohol | alcohol | alcohol | probable | alcohol | alcohol | alcohol | alcoho | alcoho | alcohol | alcoho |
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ALIGNMENTS

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R;Stover, C.K.; Pham, X.Q.; E. adman, S.; Yuan, Y.; Brody, L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequia, Reference number: A82950; M.A;Accession: F83354
                                                                     titin - rabbit (fragment)
c;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
C;Accession: S20901; I46520
R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.
EMBO J. 11, 1711-1716, 1992
A;Title: Towards a molecular understanding of titin
A;Reference number: S20897; MUID:92258380
A;Accession: S20901
A;Status: nucleic acid sequence not shown; translat
                                                                                                                                                                                                                                                                       RESULT
S20901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
F83354
                A; Molecule type: mRNA
A; Residues: 1-6805 <LAB>
A; Cross-references: EMBL: X64696
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A; Experimental source:
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A; Residues: 1-538 <STO>
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  A; Note:
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ce: strain PAO1
  sequence
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                                                                             not shown; translation
    Sew
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Pred. No.
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EMBL Data Library, February 1992
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S68061

T.; Holt, J.; Hsieh, C.L.; Francke, U.;

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A:Cross-references: EMBL:X83270; NID:g602579; PIDN:CAA58243.1; PID:g602580

A:Cross-references: EMBL:X83270; NID:g602579; PIDN:CAA58243.1; PID:g602580

A:Note: conformation and properties are reported for a synthetic peptide correspondin R; Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.

EMBO J. 11, 1711-1716, 1992

A;Title: Towards a molecular understanding of titin.

A;Reference number: $20897; MUID:92258380

A;Accession: $20898

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 13597-14200,'I',14202-14696 <LAB2>

A;Cross-references: EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193

A;Accession: $20899

A;Residues: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 16330-16382,'S',16384-16756,'F',16758-16860 <LAB3>

A;Cross-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191

A;Accession: $20899

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 'P',22278-22431,'R',22433-22448,'G',22450-22453,'Q',22455-22480,'TR',2248

A;Cross-references: EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195

A;Totle: Genomic organization of M line titin and its tissue-specific expression in talences: S63665

A;Accession: $63665

MUID:96177761

A;Accession: $63665
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A; Residues: 1-26926 < LABI>
A; Cross-references: EMBLX90568; NID:g1017424; PID:g1017425
R: Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A.
Blochemistry 34, 553-561, 1995
A; Title: Dissecting titin into its structural motifs: ident.
A; Reference number: 138345; MUID:95119041
A; Accession: 138345
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A;Title: A regular pattern of two types of 100-r A;Reference number: 146520; MUID:90238553
A;Accession: 146520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence not A;Molecule type: mRNA A;Residues: 1977-2014 <MUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Labeit, S.; Kolmerer, B. Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure A;Reference number: A57430; MUID:96026330
A;Accession: I38344
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Best Local Similarity
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C;Accession: I38344; I38345; S20898; S20897; S20899; S63665; S37393
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C; Species: H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 4235-5250 <LA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          serine/threonine-specific protein kinase (EC 2.7.1.-)
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7.3e+02;
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A; Map position: C; Function: A; Description: si C; Superfamily: t:
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C; Superfamily: light-harvesting protein alpha chain
C; Keywords: antenna complex; bacteriochlorophyll; blocked
n.1 Modified site: N-formylmethionine #status experimental
                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 205, 91/-923, 102. Eur. J. Biochem. 205, 91/-923, 102. A;Title: The primary structure of the antenna A;Title: The primary structure of the antenna A:Poference number: S23164; MUID:92249336
                                                                                                                                                                                                                                                                                                                                                                                                                            light-harvesting protein alpha chain - Ectothiorhodospira halochloris N;Alternate names: antenna pigment protein alpha chain C;Species: Ectothiorhodospira halochloris C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Au: C;Accession: S23164
                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 1-65 < WAG>
                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: S23164
                                                                                                                                                                                                                                                                                                                                                                             R:Wagner-Huber, R.; Brunisholz, R.A.; Bissig, Eur. J. Biochem. 205, 917-925, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;16780,16976,17579,17602,17667,17681,17845,17899,18121,18188,18209,18336,18670,18680,21900,21935,22295,22495,22627,22897,23024,23318,23883,24012,24177,24290,24447,24642,F;26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: structural protein forming filaments in striated muscle c;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; C;Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; gl structural protein structural protein kinase homology <KIN> F;24752-25008/Domain: protein kinase homology <KIN> F;84,177,905,2276,2378,2459,2481,2563,2669,2763,2896,3088,3179,3384,3432,3628,3772,40 98,11066,11488,11515,11635,11949,12170,12478,12526,12645,12875,13001,13036,13295,1354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:127867;
A;Map position: 2q31-2q32
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C; Genetics:
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A; Residues: 26831-26926 <GAU>
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R;Gautel, M.; Leonard, K.; Labeit,
EMBO J. 12, 3827-3834, 1993
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Pred. No. 2.8e
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WKRTSYDG

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C;Accession: A56152
R;dc Wergifosse, P.; Lintermans, P.; Limet, J.N.; Cloeckaert, A. J. Bacteriol. 177, 1911-1914, 1995
A;Title: Cloning and nucleotide sequence of the gene coding for A;Reference number: A56152; MUID:95204367
A;Accession: A56152
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A; Residues: 1-213 <DEA>
                                                                                                                                               acctylpolyamine aminohydrolase (validated) - Mycoplana ramosa C;Species: Mycoplana ramosa C;Species: Mycoplana ramosa C;Dato: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change C;Accession: T48858 R;Sakurada, K.; Ohata, T.; Fujishiro, K.; Hasegawa, M.; Aisaka, J. Bacteriol. 178, 5781-5786, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical 33K protein - pea enation mosaic virus C;Species: pea enation mosaic virus, PEMV C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 C;Accession: JQ1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:X79284; NID:g769744; PIDN:CAA55872.1; PID:g769745
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A;Status: prellminary; translated from A;Molecule type: DNA A;Residues: 1-341 <SAK> A;Cross-references: EMBL:D10463; PIDN:E A;Experimental source: ATCC 49678; stra
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T48858
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A;Experimental source: strain WSG
A;Note: this reading frame extends between two stop codons and does not A;Note: 65-Asp was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: genomic RNA
A; Residues: 1-303 <DEM>
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J. Gen. V1rol. 72, 1819-1834, 1991
A;Title: The nucleotide sequence and luteovirus-like nature
A;Reference number: JQ1382; MUID:91341468
A;Accession: JQ1386
                                                                                              A; Reference number: A; Accession: T48858
                                                                                                                                   A; Title: Acetylpolyamine amidohydrolase
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Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 08-Oct-1999
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Best Local Similarity
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ce: ATCC 49678; strain FERM
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A; Note: aphA
C; Function:
A; Description:
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conserved hypothetical protein b1345 - Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 29-Sep-1999
C;Accession: D64884
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; F.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA A;Rosidues: 1-411 <BLAT> A;Residues: 1-411 <BLAT> A;Cross-references: GB.AE000232; GB:U00096; NID:91787600; PIDN:AAC74427.1; A;Experimental source: strain K-12, substrain MG1655 C;Superfamily: hypothetical protein b1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617
A;Accession: D64884
                                                                                                                                                                                                                                            R;Perna, A..... Grotbeck, E.J.; Davis, N.M., Z..... Riller, L.; Grotbeck, E.J.; Davis, N.M., Z..... Rature 409, 529-533, 2001

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7

A;Title: Genome sequence of MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                             probable integrase for prophage CP-933R intR [imported] - Escherichia coli (strain C;Species: Escherichia coli
C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
                                                                                          A; Gene: intR
C; Superfamily:
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R; Perna, N.T.; Plun
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                                                                                                                                                  A;Cross-references: GB:AE005174; NID:g12515407; PIDN:AAG56452.1; GSPDB:GN00145; UWGP:A;Experimental source: strain 0157:H7, substrain EDL933
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A; Residues: 1-411 <STO>
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                                                                                                                                                                                                                                                                                                                         Plunkett III, G.; Burland, V.; Mau, B.; Glasner, tbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
                                                                                            hypothetical protein b1579
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A;Molecule type: DNA
A;Residues: 75-442 <KWO>
A;Cross-references: EMBL:X07734; NID:g48069;
A;Note: part of this sequence, including the
                                                                                                                R;Kwon, S.T.; Terada, I.; Matsuzawa, H.; Ohta, T. Eur. J. Biochem. 173, 491-497, 1988
A;Title: Nucleotide sequence of the gene for aqualysin I (a A;Reference number: S00620; MUID:88225062
A;Accession: S00620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A;Reference number: A72200; MUID:99287316
A;Accession: D72387
A;Accession: D72387
A;Molecule type: DNA
A;Residues: 1-264,'G',266-441 <ARN>
A;Cross-references: GB:AE001716; GB:AE000512; NID:g4980853; PIDN:AAD35451.1; PID:g498086
A;Experimental source: strain MSB8
C;Gene: TM0364
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                            A;Cross-references: GB:J90108; GB:D90108; GB:J05414; NID:g217171; PIDN:BAA14135.1; A;Note: the authors translated the codon CTG for residue 470 as Val, and GGT for reR;Kwon, S.T.; Terada, I.; Matsuzawa, H.; Ohta, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C;Accession: A35742; S00620; S00324 R;Terada, I.; Kwon, S.T.; Miyata, Y.; Matsuzawa, H.; Ohta, T. J. Biol. Chem. 265, 6576-6581, 1990
                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-513 <TER>
                                                                                                                                                                                                                                                                                                                                                           A;Title: Unique precursor structure of an A;Reference number: A35742; MUID:90216674 A;Accession: A35742
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Best Local Similarity
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A;Residues: 'A',2-23 <LIE>
R;Nelson, K.E.; Clayton, R.A.;
Garrett, M.M.; Stewart, A.M.; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Purification and characterization of a novel thermostable 4-alpha-glucanotrans A;Reference number: S23198; MUID:92331687 A;Accession: S23198
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Syst. Appl. Microbiol. 17, 297-305, 1994
A;Title: Expression in Escherichia coli and structure of the
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A; Residues: 1-441 <HEI>
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62.5%;
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  PIDN:CAA30559.1; amino and carbox;
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  carboxyl
                                                                                                                                                                thermophilic alkaline
                            PID:g602091
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hypothetical protein 2 - Haemophilus ducreyi
(;Species: Haemophilus ducreyi
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T31105
R;Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A;Reference number: 220984; MUID:99030326
A;Accession: T31105
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A; Residues: 128-170 < MATIS>
A; Residues: 128-170 < MATIS>
C; Superfamily: subtilisin; subtilisin homology
C; Superfamily: subtilisin; subtilisin; hydrolase: serine proteinase
F;1-14/Domain: signal sequence #status predicted <SIG>
F;15-127/Domain: propeptide #status predicted <PRO>
F;128-408/Product: aqualysin I #status experimental <MAT>
F;15-257/Domain: subtilisin homology <SBT>
F;25-257,281-283/Region: S1 specificity crevice #status predicted
F;409-513/Domain: carboxyl-terminal propeptide #status predicted
F;409-513/Domain: carboxyl-terminal propeptide #status predicted
C; Genetics:
                                                      A; Molecule type: DNA
A; Residues: 1-4919 <
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. Bacteriol. 180, 6013-6022, 1998
A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A;Reference number: 220984; MUID:99030326
A;Accession: T31102
                    A;Cross-references: EMBL:AF057696; NID:g3929021; PID:g3929023; PIDN:AAC79761.1
                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Haemophilus ducreyi
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
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A; Residues: 1-4152 <WAR>
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A; Rolecule type: DNA
A; Rolecule type: DNA
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A; Rolecule type: CFRA>
A; Rosidues: 1-159 <FRA>
A; Rosidues: CB: V000141; GB: J02048; NID: g58821; PIDN: CAA23457.1; PID: g58823
A; Experimental source: strain Strasbourg
A; Experimental source: strain Strasbourg
A; Experimental source: strain Strasbourg
A; Experimental source: strain Strasbourg
A; Experimental source: strain Strasbourg
A; FEBS Lett. 181, 223-228, 1985
A: Mills: Comparison of the predicted secondary structure of aphid transmission factors.
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A.Authors; Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu chudo, M.A.; Madeira, A.M.B.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, F.A.; Authors; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.F., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Silva, A.G.; Sawasak A.; Authors; da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.F.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A.Reference number: A59328
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                                                                                                                                                                                                                                                        C;Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 23-Jul-1999 C;Accession: A90799; JA0010; A93729; A94613; JN0494; A04157 R;Franck, A.; Guilley, H.; Jonard, G.; Richards, K.; Hirth, L. Cell 21, 285-294, 1980 A;Title: Nucleotide sequence of cauliflower mosaic virus DNA. A;Reference number: A90799; MUID:81001865 A;Accession: A90799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aphid transmission protein - cauliflower mosaic virus N; Alternate names: ORF II; ORF2 protein C:Species: cauliflower mosaic virus
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A;Cross-references: GB:AE004040; GB:AE003849; NID:g9107437; PIDN:AAF85076.1; GSPDB:GN001A;Experimental source: strain 985c
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Pred. No.
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9e+02;
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WKQKSYDG

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A; Reference number: A
A; Accession: JA0010
A; Molecule type: DNA
A; Residues: 1-159 < M
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A: Rolecule type: DNA
A: Residues: 1-88,'N',90-93,'R',95-104,'V',106-117,'N',119-120,'N',123-126,'D',128-159
A: Residues: 1-88,'N',90-93,'R',95-104,'V',106-117,'N',119-120,'N',123-126,'D',128-159
A: Reference number: A94613
A: Reference number: A94613
A: Recession: A94613
A: Rocession: A94613
A: Residues: 1-50,'K',52-101,'p',103-126,'DE',129-159 <GUI>
A: Residues: 1-50,'K',52-101,'p',103-126,'DE',129-159 <GUI>
A: Resperimental source: strain D/H
R: Chenault, K.D.; Melcher, U.
Gene 123, 255-257, 1993
A: Title: The complete nucleotide sequence of cauliflower mosaic virus isolate BBC.
A: Reference number: JN0493; MUID: 93154593
A: Alocession: JN0493; MUID: 93154593
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R; Gardner, R.C.; Howarth, A.J.; Hahn, P.; Brown-
Nucleic Acids Res. 9, 2871-2888, 1981
A; Title: The complete nucleotide sequence of an A; Reference number: A93729; MUID:82014878
A; Accession: A93729
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: T32510
                                                                                                                                                                                                                                                                                                                           A;Map position: 4
A;Introns: 73/3; 112/3; 137/1; 202/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C44B12.3
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A;Experimental source: strain Bristol N2; clone C44B12
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A; Residues: 1-246 <TIN>
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C. Accession: M64066

R. Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fubrmann, J.L.; Geoghagen, N.S.M.

A. Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A.; Reference number: A64000; MUID:95350630

A.; Recession: A64066

A.; Status: nucleic acid sequence not shown; translation not shown

A.; Molecule type: DNA

A.; Residues: 1-261 <TIGR>
A.; Cross-references: GB:U32724; GB:L42023; NID:g1573378; PIDN:AAC22066.1; PID:g1573380; T.; Superfamily: conserved hypothetical protein HI0360

C.; Keywords: transmembrane #status predicted <TM1>
F.; 38-54/Domain: transmembrane #status predicted <TM3>
F.88-104/Domain: transmembrane #status predicted <TM3>
F.88-104/Domain: transmembrane #status predicted <TM5>
F.168-184/Domain: transmembrane #status predicted <TM6>
F.168-202/Domain: transmembrane #status predicted <TM6>
F.168-204/Domain: transmembrane #status predicted <TM9>
F.168-204/Domain: transmembrane #status predicted <TM9>
F.240-256/Domain: transmembrane #status predicted <TM9>
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A;Residues: 1-260 <HEI>
A;Cross-references: GB:AE004282; GB:AE003852; NID:g9656626; PIDN:AAF95229.1;
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C;Genetics:
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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
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A; Map position: 1
C; Superfamily: con
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Nature 406, 477-483, 2000
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28
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A; Residues: 1-288 <WHI>
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                                                                                                                                                                                                                                                                                                                 A;Title: Genome sequence of A;Reference number: A75250; A;Accession: D75286
                                                                                                                                                                                                                                                                                                                                                                         R;White, O.; Eisen, J.A.; Heldelberg, J.F.; Hickey, I.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
C;Accession: D75286
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A;Residues: 1-262 <570>
A;Cross-references: GB:AE004962; GB:AE004091; NID:g9951826; PIDN:AAG08886.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an A;Reference number: A82950; MUID:20437337 A;Accession: F82959 A;Status: preliminary
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CCC -1-SUCH RESULT 1 CLDX_B AC 09YH92 DT 30-MAY DT 30-MA EMBL; AJ011788; CAA09776.1; ... EMBL; AF260240; AAG24512.1; ... InterPro; IPR001832; Claudin. InterPro; IPR000729; PMP22_Claudin. Pfam; PF00822; PMP22_Claudin; 1. PRINTS; PR01077; CLAUDIN. PROSITE; PS01346; CLAUDIN; 1. Tight junction; Transmembrane. 30 MAY-2000 (Rel. 39, Created) 30 MAY-2000 (Rel. 39, Last sequence update) 20-NUG-2001 (Rel. 40, Last annotation update) 20-NUG-2001 (Rel. 40, Last annotation update) CLAUDIN-LIKE PROTEIN ZF4A22 (CLAUSIN 7). Brachydanio rerio (Zebrafish) (Zebra danio). Brachydanio rerio (Zebrafish) (Zebra danio). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi. Cypriniformes; Cyprinidae; Rasborinae; Danio. MEDITIE=20525589; PubMed=11071763; Chin A.J., Tsang M., Weinberg E.S.; Chin A.J., Tsang M., Weinberg E.S.; Tsang M., Weinberg E.S.; Tsang M., Weinberg E.S.; Tsang M., Weinberg E.S.; Tsang M., Weinberg E.S.; Tsang M., Weinberg E.S.; Tsang M., Weinberg E.S.; Tsang M., Weinberg E.S.; Tsang M., Weinberg M., Weinberg E.S.; Tsang M., Weinberg E.S.; Tsang M., Weinberg E.S.; Weinberg M., Weinberg M., Weinberg M., Weinberg M., Weinberg M., Weinberg E.S.; Weinberg M., Weinberg M CLDX_BRARE Q9YH92; This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch). SEQUENCE FROM N.A. Keen T.J., Inglehearn C. Submitted (OCT-1998) to SEQUENCE FROM N.A. STANDARD; C.F.; to the EMBL/GenBank/DDBJ databases. PRT; 215 (See http://www.isb-sib.ch/announce/ A A a collaboration -

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MEDLINE-97217733; PubMed-9063744;

Roberts C., Daw S.C., Halford S., Scambler P.J.;

"Cloning and developmental expression analysis of chick Hira (Chira),
a candidate gene for DiGeorge syndrome.";

a candidate gene for DiGeorge syndrome.";

Hum. Mol. Genet. 6:237-245(1997).

-!- FUNCTION: COULD PLAY A PART IN MECHANISMS OF TRANSCRIPTIONAL
REGULATION SIMILAR TO THAT PLAYED BY YEAST HIR1 AND HIR2 TOGETHER

-!- SUBCELDULAR LOCATION: NUCLEAR (POTENTIAL).

-!- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).

-!- SIMILARITY: BELONGS TO THE HIR1 FAMILY OF WD-REPEAT PROTEINS.
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PROSITE; PS50082;
PROSITE; PS50294;
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15-JUL-1998 (Rel. 36, Last sequence
15-JUL-1999 (Rel. 38, Last annotatic
HIRA PROTEIN (TUP1 LIKE ENHANCER OF
HIRA OR TUPLE1
                                                                                                                           DOMAIN
                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                       Transcription
                                                                                                                                                                                                                                                                                                                                      EMBL; X99375; CAA67754.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIRA_CHICK P79987;
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                   1 wkxxayxg
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WKRAAYIG 104
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                                                                                                                                                                                                                                                             WD_REPEATS_1; 1. WD_REPEATS_2; 3.
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36, Last sequence update)
38, Last annotation updat
                                                                                                                                     158
202
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286
651
413
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                                                           86.1%;
62.5%;
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62.5%;
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Pred. No. 19;
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Pred. No. 4.3;
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SPLIT PROTEIN 1) (CHIRA).
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Best Local
                     LHA2_ECTHL STANDARD; PRT; 65 AA.

B80103; B80103; Created)
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (EHS-ALPHA-2)
(ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN).

Ectothhorhodospira halochloris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLD2_HUMAN
P57739;
20-AUG-2001
20-AUG-2001
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF250558; AAF98151.1; -. EMBL; AF177340; AAG17984.1; -. InterPro; IPR001832; Claudin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yu J.,
"Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Gu J.R., Wan D.F., Zhao X.T.,
Qin W.X., Huang Y., Qiu X.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reinecker H.-C., Saka
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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PF00822; PMP22_Claudin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             junction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human cDNA clone with function of inhibiting cancer cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                        4,
  Proteobacteria;
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(Rel. 40,
(Rel. 40,
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102
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Last sequence update)
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gamma subdivision; Ectothiorhodospiraceae;
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Pred. No. 13;
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Qian L.F., He L.P., Li H.N., Yu Y.,
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Q45335;
                                                                                                                                                                                                                                                                                                                                                                     LT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The primary structure of the antenna polypeptides of Ectothiorhodospira halochloris and Ectothiorhodospira halochloris and Ectothiorhodospira halophila. Four core-type antenna polypeptides in E. halochloris and E. halophila."; Eur. J. Blochem. 205:917-925(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wagner-Huber R., Brunisholz R.A., Bissig I., Frank Zuber H.;
                                                                          Cloeckaert A., Verger J.M., Grayon M., Zygmunt M.S., Grepinet O.;
"Nucleotide sequence and expression of the gene encoding the major
25-kilodalton outer membrane protein of Brucella ovis: Evidence for
untigenic shift, compared with other Brucella species, due to a
deletion in the gene.";
Infect. Immun. 64:2047-2055(1996).
                                                                                                                                                                                                                             Brucella ovis,
Bacteria; Proteobacteria;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00968; ANTENNA_COMP_ALPHA; 1.
Antenna complex; Light-harvesting polypeptide; Transmembrane;
Magnesium; Bacteriochlorophyll; Inner membrane.
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InterPro; IPR002361; Antenna_comp_alpha.
InterPro; IPR000066; LHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE:92249336; PubMed=1577009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DSM 1059;
                                                                                                                                                                                                                                                                                                15-DEC-1998
15-DEC-1998
15-DEC-1998
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                                     -I- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-I- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY. HAS A C-TERMINAL DELETION COMPARED TO THAT OF OTHER BRUCELLA SPECIES.
                                                                                                                                                          MEDLINE-96239016; PubMed-8675306;
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        OMP25
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           This SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: ANTENNA COMPLEXES ARE LIGHT-HARVESTING SYSTEMS, WHICH TRANSFER THE EXCITATION ENERGY TO THE REACTION CENTERS.
SUBUNIT: THE CORE COMPLEX IS FORMED BY DIFFERENT ALPHA AND BETA CHAINS, BINDING BACTERICCHLOROPHYLL MOLECULES, AND ARRANGED MOST PROBABLY IN TETRAMERIC STRUCTURES DISPOSED AROUND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REACTION CENTER. THE NON-PIGMENTED GAMMA CHAINS MAY CONSTITUTE ADDITIONAL COMPONENTS.
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AXIAL LIGAND TO THE BACTERIOCHLOROPHYLL MAGNESTUM (POTENTIAL).

55A4C306748E3D9A CRC64;
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POTENTIAL.
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SIGNAL
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                                                           Tight ju
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Antigen; Outer membrane; Signal
                                                                     PRINTS; PRO1077; CLAUDIN.

PROSITE; PSO1346; CLAUDIN; 1.

Tight junction; Transmembrane.
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                                                                                                                                                                                                                                                                                     MEDLINE=98311639; PubMed=9647647;
Furuse M., Fujita K., Hiiragi T., Fujimoto K., Tsukita S.;
"Claudin-1 and -2: novel integral membrane proteins localizing
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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InterPro; IPR000729; PMP22_C
Pfam; PF00822; PMP22_Claudin
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                       POTENTIAL.
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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 Brucellaceae; Brucella
         Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                      Brucella abortus
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PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
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InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claudin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gregory M., Dufresne J., Cyr D.G.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
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Sciurognathi; Muridae; Murinae; Rattus.
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Q45110;
Q45110;
15-DEC-1998 (Rel. 37, C
15-DEC-1998 (Rel. 37, L
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25 KDA OUTER-MEMBRANE I
           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                     Cloeckaert A., Verger J.M., Grayon M., Zygmunt M.S., Grepinet O.;
"Nucleotide sequence and expression of the gene encoding the major
25-kilodalton outer membrane protein of Brucella ovis: Evidence for
antigenic shift, compared with other Brucella species, due to a
deletion in the gene.";
Infect. Immun. 64:2047-2055(1996).
                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _BRUCA
                                                                                                                                       -!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                      MEDLINE=96239016; PubMed=8675306;
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J. Bacteriol. 177:1911-1914(1995).
-!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
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                                                                                                                                                                                                                                                                                                             Cloeckaert A., Vorger J.M., Grayon M., Zygmunt M.S., Grepinet O.
"Nucleotide sequence and expression of the gene encoding the maj
25-kilodalton outer membrane protein of Brucella ovis: Evidence
antigenic shift, compared with other Brucella species, due to a
deletion in the gene.";
Infect, Immun. 64:2047-2055(1996).
I-- SUBCELLULAR LOCATION: OUTER MEMBRANE.
--- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
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Cloeckaert A., Verger J.M., Grayon M., Zygmunt M.S., Grepinet O.; "Nucleotide sequence and expression of the gene encoding the major 25-kilodalton outer membrane protein of Brucella ovis: Evidence for antigenic shift, compared with other Brucella species, due to a
                                                                                                                                                                                 STRAIN-1330
                                                                                                                                                                                                                                                                                  Brucellaceae; Brucella.
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-!- SIMILARITY: BELONGS TO THE OMP25
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                                                                                                                                            MEDLINE=96239016; PubMed=8675306;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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STRAIN-ANTCC 49678 / NCIB 9440 / FERM BP-1845;

MEDLINE-89087434; PubMed-3207420;

FUJishiro K., Ando M., Uwajima T.;

"Crystallization and some properties of acetylpolyamine amidohydrolase from Mycoplana bullata.";

Biochem. Biophys. Res. Commun. 157:1169-1174(1988).

-i- FUNCTION: ACTS ON MANY TYPES OF ACETYLPOLYAMINES HAS HIGH AFFINITY TOWARDS ACETYLPUTRESCINE, ACETYLCADAVERINE, ACETYLSPERMIDINE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 1-30.
STRAIN-ATCC 49678 / NCIB 9440 / FERM BP-1845;
MEDLINE-96422009; PubMed-8824626;
Sakurada K., Ohta T., Fujishiro K., Hasegawa M., Aisaka K.;
Racetylpolyamine amidohydrolase from Mycoplana ramosa: gene and characterization of the metal-substituted enzyme.";
Bacteriol. 178:5781-5786(1996).
                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brucellaceae; Mycoplana.
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Bacteria; Proteobacteria; alpha subd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACETYLPOLYAMINE AMINOHYDROLASE.
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Infect. Immun. 64:2047-2055(1996)
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SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
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-!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY.
-!- SUBUNIT: HOMODIMER AND HETERODIMER WITH L CHAIN.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
  SEQUENCE
                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isozyme multiplicity with anomalous dimer alcohol dehydrogenase. Effects on the activ structure of residue exchanges at 'non-func
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
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                                         BINDING
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                                                                                                                                                                                                                                                                                           InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: ALCOHOL + NAD(+) = ALDEHYDE OR KETONE
-!- CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE + NAD(+) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97085413; PubMed=8931553;
Danielsson O., Shafqat J., Estonius M.,
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Pfam; pr00850; Hist_deacetyl; 1.
pr11TS; PR01270; HDASUPER.
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                                       ZINC (CATALYTIC).
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15-JUL-1999 (Rel. 3
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PUTATIVE LAMBDOID P
MGTA_THEMA
P80099;
01-AUG-1992
30-MAY-2000
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).

"In Function: INTEGRASE IS NECESSARY FOR INTEGRATION OF THE PHAGE INTO THE HOST GENOME BY SITE-SPECIFIC RECOMBINATION. IN CONJUNCTION WITH EXCISIONAES, INTEGRASE IS ALSO NECESSARY FOR EXCISION OF THE PROPHAGE FROM THE HOST GENOME (BY SIMILARITY).

"INTEGRASE FAMILY."
                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE:97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhaw G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                               EMBL; AE000232; AAC74427.1; -.
EcoGene; EG13358; intr.
Interpro; IPR002104; Phage_integrase.
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Thes 5; Conservative
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   AQL1_THEAQ
P08594;
01-AUG-1988
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLETE
ACT_SITE
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MEDLINE-99287316; PubMed-10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There use by non-profit institutions as Institutions as modified and this statement is not removed. Use entitles requires a license agreement (See httor send an email to license@isb-sib.ch).
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Liebl W., Feil R., Gabelsberger J., Kellermann J., Schleifer K.-H.;
"Purification and characterization of a novel thermostable 4-alpha-
glucanotransferase of Thermotoga maritima cloned in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGTA OR TM0364.
Thermotoga maritima
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SUBCELULAR LOCATION: CYTOPLASMIC.
SIMILARTTY: BELONGS TO FAMILY 13 O
KNOWN AS THE ALPHA-AMYLASE FAMILY.
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                                                                                                               STANDARD;
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TIVITY: TRANSFERS A SEGMENT OF A 1,4-ALPHA-D-GLUCAN אמר איז ארויביים איז ארויביים איז איז ארויביים איז איז ארויביים איז איז ארויביים איז איז ארויביים איז איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים איז ארויביים ארויביים איז ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויביים ארויבים ארויביים ארויב
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SIGNAL
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PIR; A35742; A35742.
HSSP; P06873; 3PRK.
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Eur. J. Biochem. 171:441-447(1988).

-i. FUNCTION: AQUALYSIN I IS A THERMOPHILIC ALKALINE SERINE PROTEASE.

THE OPTIMAL TEMPERATURE FOR ITS CASEINOLYTIC ACTIVITY IS 80
                                                                                                                                                                                                                                                               InterPro; IPR000209; Peptidase_S8.
Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                        PROPEP
                                                                                                                                                                                       PROSITE; PS00137; PROSITE; PS00138;
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MEDLINE=88151937; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kwon S.-T., Terada I., Matsuzawa H., Ohta T.;
"Nucleotide sequence of the gene for aqualizin I (a thermophilic alkaline serine protease) of Thermus aquaticus YT-1 and characteristics of the deduced primary structure of the enzyme."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsuzawa H., Tokugawa K., Hamaoki M., Mizoguchi M., Terada I., Kwon S.-T., Ohta T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88225062;
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DEVELOPMENTAL STAGE: SECRETED FROM THE EARLY STATIONARY PHASE UNTIL THE TIME THE CELLS CEASE TO GROW.

PTM: THE N- AND C-TERMINAL PRO-SEQUENCES ARE REMOVED THROUGH THE PROTECLYTIC ACTIVITY OF AQUALYSIN I ITSELF, IN THAT ORDER. THE C-TERMINAL PRO-SEQUENCE IS REQUIRED FOR TRANSLOCATION OF THE PROTEASES ACROSS THE OUTER MEMBRANE.
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SUBTILASE_SER;
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                                                                                                                                                            Zymogen;
CHARGE RELAY SYSTEM
                                                                              AQUALYSIN I.
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074164;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                           PRINTS; PR00071; HMGCOARDTASE.

PROSITE; PS00066; HMG_COA_REDUCTASE_1;
PROSITE; PS00318: HMG_COA_REDUCTASE_3;
PROSITE; PS01192; HMG_COA_REDUCTASE_3;
PROSITE; PS0066; HMG_COA_REDUCTASE_4;
PROSITE; PS50166; HMG_COA_REDUCTASE_4;
                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: (R)-MEVALONATE + COA + 2 NADP(+) =
HYDROXY-3-METHYLGLUTARYL-COA + 2 NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=98320604; PubMed=9647847;

Mincreased carotenoid production by the food yeast Candida utilis through metabolic engineering of the isoprenoid pathway.";

Appl. Environ. Microbiol. 64:2676-2680(1998).

-!- FUNCTION: INVOLVED IN THE CONTROL OF CHOLESTEROL BIOSYNTHESIS.
                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                            EMBL; AB012603; BAA31937.1;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REDUCTASE).
                                                                                                                                                                                                                                                                                 InterPro;
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Pro; IPR000731; HMGCR_patched_5TM
PF00368; HMG-COA_red; 1.
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Pred. No.
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21-JUL-1986
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cauliflower mosaic virus (strain W260) (CaMV). Viruses; Retroid viruses; Caulimovirus. NCBI_TaxID=31558;
Cauliflower mosaic virus (strain CM-1841) (CaMV). Viruses; Retroid viruses; Caulimovirus. NCBI_TaxID-10644;
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NON_TER 99 99
SEQUENCE 99 AA; 11049 MW;
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21-JUL-1986 (Rel. 01, Last sequence
15-JUL-1999 (Rel. 38, Last annotatio
APHID TRANSMISSION PROTEIN (PROTEIN
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SEQUENCE FROM N.A.
MEDLINE-82014878; PubMed-6269062;
Gardner R.C., Howarth A.J., Hahn P., Brown-Luedi M., Shepherd
Messing J.;
"The complete nucleotide sequence of an infectious clone of
cauliflower mosaic virus by M13mp7 shotgun sequencing.";
Nucleic Acids Res. 9:2871-2888(1981).
-!- FUNCTION: THIS PROTEIN IS INVOLVED IN VIRUS TRANSMISSION.
-!- SIMILARITY: BELONGS TO THE CAULIMOVIRUSES ORF II FAMILY.
                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics in the European Bioinformatics in the European Bioinformatics in the European Bioinformatics in the European Bioinformatics in There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                               61 WKINSYFG
                                                                                                                     1 wkxxayxg
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4; Conservative
                  January 14, 2002, 07:40:37
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Q9QQN6
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088719
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| 396 | 396 | 379 | 378 | 377 | 377 | 377 | 377 | 369 | 369 | 369 | 303 | 288 | 285 | 262 | 261 | 260 | 246 | 159 | 159 | 159 | 159 | 109 | 99 | 64 | 4919 | 4152 | 635 | 493 | 493 | 441 |
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| Q9SBA2 | 082014 | Q9FND2 | Q9JRB0 | Q9вJ33 | Q9BJ34 | Q9NJC3 | Q9NJD0 | Q9A5D4 | 024687 | Q59399 | 064761 | Q9RS05 | Q9RKH7 | Q9HT72 | Q9CP25 | Q9KQB7 | 044142 | Q9WI33 | Q83166 | Q66159 | Q83179 | Q9PB67 | Q83162 | Q83157 | Q9ZHL0 | Q9ZHL3 | Q9NKKO | 093184 | ~ | Q60035 |
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Q99KK2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO CYTIDINE MONOPHOSPHO-N-ACETYLNEURAMINIC /
O88719 PRELIMINARY;
O88719;
O1-NOV-1998 (TrEMBLrel. 08,
O1-NOV-1998 (TrEMBLrel. 08,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004606; AAH04606.1; -.
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Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Wakamatu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
"NEDO human cDNA sequencing project."
"NEDO human cDNA sequencing project."
"Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP271388; AAF76203.1.;
-InterPro; IPR00329; Cytidylyl_trans.
InterPro; IPR003329; Cytidylyl_trans.
InterPro; IPR003329; Cytidylyl_trans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CMP-N-ACETYLNEURAMINIC ACID SYNTHASE (EC 2.7.7.43).
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Transferase; Nucleotidyltransferase
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Mus musculus (Mouse).
Mus musculus (Mouse).
Thervota; Metazoa; Chordata;
Theria; Rodentia;
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MEDLINE=98356124; PubMed=9689047;
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CMP-N-ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE
CYTIDYLYLTRANSFERASE) (CMP-SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE
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-!- CATALYTIC ACTIVITY: CTP +
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Sciurognathi; Muridae;
  B303B6647EF81A3A CRC64;
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EMBL; AE004659, AA005721.1; -. InterPro; IFR000917; Sulfatase.
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R. Potocka I., Nelson W.C., Newton A., Stephans C., Phadke N.D., Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berr Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., W
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; StRCBI_TaxID-1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moonan F., Molina J.J., Mirkov T.E.;

"Sugarcane yellow leaf virus is a new virus with a genome
Polerovirus, Luteovirus, and Enamovirus properties.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF157029; AAD45687.1;
InterPro; IPR000893; Luteo_ORF5.
InterPro; IPR002929; PLRV_ORF5.
InterPro; IPR002929; PLRV_ORF5.
Prints; PR00910; LVIRUSORF6.
PRINTS; PR00910; LVIRUSORF6.
PRINTS; PR00911; PRICHEXTENSN.
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09QQN6; (TrEMBLrel. 13, Created)
01-MAY-2000 (TREMBLrel. 13, Last sequence upd.
01-JUN-2001 (TREMBLREL. 17, Last annotation upd.
putative Aphid Transmission Factor (Fragment)
sugarcane yellow leaf virus.
  Q9JH75 PRELIMINARY; PRT; 479 AA. Q9JH75; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update PUTATIVE APHID TRANSMISSION FACTOR (FRAGMENT).
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NON_TER 1 1 1
NON_TER 193 193
SEQUENCE 193 AA; 20299 MW; 2F2D8
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Pred. No. 1.3e+02;
1; Mismatches 3;
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Pred.
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Q9BRT6

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Best Local
     Q9P7A3;
Q9P7A3;
01-OCT-2000
01-OCT-2000
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StrausDerg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC006112; AAH06112.1; -.
SEQUENCE 497 AA; 54088 MW; B758E977CDA88F8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 2610017G09 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=KIDNEY ADENOCARCINOMA;
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MEDLINE-20318675; PubMed=10859394;

Smith G.R., Borg Z., Lockhart B.E.L., Braithwaite K.S., Gibbs M.J

"Sugarcane yellow leaf virus: a novel member of the Luteoviridae probably arose by inter-species recombination.";

J. Gen. Virol. 81:1865-1869(2000).

EMBL; AJ249447; CAB75437.1;

TEMBL; AJ249447; CAB75437.1;
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NCBI_TaxID=94290;
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     (TrEMBLrel. (TrEMBLrel.
                                                                            PRELIMINARY;
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Pred. No. 1.4e
1; Mismatches
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No. 1.4e+02;
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Query Match
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Matches 5; Conserv
                                                            Q9RPH6;
Q9RPH6;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                      RECB.
                                                  RECB.
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Q9HE05;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Mycobacterium smegmatis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
                                                                                                                                                                                                                                                                                  Seeger K., Harris D., Wood V., Rajandream M.A., Barrell Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AL512487; CAC19740.1; -. Interpro; IPR003613; Ubox. SMART; SM00504; Ubox; 1. SMART SM00504; Ubox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             UFD2
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=972H-;
                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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NON_TER 817 817
SEQUENCE 817 AA; 93232 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saunders D., Harris D., Wood V., Rajandream M.A., Barre Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AL163640; CAB87206.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomycetales; Schizosaccharomycetaceae;
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Schizosaccharomyces pombe (Fission yeast).
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                                                                                                                                                                           706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 706 WKQPAYFG 713
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                                                                                                                                                                         WKQPAYFG 713
                                                            (TrEMBLrel. 13,
(TrEMBLrel. 13,
(TrEMBLrel. 17,
                                                                                                                                                                                                                          Conservative
                                                                                                              PRELIMINARY;
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62.5%;
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Pred. No. 2.9e+02;
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annotation
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  Mycobacterium.
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Query Match
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Matches 4
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"In vitro transposition of Tn552: a tool for D mutagenesis.",
Nucleic Acids Res. 27:3859-3865(1999).
EMBL: AP157643; AAD46808.1; -.
HSSP; P56255; 2PJR.
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MEDLINE-99412429; PubMed: 10481025;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Euthoria; Lagomorpha; Leporidae; Oryctolagus.
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Q28733; Q28736;
Q1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
SEQUENCE 1083 AA; 117442 MW; A531F5FBA85EB748
                                                                                                                                                                EMBL; X64696; CAA45937.1; -. EMBL; X17329; CAA35207.1; -. HSSP; P56276; ITLK.
                                                                                                                                                                                                                                                                                                                                      Labeit S., Barlow D.P., Gautel M., Gibson T., Holt J., Hsieh C.L., Francke U., Leonard K., Wardale J., Whiting A., Trinick J.; "A regular pattern of two types of 100-residue motif in the sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Labeit S., Gautel M., Lakey A., Trinick J.; "Towards a molecular understanding of titin EMBO J. 11:1711-1716(1992).
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Labeit S.;
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                                                                                                                                                                                                                                                                                                                  of titin.";
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                    InterPro;
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4; Conserv
                                                                    IPR000282; Cytok_receptor_2.
IPR003962; FnIII_repeat.
IPR003961; FN_III.
IPR003598; I9_c2.
                         IPR003006;
                                           IPR003600;
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                    I9_MHC
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Pred. No. 3.1e
1; Mismatches
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Last annotation update)
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J. 3.1e+02;
3;
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RESULT
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Best Local
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PRINTS;
SMART; S
SMART; S
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                      SEQUENCE (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6555 WKKPAYDG 6562
                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 22277-25376 FROM N.A. MEDLINE-92258380; PubMed=158406; Labeit S., Gautel M., Lakey A., Tr. "Towards a molecular understanding EMBO J. 11:1711-1716(1992).
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EMBL;
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"A calmodulin_binding sequence in the
                                                                                                                                                                                                                                                                                                                                                                                               Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-HEART;
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                                                                                                                                                                                                     titin kinase.";
                                                                                                                                                                                                                                                     CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96026330;
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                                                                                                      J. BIOChem. 230:752-759(1995).

FUNCTION: THIS GIANT MUSCLE PROTEIN MAY BE INVOLVED IN MUSCLE PROTEIN FUNCTION: THIS GIANT MUSCLE PROTEIN E STRUCTURAL INTEGRITY OF ASSEMBLY AND IN MAINTAINING THE STRUCTURAL INTEGRITY OF SARCOMERES. MAY HAVE PROTEIN KINASE ACTIVITY.

ALTERNATIVE PRODUCTS: A NUMBER OF FORMS OF THIS PROTEIN ARE PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE DISTRIBUTION. DIFFERENT SIZE TRANSCRIPTS MAY ALSO EXIST WITHIN ONE TISSUE. THE SEQUENCE SHOWN HERE IS THAT OF THE HEART ISOFOFORD
                       DOMAINS
                                   SIMILARITY: BELONGS TO IMMUNOGLOBULIN C2-LIKE
                                                                      TISSUE SPECIFICITY: MUSCLE-SPECIFIC. SIMILARITY: TO THE CATALYTIC DOMAINS
                                                            KINASES
X64698;
X83270;
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SM00408;
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5; Conserv
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14; FNTYPEIII.
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Myosin; Repeat.
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A; 759127 MW;
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B.;
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                                   IMMUNOGLOBULIN SUPERFAMILY. CONTADOMAINS AND 132 FIBRONECTIN TYPE
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e C-terminus of human
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titin.";
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2.2e+03;
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                                                                       OTHER SERINE/THREONINE
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                                               CONTAINS 112
                                                                                                                                                                                                                  Pastore A.;
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RESULT
Q9NKN6
ID Q5
AC Q5
DT 0:
DT 0:
DT 0
DT 1
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Pfam; PF00041; fn3; 13.

Pfam; PF00047; fn; 95.

Pfam; PF00047; jq; 95.

Pfam; PF00049; pkinase; 1.

PRINTS; PR00726; LEAASERPTASE.

SMART; SM00040; FN3; 127.

SMART; SM00400; IG_like; 79.

SMART; SM00410; IG_like; 79.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00038; HELIX_LOOP_HEL

PROSITE; PS00039; IG_MHC; UNKNOM

PROSITE; PS00039; IG_MHC; UNKNOM

PROSITE; PS00039; IG_MHC; UNKNOM

PROSITE; PS00039; IG_MHC; UNKNOM

PROSITE; PS00039; IG_MHC; UNKNOM

PROSITE; PS00039; IG_MHC; UNKNOM
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O9NKN6; PRELIMINARY;
O1-OCT-2000 (TrEMBLrel. 15,
O1-OCT-2000 (TrEMBLrel. 17,
OJ-JUN-2001 (TrEMBLrel. 17,
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                                                                  01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 0%-JUN-2001 (TrEMBLrel. 17, Last annotation update) IRON TRANSPORT MULTICOPPER OXIDASE RELATED PROTEIN 1
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Leishmania major
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50011;
PROSITE; PS00109;
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JIPR000719; Euk_pkinase.

JIPR000377; FGCY_kin.

JIPR003962; FNIII_repeat.

JIPR003961; FN III_repeat.

JIPR003951; HLH_Myc.

JIPR003598; Ig_c2.

JIPR003598; Ig_c2.

JIPR003600; Ig_like.

JIPR003060; Ig_MHC.

JIPR0001129; Peptidase_S24.

JIPR002016; Peroxidase.
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CAA62188.1;
CAA45940.1;
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; HELIX_LOOP_HELIX; UNKNOWN_1.

; IG_MHC; UNKNOWN_1.

; PEROXIDASE_1; UNKNOWN_1.

; PROTEIN_KINASE_TYR; 1.
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9.1e+03;
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01-MAY-2000 (Tr
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Q84711;
01-NOV-1996
01-NOV-1996
01-JUN-2001
Streptomyces coelicolor
                                                                                                                                                                                                                                                                                InterPro; IPR000893; Luteo_ORF6.
InterPro; IPR002929; PLRV_ORF5.
Pfam; PF01690; PLRV_ORF5; 1.
PRINTS; PR00910; LVIRUSORF6.
                                                                                                                                                                                                                                                                                                                                  aphid non-transmissible strain of pea J. Gen. Virol. 72:1819-1834(1991). EMBL; L04573; AAA72298.1; -.
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STRAIN=FRIEDLIN;
Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock M.,
Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock M.,
Cawthra J., Marsolini F., Sunkin S., Stuart K.D.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005935; AAR39743 1; -
InterPro; IPR002355; MultiCu_oxidse2.
               FABB.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae.
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"The nucleotide sequence and luteovirus-like nature of RNA
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91341468; PubMed=1875194;
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[ (TrEMBLrel.
TYL SYNTHASE.
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
LETE CDS; ORF 2, COMPLETE CDS; ORF 3, 3
                                                           (TrEMBLrel. 13,
                                                                                    PRELIMINARY;
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_kin_actsite.
Pfam; PF00069; pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
EMBL; AL133423; CAB62722.1; -.
HSSP; P39435; IARS.
InterPro; IPR000794; Ketoacyl-synt.
Pfam; PF00109; ketoacyl-synt; 1.
SEQUENCE 429 AA; 43841 MW; 983DC0F9800582BE CR
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Cerdeno A.M., Parkhi.
Submitted (DEC-1999)
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Seeger K.J., Harris I
Submitted (DEC-1999)
                                                                                                                                                                      "Pfnck-1, a novel NIMA-related protein kinase from the parasite Plasmodium falciparum."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                         01-OCT-2000 (Tremblrel. 15, 01-OCT-2000 (Tremblrel. 15, 01-JUN-2001 (Tremblrel. 17, NIMA-RELATED PROTEIN KINASE
                                                                                                                                                                                                                SEQUENCE FROM N.A.
Dorin D., Le Roch K., Scallafandro P.,
                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5833;
                                                                                                                                                                                                                                                                                                                                               Q9NFP2
                                                              ATP-binding; Kinase;
NON_TER 432 4
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e EMBL/GenBank/DDBJ databases
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983DC0F9800582BE CRC64;
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STRAIN-MSB8 (DSM3109);
MEDLINE-92331687; PubMed=1628664;
Liebl W., Feil R., Gabelsberger J., Keller
"purification and characterization of a no
glucanotransferase of Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1995) to the EMBL/GenBank/DDBJ da
-!- CATALYTIC ACTIVITY: TRANSFERS A SEGMENT OF A
A NEW 4-POSITION IN AN ACCEPTOR, WHICH MAY B
ALPHA-D-GLUCAN.
EMBL; Z50813; CAA90693.1; -.
InterPro; IPR000461; Alpha_amylase.
Pfam; PF00128; alpha-amylase; 1.
Transferase; Glycosyltransferase.
SEQUENCE 441 AA; 51857 MW; 3D221B5234BAFBAC
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Bacteria; Thermotoga
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Heinrich P., Huber W.,
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17:297-305(1994).
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TRANSFERS A SEGMENT OF A 1,4-ALPHA-D-GLUCAN
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                                                          is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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36
1 wkxxayxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522463 seqs, 74073290 residues
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                           SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT:

SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:

SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:

SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:

SIDS2/gcgdata/geneseq/geneseqp/AA1984.DAT:

SIDS2/gcgdata/geneseq/geneseqp/AA1985.DAT:

SIDS2/gcgdata/geneseq/geneseqp/AA1987.DAT:

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SIDS2/gcgdata/geneseq/geneseqp/AA1989.DAT:

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SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search time 103.51 Seconds (without alignments)
5.725 Million cell updates/sec
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| Result No. | Score | Query Match | Query Match Length DB | DB | ID | Description |
|---------------|-------|----------------|--------------------------|----|----------|--------------------|
| | 31 | 86.1 | 275 | 22 | AAG90433 | C glutamicum prote |
| N | 30 | 83.3 | 434 | 21 | AAB28673 | Human carbohydrate |
| w | 30 | 83.3 | 434 | 21 | AAB43165 | Human ORFX ORF2929 |
| ۵ | 30 | 83.3 | 434 | 21 | AAY96100 | Human CMP-sialic a |
| ₅ | 30 | 83.3 | 434 | 21 | AAY90351 | Human glycosylatio |
| 6 | 30 | 83.3 | 434 | 22 | AAM39319 | Human polypeptide |
| 7 | 30 | 83.3 | 434 | 22 | AAB84682 | Nucleotide sequenc |
| 80 | 30 | 83.3 | 434 | 22 | AAB95213 | Human protein sequ |
| 9 | 30 | 83.3 | 448 | 21 | AAB43931 | Human cancer assoc |
| 10 | 30 | 83.3 | 461 | 22 | AAM41105 | Human polypeptide |
| 11 | 29 | 80.6 | 55 | 20 | AAY12227 | Human 5' EST secre |
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| 50 | 47 | 46 | 4 4 | ω. | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω ω | 32 | 3 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 |
|--|----------------------|-----------|--------------------|-----------|----------|-----------|----------|----------|------------|----------|----------|----------|--------------------|-----------|-------------------|----------|-----------|--------------------|----------|----------|----------|----------|-------------------|----------|-----------|----------|----------|----------|----------|----------|----------|-------------|----------|-------------|--------------------|
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| 513 934 | 513 | 343 | 211 | 10 | 10 | 10 | 10 | 10 | 9 | 89 | æ | 26926 | 5701 | 497 | 496 | 496 | 260 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 230 | 155 | 140 | 126 | 126 | 114 | 113 | 83 | 56 |
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| AAW82254 | AAR04585 AAR13181 | AAR22463 | AAY51675 | AAB06472 | AAB06463 | AAB06454 | AAB06445 | AAB06436 | AAB06420 | AAB06479 | AAB06419 | AAU05396 | AAM05328 | AAB12138 | AAB88466 | AAG81335 | AAM40643 | AAB66127 | AAB88342 | AAB87565 | AAE04207 | AAU12417 | AAM38857 | AAY84609 | AAY99378 | AAY36181 | AAY36134 | AAB54052 | AAE04228 | AAM42193 | AAM25829 | AAY12226 | AAE04281 | AAM40407 | AAE04286 |
| Aqualysin I. Ther JP10248575 Seq ID | Aquaricine I. The | polyamine | Murine clodin 1 pr | -1 cyclic | Ļ | -1 cyclic | 1 cyclic | -1 cycli | -1 cell ad | -1 cycli | in-1 ce | | Peptide #4010 enco | phobic đo | Human membrane or | | polypepti | Protein of the inv | membran | PRO1356. | | | Human polypeptide | σ, | PRO1356 (| secreted | _ | pancreat | | | | 5' EST secr | gene 1 | polypeptide | Human gene 10 enco |

ALIGNMENTS

| PI | X P X | PR | PR | PR | × | ΡF | × | PD | × | PN | × | So | × | Σ | KΨ | × | DE | × | DT | × | AC | ×× | ID | AAG | RESULT |
|---|-------------------------------|------------------------------|------------------------------|----------------------------|---|------------------------------|---|--------------|---|---------------|---|-----------------------------|---|-------------------------|--|---|--|---|---------------------------|---|-----------|----|-------------------------------------|----------|--------|
| Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H; Tateishi N, Senoh A, Ikeda M, Ozaki A; | (KYOW) KYOWA HAKKO KOGYO KK. | 03-AUG-2000; 2000JP-0280988. | 07-APR-2000; 2000JP-0159162. | 16-DEC-1999; 99JP-0377484. | | 18-DEC-2000; 2000EP-0127688. | | 20-JUN-2001. | | EP1108790-A2. | | Corynebacterium glutamicum. | | organic acid synthesis. | Coryneform bacterium; amino acid synthesis; vitamin; saccharide; | | C glutamicum protein fragment SEQ ID NO: 4187. | | 26-SEP-2001 (first entry) | | AAG90433; | | AAG90433 standard; Protein; 275 AA. | AAG90433 | ULT 1 |

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RESULT
AAB28673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression mount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                            Human; carbohydrate-modifying enzyme; CME; antidiabetic; immunosuppressive; anti-HIV; antiinflammatory; antianaemic; antiasthmatic; antiarteriosclerotic; antithyroid; hepatotropic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopat antiarthritic; antipsoriatic; uropathic; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                        Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17;
                            WPI; 2000-672729/65
                                                                                                                                                                                                                                                                  dermatological; antiulcer; cytostatic; virucide; antibacterial; fungicide; protozoacide; tranquiliser; vulnerary; diabetes; autoimmune disorder; inflammatory disorder; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
              N-PSDB;
                                                                                                                   21-APR-1999;
                                                                                                                                                                                                          WO200063351-A2
                                                                                                                                                                                                                                                                                                                                                                                                    Human carbohydrate-modifying enzyme Incyte ID No: 000422CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB28673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB28673 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                               20-APR-2000; 2000WO-US10882
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                                                                                                                                                                                                                                       sapiens
                                                        Yue H,
                                                                                    INCYTE GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH65652
              AAC65392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO: 4187; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention provides a number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                   99US-0130383
                                                      Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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62.5%;
                                                        Hillman JL,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                        Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                          osteopathic;
                                                         J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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AAB43165
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Best Local
                          31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a human carbohydrate-modifying enzyme (CME). CME polynucleotides and polypeptides are useful for treating and diagnosing diseases associated with CME such as diabetes, autoimmune/inflammatory disorders such as AIDS, Addison's disease, adult respiratory distress syndrome, allergies, anaemia, asthma, atherosclerosis, autoimmune thyroiditis, bronchitis, cholocystitis, contact dermanitis, Cron's disease, emphysema, erythroblastosis fetalis, glomerulonephritis, Good pasture's syndrome, gout, Grave's disease, mashimoto's thyroiditis, multiple sclerosis, myasthenia gravis, asthmatistic contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact descriptions of the contact 
                                                                                                                                                                                                                                                                                                                                                                                                                                            antianaemic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobiniria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
hypotensive; dermatological; immunosuppressive; antiinflammatory;
antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's Syndrome, arthritis, scleroderma, Sjogren's Syndrome, systemic lupus erythematosus, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, haemodialysis, and extracorporeal circulation, viral, bacterial, fungal parasitic, protozoal, and helminthic infections, traums or capac CMF or its astalutic or immunocenic fragment is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vulnerary; antipsoriatic; antiparkinsonian;
anticonvulsant; osteopathic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel carbohydrate modifying enzyme polypeptides and polynucleotides for diagnosis, treatment, and prevention of carbohydrate metabolism disorders, autoimmune/inflammatory disorders, and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ORFX ORF2929 polypeptide sequence SEQ ID NO:5858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 66-67;
                                                                                                                                                                   31-MAR-2000;
                                                                                                                                                                                                                          05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB43165 standard; Protein; 434 AA
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                                                                                                                                                                                                                                                                                 WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       bone damage; cartilage damage; antiinflammatory disease;
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or cancer. CME, or its catalytic or immunogenic fragment, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug screening.
                                                                                                                                                                                                                                                                                                                                                                                       contraceptive
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                                                    99US-0127636.
99US-0127636.
99US-0127728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frame; ORFX;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Lc.
. 1.5e+02;
. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 434;
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                                                                                                                                                                                                                                                                                                                                                                                                                          coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypertension
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2000US-0540763

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have actlyities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic ucids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-602362/57.
N-PSDB; AAC77374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 5028-5029; 5507pp; English.
                                                                                                                            Location/Qualifiers
Misc-difference 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                          Misc-difference
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                CMP-sialic
                                                                                                                                                                                                                                                                                                                           AAY96100;
                                                                                                                                                                                                                                                                                                                                                          AAY96100 standard; Protein; 434 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coagulation; to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397
                                                                       Misc-difference
                                                                                                     Misc-difference
                                                                                                                                                                                                                plasminogen;
                                                                                                                                                                                                                                                             Human CMP-sialic acid synthetase
                                                                                                                                                                                                                                                                                          19-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                      365
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 wkxxayxg
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5; Conser
                                                                                                                                                                                                                               acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                transferrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                      372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   œ
                                                                        /note-
147
                                                                                                                                                                                                                               synthetase; human;
                                        /note-
169
                                                                                                       136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibit thrombosis; and
                                                                                                                    /note-
                           note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.3%;
62.5%;
                           "encoded by GKT"
                                                          "encoded bu
                                                                                     "encoded by GKT"
                                                                                                                      "encoded
                                                                                                                                                                                                              e; human; sialylation; glycoprotein; thyrotropin; Na+,K+-ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30;
Pred. No.
                                                                                                                    by YAT"
                                                          YCA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
1.5e+02;
3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT
AAY90351
ID AAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycoprotein at above endogenous levels expresses at least 1
( (preferably human) enzyme selected from GlcNAc-2 epimerase, an
c enzyme catalyzing the conversion of UDP-GlcNAc to ManNAc, sialic
c enzyme catalyzing the conversion of UDP-GlcNAc to ManNAc, sialic
c enzyme stalic acid transporter at above endogenous levels. Endogenous
C N-acetylglucosaminidase activity may be suppressed A claimed
method for manipulating glycoprotein in an insect cell comprises
c enhancing the expression of 1 of the above enzymes, and a claimed
method for producing sialylated glycoproteins involves expressing
a heterologous protein (especially plasminogen, transferrin,
c nu+,K+ATPase or thyrotropin) in the insect cell. Yeast, insect,
c Na+,K+ATPase or thyrotropin host cells can be engineered to produce
new forms of sialylated glycoproteins, higher concentrations of
sialylated glycoproteins and/or elevated concentrations of donor
                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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08-DEC-1999;
                                            Human; glycosylation enzyme; glycolysis; myoglobinuria; tumour marker; immunotherapy; cosmetic surgery; metabolism; immune system disorder; haematopoletic cell deficiency; blood coagulation disorder; asthma; afibrinogenaemia; blood platelet disorder; thrombocytopaenia; neoplasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 102-103; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC (UYJO) UNIV JOHNS HOPKINS. (UYWY-) UNIV WYOMING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2000;
          allergic encephalomyelitis; allergic reaction; organ rejection;
                              autoimmune disorder; Addison's disease; multiple sclerosis; purpura;
                                                                                                                                                                     04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carbohydrate processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sialylation reaction has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant production of sialylated glycoproteins using cells in which the expression of enzymes, e.g. sialic acid synthetase, involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA50568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2000
                                                                                                                                  Human glycosylation enzyme clone HWLLM34 protein sequence.
                                                                                                                                                                                                       AAY90351;
                                                                                                                                                                                                                                       AAY90351 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                           365 wkevaylg 372
                                                                                                                                                                                                                                                                                                                                                            1 wkxxayxg 8
                                                                                                                                                                                                                                                                         u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methods involve altering the expression of enzymes involve bohydrate processing. A claimed cell producing sialylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention provides methods and recombinantly engineered ce-
producing glycoproteins having sialylated oligosaccharides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is that of human CMP-sialic acid synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-572178/53.
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5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (e.g. nucleotide
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US05313
                                                                                                                                                                     (first entry)
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99US-0169624
                                                                                                                                                                                                                                                                                                                                                                                                              83.3%;
62.5%;
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                                                                                                                                                                                                                                         434
                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB
Pred. No. 1.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      altered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jarvis
                                                                                                                                                                                                                                                                                                                                                                                                                1.5e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 434;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells
                                                                                                                                                                                                                                                                                                                                                                                               0
                                                neoplasia;
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Query Match
Best Local Similarity
"atches 5; Conserv
                                                                                                                                                                                                                                                                    CC acid synthetase. The sequences are useful as reagents for the CC differential identification of the tissues or cell types present in a CC biological sample, as immunological probes, for treating a disease or CC condition resulting from under expression of such polypeptide, for the CC detection and/or treatment of disorders involving aberrant glycolysis, Cc e.g. cramps, myoglobinuria, and as tumour marker and/or immunotherapy CC targets. They may also be used to differentiate, proliferate and attract characteristics (e.g. in cosmetic surger) or mammalian metabolism CC characteristics (e.g. in cosmetic surger) or mammalian metabolism additive or preservative. The proteins can be used to assay protein CC levels in a sample, as a marker or detector of an immune system disorder, to inhibit cytokine activity, and as a vaccine. They may further be used to treat immune system or of haematopoletic cell deficiencies or CC disorders, blood coagulation disorders (e.g. afibrinogenaemia), blood coagulation disorders (e.g. afibrinogenaemia), blood coagulation disorders (e.g. afibrinogenaemia), blood coagulation disorders (e.g. afibrinogenaemia), blood coagulation disorders (e.g. afibrinogenaemia), blood cogulation disorders (e.g. afibrinogenaemia), blood cogulation graft-versus-host disease, inflammation, CC disease, allergic encephalomyelitis), allergic reactions (e.g. asthma), CC diseases caused by viruses (e.g. hepatitis, meningitis, sepsis, typhoid, CC diseases caused by viruses (e.g. hepatitis, sepsis, typhoid, CC diseases, coccidiosis, leishmaniasis, scables, malaria, toxoplasmosis).
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a human glycosylation enzyme clone of the invention, designated HWLLM34. This protein clone is a CMP stalic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 106-108; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human glycosylation enzymes cytidine 5'-monophosphate sialic synthetase, sialic acid synthetase and aldolase and nucleic acids encoding the proteins for treating e.g., immune system disorders, microbial diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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N-PSDB; AAA37762.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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1 wkxxayxg 8
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                                                                                                                                                                                                                            434 AA;
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US05325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
169
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                                                                                            83.3%;
62.5%;
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                                                                 0;
                                                              Pred. No. 1.5e); Mismatches
                                                                                                                         Score 30;
                                                        1.5e+02;
3;
                                                                                                                      DB 21; Length 434;
                                                              Indels
                                                              0,
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Qy

Query Match Best Local Similarity

83.3%;

Score 30; Pred. No.

DB 22; . 1.5e+02;

Length 434;

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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-CCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and thrompy drug screening, and the property of the control of the sectivity of the cattivity of the control of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity of the sectivity. The section of the sectivity of the sectivi
                                                                                               assays for receptor activity, arthritis and inflammation, \textsc{C.N.S} disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; nearcopathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
Sequence
                                                   specification.
                                                                        Note: The sequence data for this patent did not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 2464; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-2001.
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The specification describes a method for manipulating carbohydrate processing pathways in cells of interest. The methods are used to manipulate multiple pathways involved with the sialylation reaction by using recombinant DNA technology and substrate feeding approaches to cenable the production of sialylated glycoproteins in the cells. The sialylation process involves the post-translational addition of the color substrate cytidine monophosphate-stalic acid (CMP-SA) onto a specific acceptor carbohydrate. The cells express at least one enzyme, caldolase, CMP-SA synthetase and CMP-SA transporter, above endogenous levels. The cells are useful for producing complex sialylated glycoproteins in cells of interest, especially insect cells. Cellsoproteins containing stalylated oligosaccharides are useful as calls of interest, especially insect cells. Stalylated stalylated glycoproteins and diagnostic tools. Cells producing complex stalylated of stalylated glycoproteins are useful for enhancing the value of
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N-PSDB; AAH28457.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the polynucleotide which comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides,
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T, Wakamatsu
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1.5e+02;
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Otsuki
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Best Local :
'antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating.
                                                                                                                      AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antiatabletic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer - \!\!\!\!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis;
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cytostatic; proliferative; vulnerary; immunomodulator;
ic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
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Pred. No. 1.5e+02;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                         Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  numan; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; lenukaccai;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotides, polypeptides, antibodiés, agónists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC7849 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                     Zhao
                                                                                                                                              WPI; 2001-442253/47.
N-PSDB; AAI60261.
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2000US-0552317.
2000US-05598042.
2000US-0620312.
2000US-0623450.
2000US-0662191.
2000US-0693036.
2000US-07273444.
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Wehrman T,
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62.5%;
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Yang Y,
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such as

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Novel nucleic acids and

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation;
AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY01602 and AAY11994 to AAY12260, respectively. The proteins given represent the
                                                                     Claim 34;
                                                                                                    New nucleic acids encoding cDNA libraries prepared from muscle, muscle and heart ti
                                                                                                                                                                                                                                                                                        01-AUG-1997;
                                                                                                                                                                                                                                                                                                                       31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                          11-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                         W09906554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 5' EST secreted protein SEQ ID NO: 540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY12227 standard; Protein; 55 AA.
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                                                                                                                                                                                        WPT; 1999-153784/13.
                                                                                                                                                                                                                       Duclert A, Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reproductive hormone regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 || |
379 wkevay1g 386
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tes 5; Conserv
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                                                                                                                                                                      AAX41060.
                                                                                                                                                                                                                                                        GENSET.
                                                                  Page 601; 622pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                         97US-0905134
                                                                                                                                                                                                                                                                                                                         98WO-IB01238
                                                                                                      heart tissue
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from kidney,
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                  immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; Alzheimer's disease; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive.
                                                                                                                                                                                                       19-NOV-1999; 99US-0166415.
30-JUN-2000; 2000US-0215136.
                                                                                                                                                                                                                                                      15-NOV-2000; 2000WO-US31162
                                                                                                                                                                                                                                                                                                                     WO200136432-A2
                                                                                                                                                                                                                                                                                                                                                                                 binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                            WPI; 2001-343793/36
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE04286 standard;
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                                                                                                                                                                        (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted protein; proliferative disorder; cancer; tumour; abnormality; developmental abnormality; haematopoietic di
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                                                                                                                                                                                                                                                                                                                                                                                   identification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.6%;
50.0%;
                                                                                                                                                                         SCI INC
                                                                                                                                          Baker KP,
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Disclosure; Page 39;

509pp;

English.

Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition

represent cDNAs corresponding

to

18

human secreted

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RESULT 1
AAM40407
ID AAM4
XX AAM4
AC AAM4
XX Huma
AC YAM
AC AAM4
XX Huma
KW Huma
KW Perii
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CC Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and CC immunosorbent assay (ELISA). The present sequence represents a human CC secreted protein fragment referred to in the disclosure of the invention.
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Best Local Similarity
   *19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                21-JAN-2000;
25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                                                                    26-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM40407 standard; Protein; 83 AA.
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                                                                                                                                                                                                                                                                                                                                 26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chemokinetic; thrombolytic; drug screening; arthritis; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The secreted proteins and their genes are useful for preventing,
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                                                            2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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                                                                                                                                                                                                                                                                    2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressant; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3552.
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50.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in gene therapy. A composition containing a polypoptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity schemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                           immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; proliferative disorder; cancer; tumou foetal abnormality; developmental abnormality; haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent \operatorname{did} not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442253/47.
N-PSDB; AAI59563.
                                                             Misc-difference
                                                                                                                                                                                                       binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE04281 standard; Protein; 113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; SEQ ID NO 3552; 10078pp; English.
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nes 4; Conserv
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                                                                                                                                                                                                                                         crine disorder; infection; wound hea
culture; chemotaxis; food additive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene 10 encoded secreted protein fragment, SEQ ID NO:145
                                                                                                                                                                                                       partner
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Wang Z,
Zhou P,
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                                                       Location/Qualifiers
                                                                                                                                                                                                          identification
/note= "Xaa equals any of the naturally occurring
                                 'label= Unknown
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50.0%;
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, Xu C,
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Pred. No.
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Xue AJ,
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; tumour;
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RESULT 1
AAY12226
SXSXEXX
SXSXEXX
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                                                                                                                                                                                                                                                                                                                                                                        A AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted CC AAE04240-AAE04297 represent human secreted protein fragments or variants. CC The secreted proteins and their genes are useful for preventing. CC The secreted proteins and their genes are useful for preventing. CC treating or amcliorating medical conditions, e.g., by protein or gene CC therapy. Pathological conditions can be diagnosed by determining the CC amount of the new protein in a sample or by determining the presence of CC amount of the new genes. Specific uses are described for each of the CC and include developing products for the diagnosis or treatment of CC proliferative disorders, cancer, tumours, foetal and developmental CC abnormalities, haematopoietic disorders, diseases of the immune system, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC cardiovascular disorders, angiogenic disorders, kidney disorders, and infections. The proteins can also be used to aid wound the healing and epithelial cell proliferation, to prevent skin ageing due to compate ligands or binding partners, and inchemotaxis, and can be used in alleviating symptoms associated with the disorders mentioned above, and compate immunessays e.g., radiommunoassay or enzyme linked CC antibodics specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and CC immunosorbent assay (ELISA). The present sequence represents a human cC secreted protein fragment referred to in the disclosure of the invention.
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Best Local Similarity
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30-JUN-2000; 2000US-0215136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-2000; 2000WO-US31162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 502; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM, Komatsoulis GA, Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                               18-JUN-1999
                                                                 AAY12226;
                                                                                                  AAY12226 standard; Protein; 114 AA.
                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                  113 AA;
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                               (first entry)
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                                                                                                                                                                                                                                                                           80.6%;
50.0%;
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Pred. No. 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for CC human secreted proteins, and encode the proteins given in AAY01602 and CC AAY11994 to AAY12260, respectively. The proteins given represent the CC signal peptide and an N-terminal fragment of a secreted protein. The CC nucleic acid sequences can be used for producing secreted human gene CC products. They can also be used to develop products for diagnosis and CC therapy. The proteins obtained may have cytokine activity, cell CC proliferation/differentiation activity, haematopoiesis regulating CC activity, tissue growth regulating activity, reproductive hormone CC regulating activity, chemotactic/chemokinetic activity, haemostatic and CC cativity, tumour inhibition activity or other activity, anti-inflammatory CC activity, tumour inhibition activity or other activities. The products CC can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 34; Page 600-601; 622pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duclert A, Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                 16-OCT-2001
                                                                                   AAM25829;
                                                                                                                   AAM25829 standard; Protein; 126
                                                                                                                                                                                                    30 wktssyvg
                                                                                                                                                    16
                                                                                                                                                                                                                                    1 wkxxayxg 8
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                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide into a membrane, or importing a polypeptide into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ú
                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                        Conservative
                                               (first entry)
                                                                                                                                                                                                      37
               sequence SEQ
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                                                                                                                                                                                                                                                                                                                                                         AA;
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                                                                                                                                                                                                                                                                                         80.6%;
50.0%;
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Pred. No. 65;
1; Mismatches
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                                                                                                                     ĀĀ
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                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                         Length 114;
                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                        Gaps
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Human protein

ID NO: 1344.

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CC AAM25963. The proteins can have activities based on the tissues and CC AAM25963. The proteins can have activities based on the tissues and CC cells they are expressed in, such as: antiinflammatory; antirheumatic; CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; CC central nervous system; virucide; anti-HIV; fungicide; antimutagen; CC cardiovascular; antianemic; antiaggregant; haemostatic; vulnerary; CC antiulcer; osteopathc; demantological; antiallergic; antiasthmatic; CC antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; CC antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; CC antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; CC encoding them can be used in gene therapy, antisense therapy and vaccine CC groduction, The proteins and polynucleotides are useful for screening for CC agonists or antagonists of a protein and for the treatment and diagnosis CC of disorders associated with the activity of a protein e.g. inflammation, CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, CC contents of a cardiac dysfunction, autoimmunity, genetic diseases, haematopoietic disorders, antaponia, nurse, ulloars, thromboortropaonia, nurse, ulloars, and contents thromboortropaonia, nurse, ulloars, and contents thromboortropaonia, nurse, ulloars, and contents thromboortropaonia.
                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; alienses; Parkinson's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                          anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                           neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-457603/49
N-PSDB; AAH99770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999;
21-JAN-2000;
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                                              * 1 wkxxayxg 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2001
                                                                                                                     Local Similarity
  73
wkqssyag 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Page 278; 1217pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                               126 AA;
                                                                                            Conservative
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2000US-0488725.
2000US-0552317.
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                                                                                                                80.6%;
                                                                                                             Score 29; DB
Pred. No. 72;
                                                                                            Mismatches
                                                                                                                                      DB
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                                                                                                                                   Length 126;
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Conservative

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Gaps

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80.6%; 50.0%;

Score 29; DB Pred. No. 72; Mismatches

22;

Length 126; Indels

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RESULT 17
AAM42193
IDM AAM421
XX AAM421
XX AAM421
XX AAM421
XX AAM421
XX Human;
XX Human;
XX Human;
XX Human;
XX Human;
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XX Human;
XX Human;
XX Leukae
XX Homo s
PN W02001
XX 26-DEC
XX 26-DEC
XX 26-DEC
XX 27-JAN
PR 25-DEC
XX 26-DEC
XX 27-JAN
PR 25-DEC
XX 26-DEC
XX 27-JAN
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XX 27-JAN
PR 25-DEC
XX 27-JAN
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Query Match
Best Local Similarity
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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-OCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                 immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                               C.N.S disorders. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-442253/47.
N-PSDB; AAI61349.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; SEQ ID NO 7124; 10078pp; English.
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Wang Z,
, zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYSEQ INC
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Yang Y,
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Zhang J;
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          The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoletic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzhelmer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive;
                                                                                                                                                                                                AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants.
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                                                                                                                                                                                                                                                                  Claim 11; Page 459; 509pp; English.
                                                                                                                                                                                                                                                                                                     used
                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid molecule encoding a human secreted protein
                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                 in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                     2001-343793/36.
                                                                                                                                                                                                                                                                                                                                                                                                        SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                      Komatsoulis
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2000US-0215136.
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25..140
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developmental abnormality; haematopoietic disorder;
cognitive disorders,
                                                                                                                                                                                                                                                                                                                                                                                                      GA,
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RESULT :
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; diagnosis; identification; cytostatic; neuroprotective nootropic; immunomodulatory; relaxant; contraceptive; gynaecolog antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic neural; immune system; muscular; reproductive; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  skin disorders (e.g., psoriasis), sepsis, diabetes, atl cardiovascular disorders, angiogenic disorders, kidney
AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contracepy gynaecological, cardiant and antiinflammatory activities, and can
                                                                                                       Claim
                                                                                                                                                      New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pancreatic cancer antigen protein sequence SEQ ID NO:504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB54052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB54052 standard; Protein; 155
                                                                                                                                         cancer,
                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                 Rosen
                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                    12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200055320-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pulmonary; cardiovascular; renal; proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 wktssyvg 37
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                                                                                                                                                                                                            2000-579444/54.
DB; AAC98817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                               CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pancreas; pancreatic cancer; pancreatic cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                         or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                       Page 942-943; 1379pp; English
                                                                                                                                                                                                                                                                 Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                      2000WO-US05989
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Pred. No.
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                                                                        cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective;
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13-NOV-1997;
17-DEC-1997;
AAY36129-Y36222 represent novel human secreted proteins encoded by the extended cDNA sequences represented in AAX97813-X97906. The proteins of the invention have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of
                                                                                                                                                                                                                                                                                                                                 WPI; 1999-347472/29.
N-PSDB; AAX97818.
                                                                                                                                                                                                                                                       Extended cDNAs encoding secreted proteins
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13-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic; gene therapy; chromosome mapping; secretion vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic;
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                                                                                                                                                                                     Page 234-235;
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97US-0066677.
97US-0069957.
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| 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 |
| 6. | 6. | φ. | <u>ი</u> | 9 | σ, | 66.7 | 6. | 9 | 9 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 | 69.4 |
| 422 | 422 | 422 | 422 | 422 | 345 | 345 | 222 | 1663 | 1663 | 1663 | 1620 | 1620 | 645 | 556 | 554 | 464 | 432 | 344 | 344 | 237 | 237 | 237 |
| ហ | 4 | ω | ω | N | 4 | ω | 4 | 4 | 4 | N | 4 | <u>,</u> | ۳ | ш | ب | N | N | ນ | Ν | 4 | 4 | N |
| PCT-US94-01826A-6 | 186-414 | US-08-479-869-6 | US-08-477-459-6 | US-08-484-575A-6 | US-09-222-786-2 | US-09-222-817-2 | US-09-140-804-7 | US-09-142-334-22 | US-09-132-271-1 | US-08-793-126-1 | US-09-100-089-2 | US-08-542-363-2 | US-07-779-172A-3 | US-08-445-586-2 | US-08-445-586-7 | US-09-021-323-3 | US-08-677-049-8 | US-07-857-224B-93 | US-07-857-224B-92 | US-09-196-131-16 | us-09-196-131-2 | US-08-417-226-16 |
| Sequence 6, Appl | Sequence 6, Appl | Sequence 6, Appl. | Sequence 6, Appl | Sequence 6, Appl | Sequence 2, Appl | Sequence 2, Appl | Sequence 7, Appl. | Sequence 22, App. | Sequence 1, Appl | Sequence 1, Appl | Sequence 2, Appl | Sequence 2, Appl | Sequence 3, Appl | Sequence 2, Appl | Sequence 7, Appl | Sequence 3, Appl | Sequence 8, Appl | • | • | Sequence 16, App | Sequence 2, Appl. | Sequence 16, App |

ALIGNMENTS

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RESULT 1
US-08-608-241-2
                                                                    ; MOLECULE TYPE: protein US-08-608-241-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Patent No.
                                                                                                      TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
TYPE: amino acid
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dononue, Lincoll, APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
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STREET: 1 South Pinckney Street
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 75.0%;
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 Score
Pred.
 27;
No.
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 DB 1;
1.9e+02;
                 Length 376;
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US-08-919-953-2
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                                                                                                       Sequence 2, Application US/08919953 Patent No. 5837481
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acid
       APPLICANT: Donohue, Timothy
APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBLY
TITLE OF INVENTION: SENSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 608-251-5000
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PRIOR APPLICATION NUMBER:
 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                  316 WKGSAFGG 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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CITY: Madison
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Barber, Robert
                                                                                                                                                                                                                                                              Conservative
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50.0%;
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            MICROBIAL SYSTEM FOR FORMALDEHYDE SENSING AND REMEDIATION
                                                                         Timothy J
SENSING AND 7
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Pred. No. 1
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APPLICANT: Donohue, Timothy
APPLICANT: Barber, Robert
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: Microbial System for Formaldehyde Sensing and
TITLE OF INVENTION: Remediation
FILE REFERENCE: 960296.95505
CURRENT APPLICATION NUMBER: US/09/192,983A
CURRENT TILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/919,953
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 08/608,241
EARLIER FILING DATE: 1996-02-28
NUMBER OF SEQ ID NOS: 7
                                                                                                        ; ORGANISM: Rhodobacter sphaeroides US-09-192-983-2
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Best Local Similarity
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Query Match
Best Local Similarity 50...
Conservative
                                                                                                                                                    SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 376
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09192983A Patent No. 6242244
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                        TYPE: PRT
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MEDIUM TYPE: Floppy
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REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
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OPERATING SYSTEM:
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CITY: Madison
STATE: WI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/608,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 wkxxayxg 8
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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50.0%;
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50.0%;
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Pred. No. 1.9e
1; Mismatches
                    Score 27; DB 4; Le Pred. No. 1.9e+02; 1; Mismatches 3;
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..9e+02;
3;
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                       Indels
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                       0;
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                       Gaps
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                       0;
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wkxxayxg

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RESULT 6
US-08-637-759B-89
: Sequence 89, Application US/08637759B
: Patent No. 5876931
: GENERAL INFORMATION:
: APPLICANT: David William Holden
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US-07-857-224B-84
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US-07-857-224B-84
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SEQUENCE CHARACTERISTICS:
LENGTH: 374
                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: (note: this is an international post code) CH-8092 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Benner, Stev
TITLE OF INVENTION: Pro
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                       314 WKGAIYGG 321
                                                                                                                                                                                                                                                                                                  PAGES: 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntos
                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Joernvall, H.
AUTHORS: Porsson, M.
AUTHORS: Jeffery, J.
TITLE: Alcohol dehydrogenases
                                                                                                                                                                                                                 Local Similarity 50.
                                                                                                                                                                                                                                                                                                                                         VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS:
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o. 5958784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               M: human
Alcohol dehydrogenase,
                                                                                                                                                                                                                                                                                                                            4226-4230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          none
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                                                                                                                                                                                                                                                                                                                                                       Proceedings of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steven A. Benner
dlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steven A.
                                                                                                                                                                                                                                72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MacIntosh 7.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84:
                                                                                                                                                                                                                                                                                                                                                      the National Academy of Sciences, USA
                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                Score 26; DB 2;
Pred. No. 3e+02;
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Table 3 Column
                                                                                                                                                                                                                                             Length 374;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                Gaps
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; MOLECULE TYPE:
; HYPOTHETICAL:
US-08-637-759B-89
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                                                                                                                                                                                                                                                                                                      Patent No. 6015669
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       Sequence 89, Application US/08871355A Patent No. 6015669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (404) 873-879
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: PABSE, PALTES I.
REGISTRATION UNMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Genes NUMBER OF SEQUENCES: 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
FILING DATE: 11-DEC-
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
STREET:
CITY: A
                                                                                                                                                                                ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                   COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                  CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                         30 WKPAAFQG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 03-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
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                                                                                                                                                   Georgia
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1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           759 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (404) 873-8795
                                                                                                                                                                                                                                                                                    David William Holden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-1995
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50.0%;
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US/08/871,355A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 2;
Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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PRIOR APPLICATION DATA:

CLASSIFICATION:

FILING DATE:

09-JUN-1997

APPLICATION NUMBER: FILING DATE: 11-DEC

11-DEC-1995

PCT/GB95/02875

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US-08-970-269A-29
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Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/08970269A Patent No. 5976803
                                                                                                                   TELEFAX: 713-777-6908 INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO:
TOPOLOGY: 11
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2987 amino acids
                                                                                                                                                                                                                                                 COMPUTER: APP1e

OPERATING SYSTEM: Macintosh
SOSTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,269A
FILING DATE: NO. 5976803ember 14, 1997
CLASSIFICATION: 435
                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 713-777-2321
                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Katheryn Meek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 759 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Genetic Test For Equine Severe TITLE OF INVENTION: Combined Immunodeficiency Disease
                                               STRANDEDNESS:
                                                                                                                     TELEPHONE: /13 777-6908
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 8011 (CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 77071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 WKPAAFQG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: li
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                                                                              LENGTH:
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                                                                amino acid
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8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  759 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           دع: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                 linear
               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.2%;
50.0%;
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Pred. No. 5.6e+02;
1; Mismatches 3
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US-09-407-562-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/09407562 Patent No. 6294334 GENERAL INFORMATION:
                                                      Matches
                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                  TELEFAX: 713-777-6908 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2840 WKSLAY 2845
                                                                                                                                         ANTI-SENSE: no ORIGINAL SOURCE: FEATURE:
                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL: I
ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/970,269
FILING DATE: No. 6294334ember 14,
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: no
ORIGINAL SOURCE:
2840 WKSLAY 2845
                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2987 amino acids
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: D5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UC
                                                                                                                                                                                                                                                                                    TELEPHONE: /13 ... 713-777-6908
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: CLASSIFICATION:
                                                                  Local Similarity
                          1 wkxxay 6
                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/407,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 8011 CCITY: Houston
                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Katheryn Meek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                      Conservative
                                                                                                                                                                                                                linear
                                                                                                                                                                                    no
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                                                                  72.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetic Test For Equine Severe
Combined Immunodeficiency Disease
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66.7%;
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                                                                                                                                                                                                                                                                                    29:
                                                      Score 26; DB Pred. No. 1.9 0; Mismatches
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Pred. No. 1.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                1997
                                                                   .9e+03;
                                                                                 Length 2987;
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                                                        Indels
                                                        0;
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                                                      Gaps
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                                                        0;
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US-09-407-562-30
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Patcot No. 5976803
GENERAL INFORMATION:
APPLICANT: Katheryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             Sequence 30, Application US/09407562 Patent No. 6294334
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple
                                                                                                                                                                                                                                                                                                                                                                           2840 WKSLAY 2845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: D5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple
                                                                                                                                                       APPLICANT: Katheryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microsoft word for Macintosh CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: no ANTI-SENSE: no
                                                                                                        STREET: 8011 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple
OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 77071
                                                        COUNTRY: U
                                                                                             STATE:
                                                                                                                        ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: No. 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                            1 wkxxay 6
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4; Conserv
                                                                                         Texas
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8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3959 amino acid
                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 5976803ember 14, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.2%;
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Pred. No. 2.5e+03;
0; Mismatches 2;
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RESULT 12
US-08-993-228-14
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/993,228
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: p:
HYPOTHETICAL: no
ANTI-SENSE: no
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NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2840 WKSLAY 2845
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APPLICATION NUMBER: 08/970,269
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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SOFTWARE: Microsoft Word for Macintosh
                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                             STREET: 87 Cambi
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CLASSIFICATION:
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                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
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02140
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5976838
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                                                                                                                                                                                                                                                                             87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Racie, Lisa A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCoy, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LaVallie, Edward R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                 Genetics Institute, Inc.
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66.7%;
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; Pred. No. 2.5e
0; Mismatches
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2.5e+03;
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TELECOMMUNICATION INFORMATION:

TELEPHONE:

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; STRANDEDNESS: TOPOLOGY: linear; MOLECULE TYPE: protein US-08-993-228-14
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US-07-971-160-4
; MOLECULE TYPE: peptide US-07-971-160-4
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Best Local Similarity 50.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                  TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/879,689

PILING DATE: 05-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: Ogden, Stasia L.

REGISTRATION NUMBER: 36,228
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Plessis, Anne
APPLICANT: Thierry, Agnes
TITLE OF INVENTION: Nucleotide
TITLE OF INVENTION: I-SCEI and
NUMBER OF SEQUENCES: 52
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: UPFILING DATE: 19921105
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 WKHVRYRG 58
                                                                                                                                                    REFERENCE/DOCKET NUMBER: 034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
                               TOPOLOGY:
                                                             LENGTH:
                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                            amino acid
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(617) 876-807
                                                                 235 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fairhead, Cecile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colleaux, Laurence
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                                                                                                                  202-408-4400
                               linear
                                                                                                                                    202-408-4000
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Pred. No.
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the Uses
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RESULT 15
US-08-465-273-4
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US-08-336-241-4
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Best Local Similarity 66./
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                                                                                                                        Matches
                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/336,241
FILING DATE: 07-NOV-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,160
FILING DATE: 05-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/879,689
APPLICATION NUMBER: US 07/879,689
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                                                                                                                                                                                                                                                                                          TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                     NAME: POTTER, Jane E.R. REGISTRATION NUMBER: 33,332 REFERENCE/DOCKET NUMBER: 03 TELECOMMUNICATION INFORMATION: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nicolas, Jean-Francois
TITLE OF INVENTION: Nucleotide Sequence Encoding the Enzyme
Lent No. 5792632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: I-SCEI and the Uses Thereof NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1300 I STATE: D.C.
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                                                             62 WKNKAY 67
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                                                                                                                      Similarity 4; Conserv
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1300 I Street, N.W.
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Dujon, Bernard
                                                                                                                        Conservative
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                                                                                                                                      69.4%;
66.7%;
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66.7%;
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Pred. No. 3.1e+02;
0; Mismatches 2;
                                                                                                                                      Score 25;
Pred. No.
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                                                                                                                     Length 235
                                                                                                                                                   Length 235;
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; Sequence 4, Application US/08465273

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                                                                                                                                                                     RESULT
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Matches
                                                                                                             Sequence 4, Applic Patent No. 5948678
                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US 08/336,241
FILING DATE: 07-NOV-1994
CLASSIFICATION 1800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,160
APPLICATION NUMBER: US 07/971,160
FILING DATE: 05-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/879,689
FILING DATE: 05-MAY-1992
FILING DATE: 05-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5866361
TITLE OF INCENTION: I-SCEI and the Uses Thereof NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                  GENERAL INFORMATION:
APPLICANT: Choulike, Andre
APPLICANT: Perrin, Arnaud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495-0111-06000
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Nucleotide Sequence Encoding the Enzyme
APPLICANT: Nicolas, Jean-Francols
TITLE OF INVENTION: Nucleotide Sequence Encoding the Enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
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                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1300 I S
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                            62 WKNKAY 67
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Potter, Jane I REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                               1 wkxxay 6
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                                                                                                                                Application US/09119024
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Dujon, Bernard
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                                     Perrin, Arnaud
Dujon, Bernard
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                                                                                                                                                                                                                                                                                                                                                                                                               peptide
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                                                                                                                                                                                                                                                                                                                      69.48;
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Pred. No. 3.1e+02;
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Best Local S
Matches 4
                                                                                                                                              TITLE OF INVENTION: Nucleotide Sequence Encoding the Enzyme Patent No. 5962327
TITLE OF INVENTION: I-SCEI and the Uses Thereof
                                                                                                                                                                                                                                                                            Sequence 4.
Patent No.
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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FILING DATE: 07-NOV-1994
APPLICATION NUMBER: US 07/
FILING DATE: 05-NOV-1992
PRIOR APPLICATION DATA:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 235 amino acid
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                                                                                                              NUMBER OF SEQUENCES: 5
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                                                            ADDRESSEE: Finnegan, Hender
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 66. 
nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: POtter, Jane E.R. REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                             CITY: Washington STATE: D.C.
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                 COUNTRY:
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20005-3315
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1300 I Street, N.W.
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Dujon, Bernard
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                                                                                           Finnegan, Henderson,
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Pred. No. 3
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                                                                                                Farabow, Garrett
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COMPUTER READABLE FORM:

MEDIUM TYPE:

OPERATING SYSTEM: SOFTWARE: Patent!

PatentIn Release #1.0, Version #1.25

:: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS

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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-417-226-4
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                                                                                                                                                                                                                                                                                                                                            Patent No. 6238924
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APPLICANT: Choulika, Andre
APPLICANT: Perrin, Arnaud
APPLICANT: Dujon, Bernard
APPLICANT: Nicolas, Jean-
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                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: I-SCEI and the Uses Thereof NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07
FILING DATE: 05-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 05-MAY-1992
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/336,241
FILING DATE: 07-NOV-1994
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APPLICATION NUMBER: US,
FILING DATE: 05-APRIL-
              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Nicolas, Jean-Francois
TITLE OF INVENTION: Nucleotide Sequence Encoding the Enzyme
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LENGTH: 235 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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                                                                                                                                                                       STREET: 1300 I STREET: Washington STATE: D.C.
                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                  ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
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APPLICATION NUMBER:
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us/09/196,131
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Pred. No. 3.1e+02;
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RESULT 19
US-07-971-160-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                       APPLICATION NUMBER: US/07/971,160
FILING DATE: 19921105
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/879,689
FILING DATE: 05-MAY-1992
                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                       FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                       STREET: 1300 I St
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                            NAME: Ogden, Stasia L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                            STATE:
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               REFERENCE/DOCKET NUMBER:
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1300 I Street, N.W.
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VENTION: Nucleotide
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                                                                                                                                                                                                   IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                       Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.4%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                     I-SCEI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        us 07/879,689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08/417,226
                            36,228
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               03495-0111-01000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 4;
Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Encoding the Enzyme the Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

WEDIUM TYPE: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION OF 19921105
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/879,689
FILING DATE: 19921109:
APPLICATION NUMBER: US 07/879,689
FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: 03495-0111-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
INFORMATION ENGRES 10 NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: peptide
US-07-971-160-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 202-408-4000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
TYPE: amino acid
HOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-971-160-2
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US-07-971-160-16
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/07971160 Patent No. 5474896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 69.4%; Score 25; DB 1; Length 237; Best Local Similarity 66.7%; Pred. No. 3.1e+02; Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dujon, Bernard
APPLICANT: Choulika, Andre
APPLICANT: Choulika, Andre
APPLICANT: Colleaux, Laurence
APPLICANT: Pairhead, Cecile
APPLICANT: Perrin, Arnaud
APPLICANT: Piessis, Anne
APPLICANT: Thierry, Agnes
TITLE OF INVENTION: Nucleotide Sequence Encoding the Enzyme
TITLE OF INVENTION: 1-SCEI and the Uses Thereof
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1300 I St
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
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    69.4%;
66.7%;
Score 25; DB 1; Length 237; Pred. No. 3.1e+02;
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Search completed: January 14, 2002, 07:23:42 Job time: 73 sec

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Result
No.
                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries
                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                             seq
    protein search,
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length: 2000000000
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Query
Match
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35
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pir2:*
pir3:*
pir4:*
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    GenCore version 4.5 (c) 1993 - 2000 Comm
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JC4967
S51187
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D70475
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                                                                                    DERTA
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                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compugen Ltd
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9.586 Million cell update
major 25k outer me cerebellin-like gl probable Serine/Th clathrin-associate prostaglandin-endo prostaglandin-endo prostaglandin-endo light-harvesting palcohol dehydrogen alcohol dehydrogen
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| 50 | 49 | 48 | 47 | 46 | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω ω | 32 | 31 | 30 |
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| 26 | 26 | 26 | 26 | 26 | 26 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 |
| 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 |
| 246 | 224 | 200 | 199 | 159 | 135 | 1956 | 1083 | 733 | 599 | 441 | 415 | 415 | 396 | 386 | 381 | 381 | 381 | 379 | 379 | 379 |
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| T32510 | B85584 | T02779 | TJBPKL | QQCV2 | JQ1225 | T16416 | S54293 | S33643 | T18316 | B84854 | C72026 | A86599 | S31959 | S31140 | T04164 | T03289 | JN0447 | A71479 | H81741 | D81515 |
| hypothetical prote | probable tail comp | y4dP protein - Rhi | tail assembly prot | - | UncI protein homol | hypothetical prote | regulator protein | transforming prote | hypothetical prote | hypothetical prote | rod shape protein | rod shape protein | acyl-[acyl-carrier | alcohol dehydrogen | formaldehyde dehyd | formaldehyde dehyd | alcohol dehydrogen | probable rod shape | cell shape-determi | cell shape-determi |

ALIGNMENTS

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A; Molecule type: DNA
A; Residues: 1-528 <PAR>
A; Cross-references: EMB
                                                       A;Reference number: Z16918
A;Accession: T45418
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                phosphoglycerate dehydrogenase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                  RESULT
T45418
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G70854
                                                                                                                          submitted to the EMBL Data
                                                                                                                                           C; Accession: T45418
R; Parkhill, J.; Barrell, B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL021287; GB:AL123456; NID:g3261508; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-528 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.;
A;Title: Deciphering the biology of Mycobacterium
A;Reference number: A70500; MUID:98295987
A;Accession: G70854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: G70854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable serA protein - Mycobacterium tuberculosis (strain H37RV)
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :Genetics:
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    EMBL: 299263;
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62.5%;
                                                                                                                        Library, Septem
    PIDN:CAB16440.1
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 528;
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cosmid B637

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C;Accession: A35512; A25223; A24421; A33081
R;Birchmeier, C.; O'Neill, K.; Riggs, M.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 4799-4803, 1990
A;Title: Characterization of ROS1 cDNA from a human glioblastoma A;Reference number: A35512; MUID:90280463
A;Accession: A35512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein aq_2044 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000
C;Accession: D70475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: C; Genetics:
A; Note: serA
C; Superfamily: Bacillus
                                                                                                           A; Title: Human c-ros-1 gene homologous to A; Reference number: A25223; MUID:87064611 A; Accession: A25223
                                                                                                                                                                         A; Experimental source: glioblastoma cell line SW-1088 R; Matsushime, H.; Wang, L.H.; Shibuya, M. Mol. Cell. Biol. 6, 3000-3004, 1986
                                                                                                                                                                                                                                         A;Molecule type: mrNA
A;Residues: 1-2212,'N',2214-2227,'QC',2229-2347 <BIR>
A;Cross-references: GB:M34353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; molecule type: DNA
A; Residues: 1-392 <AQF>
A; Cross-references: GB: AE000769; NID: g2984262; PIDN: AAC07799.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666
A;Accession: D70475
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Cross-references: GB:M13368
A;Experimental source: placen
A;Note: the differences after
                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 07-Oct-1994 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase-related protein ros-1 precursor - human
N;Alternate names: protein-tyrosine kinase mcf3 (activated ros-1)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) ros-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: D70475
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 멍
                                                                    A; Molecule type: DNA
A; Residues: 1790-2245, 'KFDSSEFSSFRCTVN'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 392,
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5; Conser
                         source: placenta
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    after residue
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62.5%;
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Pred. No.
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    2245 result from
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                                                                                                                                                         the v-ros sequence of UR2 sarcoma virus
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46;
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    the authors'
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    misinterpretation
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F;335-378/Domain: LDL receptor YWTD-containing repeat homology <YWA>
F;466-503/Domain: LDL receptor YWTD-containing repeat homology <YWA>
F;715-757/Domain: LDL receptor YWTD-containing repeat homology <YWA>
F;715-757/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;758-798/Domain: LDL receptor YWTD-containing repeat homology <YW4>
F;483-888/Domain: LDL receptor YWTD-containing repeat homology <YW4>
F;843-888/Domain: LDL receptor YWTD-containing repeat homology <YW5>
F;893-933/Domain: LDL receptor YWTD-containing repeat homology <YW5>
F;1532-1574/Domain: LDL receptor YWTD-containing repeat homology <YW6>
F;1532-1574/Domain: LDL receptor YWTD-containing repeat homology <YW6>
F;1543-247/Domain: transmembrane #status predicted <TMN>
F;1884-2347/Domain: intracellular #status predicted <INT>
F;1943-2222/Domain: protein kinase homology <KIN>
F;1943-2222/Domain: protein kinase ATP-binding mottif
F;52,114,123,324,352,471,607,628,706,714,732,939,961,1015,1087,1090,1211,1272,1330,14
F;1980/Active site: Lys #status predicted
F;1980/Active site: Lys #status predicted
F;19160/Active site: Lys #status predicted
F;19160/Active site: Lys #status predicted
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A:Introns: 1853/1; 1881/1; 1926/2; 1980/3; 2002/2; 2045/3; 2078/2; 2145/2; 2190/2
C:Superfamily; kinase-related protein ros; LDL receptor YWTD-containing repeat hom C:Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming pr C:Keywords: Signosin: signal sequence #status predicted <Signosin: signal sequence #status predicted <Signosin: kinase-related protein ROS1 #status predicted <MAT>
F:37-1859/Domain: extracellular #status predicted <EXTP
                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Urade, Y.; Oberdick, J.; Molinar-Rode, R.; Morgan, J.I.
Proc. Natl. Acad. Sci. U.S.A. 88, 1069-1073, 1991
A;Title: Precerebellin is a cerebelline-specific protein with similarity to the globul A;Reference number: A37873; MUID:91126057
A;Accession: A37873
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A; Residues: 1854-2261, 'A', 2263-2347 <BI2>
A; Cross references: GB:M13880; NID:9337482;
A; Experimental source: tumor cells
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A; Title: Characterization of an activated
A; Reference number: A24421; MUID:87064625
                                                                                                                                                                                                                                                             A;Cross-references: GB:M58583; NID:9180250; PIDN:AAA35676.1; PID:9180251
C;Superfamily: complement subcomponent Clq chain A; complement Clq carbo
F;63-192/Domain: complement Clq carboxyl-terminal homology <ClQ>
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A;Cross-references: GDB:120351;
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A; Residues: 1-193 <UR
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Mol. Cell. Biol.
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180 WKYSTFSG 187
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                                                                                                                       Score 28; DB Pred. No. 39; 1; Mismatches
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cerebellin-like glycoprotein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993
C;Accession: A60032
R;Moda, C:, Ohtani, H.
Brain Res. Mol. Brain Res. 9, 71-77, 1991
A;Title: Molecular cloning of rat cerebellin-like pa;Reference number: A60032; MUID:91203483
                                                      A;Title: Molecular cloning of A;Reference number: A60032; A;Accession: A60032
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R;White, O.; Elsen, J.A.; Heldelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896
A;Accession: H75258
                                                                                                                                                                                                                                            A60032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-213 <DEA>
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A;Title: Cloning and nucleotide sequence of the gene coding fareference number: A56152; MUID:95204367
A;Accession: A56152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            major 25k outer membrane protein precursor - Brucella abortus
                               A:Status: not compared with conceptual translation
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A;Experimental source: strain R1
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A; Residues: 1-206 <WHI>
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C;Species: Dainococcus radiodurans
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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Molecule type: mRNA Residues: 1-224 <WA
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Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 08-Oct-1999
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Utterback, T.; Zalewski,
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clathrin-associated protein complex medium chain · yeast (Saccharomyces cerevisiae) N;Alternate names: protein P0394; protein YPL259c C;Species: Saccharomyces cerevisiae C;Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 20-Jun-2000 C;Accession: S65290; S65292; S19692; S17028 R;Messenguy, F.; Dubois, E.; Vierendeels, F.; Scherens, B. submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
                   A;Cross-references: EMBL:Z73615; NID:g1370535; PIDN:CAA97989.1; PID:g1370536; MIPS:YPA;Experimental source: strain S288C (A8972)
R;Duesterhoeft, A.; Floeth, M.; Fritz, M.; Hilbert, H.; Moestl, D. submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
S65290
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C; Superfamily: clathrin
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                                                                                                                               A; Molecule type: DNA
A; Residues: 1-475 <MES>
                                                                                                                                                                                    A; Reference number: S64935
A; Accession: S65290
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-428 <STO>
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1; Mismatches
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Pred. No.
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83;
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Maiti, R.; Me
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A; Molecule type: DNA
A; Residues: 305-475 < DUE>
A; Cross-references: EMBL:273615; MIPS:YPL259c
A; Cross-references: Extrain $288C (AB972)
R; Nakayama, Y; Goebl, M; O'Brine Greco, B; Lemmon, S; Pingchang Chow, E; Kirchl
R; Nakayama, Y; Goebl, M; O'Brine Greco, B; Lemmon, S; Pingchang Chow, E; Kirchl
R; Title: The medium chains of the mammalian clathrin-associated proteins have a home
A; Reference number: $19692; MUID:92104180
A; Recession: $19692
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-213, 'I', 215, 'H', 217-221, 'K', 223-421, 'S', 423-475 < NAK>
A; Cross-references: EMBL:X60288
R; Makayama, Y; Goebl, M; O'Brine Greco, B; Lemmon, S; Pingchang Chow, E; Kirchl
S; Submitted to the EMBL Data Library, September 1991
A; Description: The medium chains of the mammalian clathrin associated proteins have
A; Recession: $17028
A; Roclecule type: DNA
A; Residues: 1-213.'I', 215, 'H', 217-221, 'K', 223-432, 'R', 434-439, 'M', 441-449, 451-475 < Nakayama, Y; Cross-reference number: $17028
A; Roclecule type: DNA
A; Residues: 1-213.'I', 215, 'H', 217-221, 'K', 223-432, 'R', 434-439, 'M', 441-449, 451-475 < Nakayama, Y; Cross-reference number: $17028
A; Roclecule type: DNA
A; Residues: 1-213.'I', 215, 'H', 217-221, 'K', 223-432, 'R', 434-439, 'M', 441-449, 451-475 < Nakayama, Y; Cross-reference number: $17028
A; Roclecule type: DNA
A; Residues: 1-213.'I', 215, 'H', 217-221, 'K', 223-432, 'R', 434-439, 'M', 441-449, 451-475 < Nakayama, Y; Cross-reference number: $17028
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A;Residues: 1-213,'I',215,'H',217-221,'K',223-432,'R',434-439,'M',441-449,451-475
A;Cross references: EMBL:X60288; NID:g4799; PIDN:CAA42828.1; PID:g4800
C;Genetics:
                        RESULT
A28960
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C;Keywords: oxidoreductase
F;1-23/Domain: signal sequence #status predicted <SIG>
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J. Biol. Chem. 263, 3550-3553, 1988
A;Title: Isolation and characterization of the complementary DNA
A;Reference number: A29947; MUID:88153641
A;Accession: A29947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - sheep N;Alternate names: prostaglandin endoperoxide synthetase C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep) C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 10-D C:Accession: A29947
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A;Cross-references: SGD
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C;Superfamily: human prostaglandin-endoperoxide synthase;
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A; Residues: 1-599 <MER>
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prostaglandin-endoperoxide synthase (EC 1.14.99.1) G/H precursor -
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R;DeWitt, D.L.; Smith, W.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1412-1416, 1988
A;Title: Primary structure of prostaglandin G/H synthase
A;Reference number: A28960; MUID:88144447
A;Accession: A28960
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C;Superfamily: human prostaglandin-endoperoxide synthase;
C;Keywords: oxidoreductase
F;36-69/Domain: EGF homology <EGF>
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C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 10-Dec-1999
C;Accession: A28960
R;DeWitt, D.L.; Smith, W.L.
                                                                                                                                                                                                                                         ugnt-narvesting protein alpha chain - Ectothiorhodospira halochloris
N;Alternate names: antenna pigment protein alpha chain
C;Species: Ectothiorhodospira halochloris
C;Date: 19-Mar-1997 #sequence revision 10-M-1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Y00750; NID:g1361; PIDN:CAA68719.1; PID:g1362
A;Note: part of this sequence, including the amino end of the mature protein, was A;Note: 97-His, 164-Gly, 456-Gln, 520-Gln, 520-Lys, and 525-Ile were also found C;Superfamily: human prostaglandin-endoperoxide synthase; EGF homology C;Keywords: oxidoreductase
E;1-24/Domain: signal sequence #status predicted <SIG>
F;25-600/Product: prostaglandin-endoperoxide synthase #status experimental <MAT>
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A; Residues: 1-600 < DEW>
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A;Accession: S00561
                                                                                                                           Eur. J. Biochem. 205, 917-925, 1992
A;Title: The primary structure of the antenna polypeptides of Ectothiorhodospira halo
A;Reference number: S23164; MUID:92249336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Yokoyama, C.; Takai, T.; Tal
FEBS Lett. 231, 347-351, 1988
C;Superfamily: light-harvesting protein alpha chain
C;Keywords: antenna complex; bacteriochlorophyll; blocked
                                            A; Molecule type: protein A; Residues: 1-65 < WAG>
                                                                                                                                                                        R;Wagner-Huber, R.; Brunisholz, R.A.; Bissig, Eur. J. Biochem. 205, 917-925, 1992
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Pred. No. 1.2e+02;
1; Mismatches 3
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                                                                                                                                                                                                       G.; Suter, F.;
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end; light-harvesting

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C; Genetics:
A; Gene: soxA
C; Keywords:
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A:Residues: 1-168 <LUE>
A:Cross-references: EMBL:X62643;
                                                                                                                                                                                                                       A;Title: An archaebacterial A;Reference number: S21041; A;Accession: S21041
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                                                                                                                                                                                                                                                                                                                                             cytochrome-c oxidase (EC 1.9.3.1) chain II -
C:Specles: Sulfolobus acidocaldarius
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A;Molecule type: DNA
A;Residues: 1-126 <KUE>
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                                                        Query Match
Best Local
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Date: 13-Jan-1996 #sequence_revision 01-Mar-1996
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28;
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A;Accession: S00324
A;Accession: S00324
A;Molecule type: protein
A;Residues: 128-170 <MATS>
C;Superfamily: subtilisin; subtilisin homology
C;Keywords: extracellular protein; hydrolase; ser
F;1-14/Domain: signal sequence #status predicted
F;15-127/Domain: propeptide #status predicted <PR
F;128-408/Product: aqualysin I #status experiment
F;157-364/Domain: subtilisin homology <SBT>
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Best Local Similarity
A; Conserv
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A; Residues: 1-513 <TER>
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A; Map position:
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A; Residues: 1-206 <WHI>
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50.0%;
               I #status experimental <MAT>
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A;Cross-references: GB:J90108; GB:D90108; GB:J05414; NID:g217171; PIDN:BAA14135.1; PI A;NOte: the authors translated the codon CTG for residue 470 as Val, and GGT for resilue 470 as Val, and GGT for resilue 7. St.; Terada, I.; Matsuzawa, H.; Ohta, T.

Eur. J. Blochem. 173, 491-497, 1988
A;Title: Nucleotide sequence of the gene for aqualysin I (a thermophilic alkaline ser A;Reference number: $00620; MUID:88225062
A;Accession: $00620
A;Molecule type: DNA
A;Residues: 75-442 <KWO>
A;Cross-references: EMBL:X07734; NID:g48069; PIDN:CAA30559.1; PID:g602091
A;Note: part of this sequence, including the amino and carboxyl ends of the mature pr R;Matsuzawa, H.; Tokugawa, K.; Hamaoki, M.; Mizoguchi, M.; Taguchi, H.; Terada, I.; K
Eur. J. Blochem. 171, 441-447, 1988
A;Title: Purification and characterization of aqualysin I (a thermophilic alkaline se A;Reference number: $00324; MUID:88151937
A.Accession: $00324
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A;Title: Genome sequence of the radioresistant bacterium A;Reference number: A75250; MUID:20036896
A;Accession: H75258
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J. Biol. Chem. 265, 6576-6581, 1990
A:Title: Unique precursor structure of an
A:Reference number: A35742; MUID:90216674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Thermus aquaticus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A35742; S00620; S00324
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: H75258
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Pred. No.
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Utterback,
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T.; Zalewski,
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A; Experimental:
C; Genetics:
A; Gene: Rv3170
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                                                                                                                                                                                                                 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, A:Title: Deciphering the biology of Mycobacterium tuberculosis from the cc A;Reference number: A70500; MUID:98295987
A;Accession: H70947
                                                                                                                                                                                                                                                                                      R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                               C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: H70947
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E85798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
C;Accession: E85798
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                                                                                                                                               A;Cross-references: GB:AL021646; GB:AL123456; NID:g3242278;
                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-448 <COL>
                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Rv3170 - Mycobacterium tuberculosis (strain H37RV)
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A; Residues: 1-261 <S
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C;Species: Escherichia coli
Query Match
Best Local S
Matches 4
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 Similarity 4; Conserv
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                                                                                                                               source:
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62.5%;
                80.6%;
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62.5%;
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Score 29; DB Pred. No. 43; 0; Mismatches
 0;
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Pred.
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Pred. No.
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No.
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43;
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15;
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lanta, E.;
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K.; Apodaca,
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A; Reference number: Z15391
A; Accession: T04949
A; Molecule type: DNA
A; Residues: 1-648 < BEV
A; Cross-references: EMBL: ALO21960
A; Experimental source: cultivar Columbia; BA
C; Genetics:
A; Map position: 4
A; Introns: 44/3; 76/3; 128/3; 174/3; 194/1;
A; Note: F7J7.120
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C;Species: Ectothiorhodospira halochloris
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S23164
R;Wagner Huber, R.; Brunisholz, R.A.; Bissig, I.; Frank, G.; Suter, F.; Zube Eur. J. Biochem. 205, 917-925, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-822 <STO>
A; Cross-references: GB: AEO05176; NID: g12724499;
A; Experimental source: strain IL1403
C; Genetics:
A; Gene: ptk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The complete genome sequence of A;Reference number: A86625 A;Accession: F86812 A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphoketolase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C;Accession: F86812
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Best Local Similarity
Thes 4; Conserv
                                                                                                                light-harvesting protein alpha chain - Ectothiorhodosp N; Alternate names: antenna pigment protein alpha chain
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Best Local :
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                            I.; Frank, G.; Suter, F.; Zuber,
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R;Heldelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolacva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;fittle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;eterence number: A82035; MUID:20406833

A;Accession: B82091

A;Accession: B82091

A;Status: prcliminary
A;Molecule type: DNA
A;Residues: 1-1208 <HEI>A;Cross-references: GB:AE004303; GB:AE003852; NID:99656890; PIDN:AAF95464.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Gene: Vc2320

A;Map position: 1
C;Superfamily: exodeoxyribonuclease V 135K chain
                                                                                                    hypothetical protein PH0727 - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999 C;Accession: H71119
                                      R:Kawarabayasi, Y.; Sawada, M.;
M.; Ohiuku, Y.; Funahashi, T.;
DNA Res. 5, 55-76, 1998
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H71119
A; Title: Complete sequence and gene organization of the A; Reference number: A71000; MUID: 98344137
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C;Date: 18-Aug-2000 #sequence_revision
C;Accession: B82091
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A;Residues: 1-1180 <STO>
A;Cross references: GB:AE005174; NID:g12517302; PIDN:AAG57931.1;
A;Experimental source: strain O157:H7, substrain EDL933
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85933
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C:Species: Es
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;Species: Escherichia coli
;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
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                                                             Tanaka, T.;
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                                                         H.; Haikawa, Y.; Hino, Y.; .; Kudoh, Y.; Yamazaki, J.;
                                                                                                                                                                                                                                                                                                                                                                                        DB 24;
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23;
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A;Gene: yebI
C;Superfamily: conserved hypothetical protein HI0360
C;Superfamily: conserved hypothetical protein protein
F;11-27/Domain: transmembrane #status predicted <TM1)
F;38-54/Domain: transmembrane #status predicted <TM2)
                                                                                                                                                                                                                                                                                                                                                              probable membrane protein yebI - Escherichia coli
C.Sepcles: Escherichia coli
C.Sepcles: Escherichia coli
C.Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C.Accession: C64948
R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; I
R.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A.Reference number: A64720; MUID:97426617
A.Recession: C64948
A.Status: nucleic acid sequence not shown; translation not shown
A.Molocula truck of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
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A;Cross-references: GB:AE000280; GB:U00096; NID:91788163;
A;Experimental source: Strain K-12, substrain MG1655
C;Genetics:
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A;Status: preliminary; nucleic acid sequence not shown; translation not A;Status: preliminary; nucleic acid sequence not shown; translation not A;Status: preliminary; nucleic acid sequence not shown; translation not A;Residues: 1-278 <KAW>
A;Residues: 1-278 <KAW>
A;Cross references: GB:AP000003; NID:g3236130; PIDN:BAA29818.1; PID:d103 A;Experimental source: strain OT3
A;Status: preliminary; nucleic acid sequence replaces an interim accession for a sequence replaces an interim accession for a sequence replaces.
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2002, 07:37:28; Search time 63.57 Seconds (without alignments)

9.586 Million cell updates/sec

Title: 09-185908-1E

Perfect score: 36
Sequence: 1 wrxxsyxg 8

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 08

Maximum Match 100% Listing first 50 summaries

: PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | . 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | ъ | 4 | ω | 2 | | Result |
|--------------------|--------|--------|--------------------|--------|--------------------|--------------------|--------------------|---------|--------|---------|--------------------|--------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------|--------------------|--------|--------|--------|--------|--------------------|------|---------------------|
| 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 29 | 29 | 29 | 30 | 30 | 31 | 31 | 32 | 32 | 32 | Score |
| 75.0 | | 5. | 75.0 | 5 | 5 | 5 | 5 | 5 | 75.0 | 7. | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 77.8 | 7. | 7. | 0 | 0 | 80.6 | ω | ω | 86.1 | 5 | 88.9 | 8 | 88.9 | % Query Match |
| 246 | 241 | 199 | 187 | 175 | 159 | 154 | 154 | 116 | 116 | 1289 | 988 | 700 | 669 | 513 | 206 | 168 | 126 | 65 | 822 | 648 | 448 | 261 | 261 | 551 | 278 | 1208 | 1180 | 1180 | Length E |
| N | N | 2 | N | ν | 1 | 2 | Ν | ۲ | Н | 2 | 2 | N | ۳ | μ. | N | N | N | N | Ŋ | N | N | N | 2 | 2 | N | 2 | 2 | μ, | DB |
| T32510 | B83447 | F96737 | H72503 | T11179 | QQCV2 | E81218 | E81795 | Q4 ADE5 | Q4ADE2 | T18212 | H71338 | T06088 | S62919 | A35742 | H75258 | S21041 | S58121 | S23164 | F86812 | T04949 | H70947 | E85798 | C64948 | T16557 | H71119 | в82091 | G85933 | | ID |
| nypornetical proce | | · | hypothetical prote | ā | aphid transmission | RNA methyltransfer | probable tRNA/rRNA | 4 | E4 11K | oral cr | conserved hypothet | | probable membrane | aqualysin (EC 3.4. | probable 3-demethy | cytochrome-c oxida | Ig heavy chain V r | Щ | O | hypothetical prote | | hypothetical prote | Ħ | | | Ē | hypothetical prote | nucl | Description |

RESULT G85933

ALIGNMENTS

A; Molecule type: DNA
A; Rosidues: 1-1180 cFIN>
A; Cross-references: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42682
A; Cross-references: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42682
A; Cross-reference: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42682
A; Cross-reference: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42682
A; Rose, D.J.; Mau, B.; Shao, Y.
Science: 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:g7426617
A; Reference: B65064
A; Accession: B65064 R;Finch, P.W.; Storey, A.; Chapman, K.E.; Brown, K.; Hickson, I.D.; Emmerson, P.T. Nucleic Acids Res. 14, 8573-8582, 1986
A;Title: Complete nucleotide sequence of the Escherichia coli recB gene.
A;Reference number: A25532; MUID:87066729
A;Accession: A25532 exodeoxyribonuclease V (EC 3.1.11.5) 135K chain - Escherichia coli N;Alternate names: exonuclease 135K polypeptide; recBC DNase 135K polypeptide C;Species: Escherichia coli C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 19-Jan-2001 C;Accession: A2532; E65064 C;Accession: A25322; E65064 C;Accession: A25322; E65064 C;Accession: A25322; E65064 C;Accession: A25322; E65064 C;Accession A;Map position: 61 min C;Superfamily: exodeoxyribonuclease V 135K chain C;Keywords: ATP; DNA repair; hydrolase; nucleotide binding; P-loop F;23-30/Region: nucleotide-binding motif A (P-loop) A; Molecule type: DNA
A; Residues: 1-1180 <BLAT>
A; Residues: 1-1180 <BLAT>
A; Cross-references: GB:AE000365; GB:U00096; NID:g2367163; PIDN:AAC75859.1; PID:g17891
A; Cross-references: strain K-12, substrain MG1655
A; Experimental source: strain K-12, substrain MG1655
C; Comment: This enzyme is required for efficient DNA repair; it catalyzes the unwindi ll of these activities require concomitant hydrolysis of ATP. 밁 QYA; Gene: recB C; Genetics: A;Status: preliminary; nucleic acid sequence not shown; translation not shown Query Match
Best Local Similarity
Matches 5; Conserv 901 WRVTSYSG 908 1 wrxxsyxg 8 Conservative 88.9%; 62.5%; Score 32; DB Pred. No. 23; Mismatches 1; ω •• Length 1180; Indels 0, Gaps 0;

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á
Search completed: January 14, 2002, 07:23:43 Job time: 74 sec
                                                                                                              Best Local Similarity 50.0%; Pred. No. 3.5e+02; Matches 4; Conservative 0; Mismatches 4; Indels
                                                             0; Gaps
                                                                                                              0;
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82:

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RESULT 19
US-07-857-224B-85
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                                                                                                                                                              TELEFAX: (International TELEX: none INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
DESCRIPTION: protein
                                              MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 374
                                                                                                                                                                                                                               PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: human FEATURE: Alcohol dehydrogenase, PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
FEATURE: Alcohol dehydrogenase, Table 3 Column 6 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 WKGAIFGG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL: F1
                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 03/25, CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacInto:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGES: 4226-4230
DATE: 1981
                              ORGANISM:
                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 4; Conserv
                                                                                                 TOPOLOGY:
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                                                                                                               amino acid
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                                mouse
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                                                                                                                                                                                                                                                                             NUMBER: US/07/857,224B
03/25/92
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Pred. No. 3
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                                               US-07-857-224B-86
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Best Local :
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Query Match
                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MacIntosh 7.0 SOFTWARE: Microsoft Word CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/857,224B FILING DATE: 03/25/92
                                                                                                                                                                                           FEATURE: Alcohol denyur.
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                             MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 mb storage
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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VOLUME: 78
PAGES: 4226-4230
DATE: 1981
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AUTHORS:
TITLE: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntos
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                                                                                                                                                                                                    ORGANISM: rat
ATURE: Alcohol dehydrogenase, Table 3 Column
                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Hadla
CITY: Zurich
                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                         VOLUME:
                                                                                                                      TITLE:
                                                                                                                                                                     AUTHORS:
                                                                                                         JOURNAL:
                                                                                                                                     AUTHORS:
                                                                                                                                                                                   AUTHORS:
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L: Proceedings of the National Academy of Sciences, USA
                                                                                                Alcohol dehydrogenases
5: Proceedings of the National Academy of Sciences, USA
                                                                                                                                                                                                                                                                                                                                                                    none
                                                                             4226-4230
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                                                                                                                                       Jeffery, J.
                                                                                                                                                    Persson, M.
                                                                                                                                                                     Joernvall, H.
                                                                                                                                                                                                                                                                                                                                                                                (International) 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steven A. Benner
dlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                (International)
                                                                                                                                                                                                                                                            protein
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   71.4%;
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Pred. No.
   Score
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    25;
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    2:
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   Length 375;
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US-07-857-224B-80
                                                                                                                                                                                                                 Sequence 81, Application US/07857224B Patent No. 5958784 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                         07-857-224B-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: none
INFORMATION FOR SEQ ID NO:
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                            APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: Alcohol dehydr PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple MacIntosh 7.0 OPERATING SYSTEM: MacIntosh 7.0 SOFTWARE: Microsoft Word CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/857, 2: FILING DATE: 03/25/92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: (note: this is an international post code) CH-8092 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Benner, ITTLE OF INVENTION:
                                                         COUNTRY:
                                                                                           STREET: Hadlaubstrusse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAGES: 4226-4230
DATE: 1981
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TELEFAX: (International) 41 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION: protein
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STREET: Hadlaubstrasse 151
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Alcohol dehydrogenase, Table 3 Column
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Proceedings of the National Academy of Sciences, USA
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                                                         Switzerland
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                                                                                                                               Steven A. Benner
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0; Mismatches
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1 1 262 2437
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US-07-857-224B-82
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US-07-857-224B-81
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 82, Appli
Patent No. 5958784
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Best Local Similarity
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                                                                                                                  COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntos
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                              ZIP: (note: this is an international post code) CH-8092 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                        PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
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                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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AUTHORS: Jeffery, J.
AUTHORS: Alcohol dehydrogenases
TITLE: Alcohol dehydrogenases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES: 42
TELEFAX:
                                                                                   APPLICATION NUMBER: US
FILING DATE: 03/25/92
                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                STATE:
                                                                          CLASSIFICATION:
                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 wkxxafxg 8°
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3.5e+02;
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                                                                                      LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-278-1
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Best Local Similarity 50...
"--+-hes 4; Conservative
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SEQ ID NO 12
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APPLICANT: Mikiko SUGA,
Query Match
Best Local Similarity
Abes 4; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, TSUYOSHI OSUMI, TSUY TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION CURRENT APPLICATION NUMBER: US/09/222,786A CURRENT FILING DATE: 1998-12-30 EARLIER APPLICATION NUMBER: JP 10-3751 EARLIER APPLICATION NUMBER: JP 10-3751 EARLIER FILING DATE: 1998-01-12 EARLIER FILING DATE: 1998-12-11 NUMBER OF SEQ ID NOS: 14
                                                                                                                                               SOFTWARE:
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/214,278
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                            APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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Pred. No. 1.8e+02;
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                         Score 25; DB 4;
Pred. No. 2.1e+02;
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Best Local Similarity
"hes 4; Conserv
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                                                    RESULT 16
US-07-857-224B-80
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Sequence 80, Application US/07857224B Patent No. 5958784 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 01 FILING DATE: 17-JAN-1995 ATTORNEY/AGENT INFORMATION:
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                                                                                                                             219 WKLTAF 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
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Song, Wen-Yuang
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NO: 16:
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Pred. No. 2.6e+02;
0; Mismatches 2;
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US-09-222-817-12
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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-222-786-2
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; Sequence 2, Application US/09222817

; Patent No. 6037154
                                                                                                      RESULT
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                  Sequence 12, Application US/09222817 Patent No. 6037154 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: JP 10-353513
EARLIER FILING DATE: 1998-12-11
NUMBER OF SEO ID NOS: 14
SOFTWARE: PATCHTIN VCr. 2.0
SEO ID NO 2
                                                                                                                                                                                                                                          Matches
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Best Local :
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Patent No. 6258573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MIKIKO SUGA, MASBARZU SUGIMOTO, TSUYOSHI OSUMI, TSUYOSHI NAKAMATSU, TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION FILE REFERENCE: OPB12 CURRENT APPLICATION NUMBER: US/09/222,786A CURRENT FILING DATE: 1998-12-30 EARLIER APPLICATION NUMBER: JP 10-3751 EARLIER FILING DATE: 1998-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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FILE REFERENCE: OP813
CURRENT APPLICATION NUMBER: US/09/222,817
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER APPLICATION NUMBER: JP 10-353521
EARLIER APPLICATION NUMBER: JP 10-353521
NUMBER OF SEQ ID NOS: 18
COCRUMANDE: DEFORT: US- 2 0
    APPLICAUT: Mikiko SUGA,
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                                                                                                                                                          132 WKRSSFNG 139
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nes 4; Conserv
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50.0%;
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50.0%;
Masakazu SUGIMOTO, Tsuyoshi OSUMI,
                                                                                                                                                                                                                                    Score 27; DB
Pred. No. 1.2e
1; Mismatches
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Pred. No. 1.2e+02;
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  Tsuyoshi NAKAMATSU
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; TYPE: PRT ; ORGANISM: Brevibacterium flavum US-09-222-817-14
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US-09-222-817-14
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; TAPRISM: Brevibacterium flavum
US-09-222-817-12
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Sequence 12, Application US/0922786A
Patent NO. 6258573
GENERAL INFORMATION:
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuy
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION
FILE REFERENCE: OP812
CURRENT APPLICATION NUMBER: US/09/222,786A
CURRENT APPLICATION NUMBER: US/09/222,786A
CURRENT FILING DATE: 1998-12-30
EARLIER RAPLICATION NUMBER: UP 10-3751
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 14
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Best Local Similarity
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EARLIER FILING DATE: 198-12-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
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CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER FILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: JP 10-353521
EARLIER FILING DATE: 1998-12-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/222,817
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER FILING DATE: 1998-01-12
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Pred. No. 1.8e
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Pred. No.
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1.8e+02;
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1.8e+02;
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US-08-871-355A-89
Sequence 89, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
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Best Local Similarity
"hes 5; Conserve
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; HYPOTHETICAL:
US-08-637-759B-89
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 89, Application US/08637759B Patent No. 5876931
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: David William Holden TITLE OF INVENTION: Identificati
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                                                    TITLE OF INVENTION: Identification of Genes NUMBER OF SEQUENCES: 501
                                                                       APPLICANT: David William Holden TITLE OF INVENTION: Identificat:
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FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                         30 WKPAAFQG 37
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62.5%;
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Pred. No. 96;
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; MOLECULE TYPE:
; HYPOTHETICAL:
US-08-871-355A-89
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Best Local Similarity
"-+hes 5; Conserv
                                                                                                                      ; ORGANISM: Rattus norvegicus US-09-140-804-7
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-140-804-7
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APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
APPLICANT: HUMES, JACQUELINE M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09140804 Patent No. 6197930
                                    Matches
                                                    Query Match
Best Local Similarity
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FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101 COI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 89:
                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
                                                                                                                                                       TYPE: PRT
                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: US.
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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ZIP: 30309-3450
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amino acid
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50.08;
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62.5%;
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                                                    Score 27;
Pred. No.
                                      Mismatches
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                                      Gaps
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US-08-919-953-2
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US-08-922-182-2
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Best Local Similarity 02...
5; Conservative
                                                                                             Sequence 2, Application US/08919953
Patent No. 5837481
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Seay, Nicholas J
RECISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 608-251-9166 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
             APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APRLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICKOBIAL
TITLE OF INVENTION: SENSING AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equence 2, Application US/08922182 tent No. 5834300
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,182
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION MABER: 08/608,241
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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CITY: Madison
STATE: WI
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Barber, Robert D
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                 MICROBIAL SYSTEM FOR FORMALDEHYDE SENSING AND REMEDIATION
                                                                                                                                                                                                                                                                                               85.7%;
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                                                                                                                                            SEQ ID NO 2
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GENERAL INFORMATION:
APPLICANT: Donohue, Timothy
APPLICANT: Barber, Robert
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: Microbial System for Formaldehyde Sensing and
TITLE OF INVENTION: Microbial System for Formaldehyde Sensing and
TITLE OF INVENTION: NUMBER: US/09/192,983A
CURRENT APPLICATION NUMBER: US/09/192,983A
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/919,953
EARLIER FILING DATE: 1997-08-29
EARLIER FILING DATE: 1997-08-29
EARLIER FILING DATE: 1996-02-28
                                                                                        LENGTH: 376
; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-09-192-983-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-919-953-2
Query Match 85.7
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09192983A Patent No. 6242244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
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OPERATING SYSTEM:
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CITY: Madison
STATE: WI
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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62.5%;
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Pred. No.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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6: /cgn2_6/ptodata/2,
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Listing first 50 summaries
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Copyright (c) 1993 - 2000 Comp
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US-08-608-241-2
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US-08-887-234B-86
US-08-487-753-2
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US-08-487-753-5
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| | 71 4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 |
| | 2987 | 2987 | 1347 | 1257 | 1248 | 1240 | 1238 | 1212 | 1148 | 1079 | 1065 | 1055 | 985 | 980 | 604 | 604 | 604 | 604 | 604 | 604 | 604 | 604 | 604 |
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| | -09 | US-08-970-269A-29 | US-09-058-489-24 | US-08-611-729A-8 | US-08-882-046-6 | US-09-058-489-23 | US-09-214-278-5 | US-09-214-278-3 | US-08-882-046-4 | US-09-058-489-22 | US-08-400-159-8 | US-09-214-278-2 | US-08-473-553A-2 | US-08-473-553A-6 | PCT-US93-09167-5 | PCT-US93-09167-4 | PCT-US93-09167-2 | US-08-930-589A-18 | US-08-487-744-5 | US-08-487-744-4 | US-08-487-744-2 | US-08-480-065-5 | US-08-480-065-4 |
| | • | Sequence 29, Appl | Sequence 24, Appl | Sequence 8, Appli | Sequence 6, Appli | ~ | Sequence 5, Appli | - | Sequence 4, Appli | Sequence 22, Appl | Sequence 8, Appli | • | Sequence 2, Appli | Sequence 6, Appli | Sequence 5, Appli | • | Sequence 2, Appli | Sequence 18, Appl | Sequence 5, Appli | | Sequence 2, Appli | ` | Sequence 4, Appli |

ALIGNMENTS

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; MOLECULE TYPE: protein US-08-608-241-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08608241; Patent No. 5747328
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US-08-608-241-2
                                                          TELEFAX: 608-22-1 NO: 2
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1 FINGTH: 376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Witthuhn, Vernon TITLE OF INVENTION: MICROBIT TITLE OF INVENTION: SENSING NUMBER OF SEQUENCES: 7
                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Seay, NICHOLAS J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/608,241
                                                    amino acid
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Barber, Robert
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Robert D
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Query Match Best Local Similarity

85.7%; 62.5%;

Score Pred.

30; DB 1; No. 31;

Length 376;

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                                    Score 30; DB Pred. No. 77; 0; Mismatches
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Search completed: January 14, Job time: 811 sec 2002, 07:36:00

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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUL-2000;
14-SEP-2000;
                                                                      Tang YT,
Wang J,
Zhao QA,
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WPI; 2001-442253/47.
N-PSDB; AAI60879.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM41723 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                           Qian XB,
Yang Y,
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                                                                                           Zhang
                                                                                                                  Ren F,
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                                                                                             J.
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                                                                                                                  Wang
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RESULT
AAG17084
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Matches 5
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25-MAR-1999
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06-APR-1999
19-APR-1999
19-APR-1999
21-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathles and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                    25-FEB-2000;
                                                                                                                                                                                                                                                              06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hvhridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 17971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG17084 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, usuch as central nervous system injuries
                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                             termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG17084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) the encoded polypeptides (AAM38642-AAM42213) with nootropic, timmunosuppressant and cytostatic activity. The polynucleotides at timmunosuppressant and cytostatic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || || || || 45 wkvtafig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 62.55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235
                                                                                                                                                                                                                                   2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
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99US-0123180.
99US-0123548.
99US-0125788.
99US-0126564.
99US-01267785.
99US-01267785.
99US-012677462.
99US-0128714.
99US-0128734.
99US-0128714.
99US-0130510.
99US-0130510.
99US-0131449.
99US-0132048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB Pred. No. 71; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 235;
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Best Local Similarity
"hes 5; Conservations
RESULT 16
AAB66183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein_membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes.
                                                                                                                                                                                               20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
29-CCT-1999;
30-NOV-1999;
02-DEC-1999;
16-DEC-1999;
05-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                             Gao
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                         Secreted and transmembrane proteins and nucleic acids designated PRO useful as hybridization probes, in chromosome and gene mapping and general probability.
                                                                                                                                                                                                                                                                                                                                                                                                                 WO200078961-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted; transmembrane; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein of the invention #95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB66183;
                                                                                                                                          Baker KP,
                                                                                                                                                                                                                                                                                                                              23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                          18-FEB-2000; 2000WO-US04342.
                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-2000.
                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                      2001-071395/08
                                                                                              Paoni NF, Roy
e CK, Williams
                                                                                                 P, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D; CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                 99WO-US28551.
99WO-US30095.
2000WO-US00219.
2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                       99US-0144758.
99US-0145698.
99WO-US20111.
99US-0162506.
99WO-US28313.
                                                                                                                                                                                                                                                                                                                                99US-0141037
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ID AABSO99
XX AABSO99
XX AABSO9
XX AABSO9
XX YA HUMAN
DT 21-MAR
XX HUMAN
XX HUMAN
KW ANTIIN
KW PRO a9
OS HOMO S
XX WO2000
XX WO2000
XX WO2000
XX O2-JUN
PR 22-JUN
PR 10-SEE
PR 01-SEE
PR 01-SEE
PR 01-SEE
PR 01-SEE
PR 11-FEE
PR 01-DEC
PR 02-DEC
PR 11-FEE
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Thehes 5; Conserv
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01-SEP-1999;

08-SEP-1999;

08-SEP-1999;

29-OCT-1999;

20-DEC-1999;

01-DEC-1999;

02-DEC-1999;

01-DEC-1999;

06-JAN-2000;

01-FEB-2000;

11-FEB-2000;

18-FEB-2000;

18-FEB-2000;

18-FEB-2000;

18-FEB-2000;

19-MAR-2000;

10-MAR-2000;

10-MAR-2000;

11-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general; antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant; PRO agonist; cancer; inflammatory disorder; immunological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB50968 standard; Protein; 220 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO1488 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB50968;
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23-JUN-1999;
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                                                                                Baker KP,
                                                                                                                              (GETH ) GENENTECH INC
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                                                   DL,
                                                      Goddard
,, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 AA;
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                                                                                                                                                                             2000WO-US00376.
2000WO-US04341.
2000WO-US04341.
2000WO-US04342.
2000WO-US04342.
2000WO-US05841.
2000WO-US05814.
2000WO-US05814.
2000WO-US05884.
2000WO-US05884.
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99WO-US28313.
99WO-US28634.
99WO-US28551.
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99WO-US20594.
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                                                        Gurney AL, I
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30; DB
Pred. No. 67;
                                                           Hebert C,
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Length 220;
                                                                                Henzel W,
                                                                                     Kabakoff RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Claim

Fig

773pp; English.

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Best Local (
                                                                                                                                                                                                                             21-JAN-2000;
25-APR-2000;
09-JUL-2000;
                                                                                                                    Tang YT,
Wang J,
                     Example 4;
                                          Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzholmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                     (HYSE-)
                                                                                                                                                                                                                  19-JUL-2000;
                                                                                                                                                                                                                                                                         26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                 26-JUL-2001.
                                                                                                                                                                                                                                                                                                                    WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                       chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM39937 standard;
                                                                                                                                                                                                                                                                                                                                                                leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                    2001-442253/47.
                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wkvtafig 37
                                                                                                                                                                                                                                                                                                                                                                                                                nootropic; immunosuppressant; cytostatic; gene therapy;
                                                                           AAT59093.
                                                                                                                                                    HYSEQ INC
                                                                                                        Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
5; Conserv
                      SEQ
                                                                                                                                                                         2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0598042
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                     ID NO
                                                                                                                    Asundi V,
Wehrman T,
                                                                                                          Goodrich R,
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                     3082;
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                                                                                                        Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
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Pred. No.
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                                                                                                                  Qian XB,
Yang Y,
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                                                  treating
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                                                                                                                            Ren F,
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The invention relates

to human nucleic acids (AAI57798-AAI61369) and

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Best Local
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral scclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate CDNA sequences of the invention. The invention also includes methods the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the
                                                                                                           This invention relates to nucleic acid sequences AAF93744 -
                                                                                                                                                  Claim 1;
                                                                                                                                                                            Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development - \,
                                                                                                                                                                                                                                                                                                                                                                                                              07-JUL-2000; 2000EP-0114090
                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1067182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secretory protein; membrane protein; vaccine;
rheumatoid arthritis; diabetes.
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                                                                                                                                                                                                                                2001-093989/11.
DB; AAF93746.
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                                                                                                                                             SEQ ID 6; 609pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220
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62.5%;
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Pred. No. 67;
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                                                               AAF62235 which are used to isolate
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transmembrane; secretion; immunoa
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immunoadhesion; pharma
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pharmaceutical;
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       01-CCT-1998;
02-CCT-1998;
06-CCT-1998;
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28-CCT-1998;
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29-CCT-1998;
21-CCT-1998;
21-CC
                 New mammalian DNA sequences secreted PRO polypeptides, usmall molecule inhibitors of
                                                                         WPI; 2000-237871/20.
N-PSDB; AAA37116.
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98US-0103679

98US-0105002

98US-01055002

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                    of
                  is encoding transmembrane, receptor or
   useful for screening of potential peptide o:
   of the relevant receptor/ligand interactions
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17-AUG-1999;
09-NOV-1999;
            cell proliferative disorders e.g. arterioscierosis and cancers; autoimmune or inflammatory disorders e.g. Addison's disease and acquired immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic, protozoal and helminthic infections; gastrointestinal disorders e.g. dysphagia and tritable bowel syndrome; neurological disorders e.g. epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob disease and mental disorders e.g. anxiety, schizophrenia and Tourette's
                                                                                                                            intracellular signalling molecules INTRA1 - INTRA52, represented in AAB64369 - AAB64420. Modulators of the intracellular signalling molecules of the invention exhibit immunosuppressive; cytostatic; neuroprotective; nootropic; antiarteriosclerotic; antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal; antiviral; antiparasitic; nantihelminthic; and antiparkinsonian activity. INTRA polypeptides their agonists and antagonists are useful for the treatment of a condition associated with decreased or increased expression of functional INTRA. Disorders associated with abnormal INTRA expression or activity include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; neuroprotective; nootropic; antiarteriosclerotic; cance antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal; antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell proliferative disorder; arteriosclerosis autoimmune; epilepsy; inflammatory disorder; Addison's disease; gastrointestinal disorder; neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;
                                                                                                                                                                                                                                                                             Sequences AAF32638 - AAF32689 represent cDNA encoding human
                                                                                                                                                                                                                                                                                                                                          inflammatory, neurologic developmental disorders
                                                                                                                                                                                                                                                                                                                                                      New human intracellular signaling molecules, useful for the diagnosis, prevention and treatment of cell proliferative, autoimmune, inflammatory, neurological, gastrointestinal, reproductive and developmental disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mental disorder; schizophrenia; anxiety.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid
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99US-0149640.
99US-0164417.
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J, Reddy R,
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62.5%;
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Pred. No.
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Lu DAM;
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INTRA
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel murine nucleic acid sequences encoding to clodin family of tight junction (TJ)-constituting membrane protein can be used in medical field. This sequence represents the clodin 6 protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tight junction-constituting membrane protein clodin family - useful in the medical field
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-285512/25
N-PSDB; AAZ89153.
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                                                                                              AAY99434;
                                                                                                                                     AAY99434 standard; Protein;
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5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 17-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             murine; tight junction-constituting membrane protein;
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Human PRO1488 (UNQ757) amino

acid sequence SEQ

ID

NO:330

Length 126;

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DЬ
                                        The polynucleotide sequence given in AAA78381 to AAA78432 encode the CC human secreted proteins given in AAB24437 to AAB24604. Human secreted proteins have activities based on the tissues and cells the genes are CC expressed in Examples of activities include: cytostatic; antianaemic; antidiabetic; antiinflammatory; ophthalmological; antirheumatic; CC antidritritic; antipsoriatic; antimicrobial and antiparkinsonian.

CC uncotropic; neuroprotective; antimicrobial and antiparkinsonian.

CC Human secreted protein polynucleotides, polypeptides, antagonists and/or agonists may be useful in treating, preventing, and/or diagnosing other CC diseases, disorders, and/or conditions such as: (a) cancers; (b) CC disorders of the immune system; (c) angiogenesis disorders; (d) myperproliferative disorders; (e) cardiovascular disorders; (f) diseases associated with increase apoptosis; (g) neurological diseases; and CC (h) infectious diseases. They are also used to promote wound healing. AAA78372 to AAA78380 and AAB24436 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB24453
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Best Local
                                                                                                                                                                                                                                                                                                                                              Forty seven human nucleic acids encoding secreted proteins, useful the treatment, prevention and diagnosis of cancers, disorders of timmune system, angiogenesis disorders, neurological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective; antimicrobial; antiparkinsonian; cancer; immune system disorder; angiogenesis; hyperproliferative disorder, cardiovascular disorder; apoptosis; neurological disease; cardiovascular disorder; apoptosis; neurological disease;
                                                                                                                                                                                                                                                                                                    Claim
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18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory; ophthalmological; antirheumatic; antiarthri
antipsoriatic; antiangiogenic; cardiant; anti-HIV; nootropic;
                                                                                                                                                                                                                                                                                                                                 hyperproliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infectious disease; wound healing.
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98US-0113006
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62.5%;
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Shi Y, Lafleur DW, Olsen
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sen HS, Florence
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                                                                                                                                                                                                                                                                                                                                                       The polynucleotide sequence given in AAA78381 to AAA78432 encode the human secreted proteins given in AAB24437 to AAB24604. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; antianaemic; antidiabetic; antiinflammatory; ophthalmological; antirheumatic; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation; antistation
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                                                                                 associated with increase apoptosis; (g) neurological diseases; and (h) infectious diseases. They are also used to promote wound heali AAA78372 to AAA78380 and AAB24436 represent sequences used in the
                                                                                                                                                                                                                    antiarthritic; antipsoriatic; antianglogenic; cardiant; anti-HIV; nootropic; neuroprotective; antimicrobial and antiparkinsonian. Human secreted protein polynucleotides, polypeptides, antagonists agonists may be useful in treating, preventing, and/or diagnosing diseases, disorders, and/or conditions such as: (a) cancers; (b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Forty seven human nucleic acids encoding secreted proteins, useful in
the treatment, prevention and diagnosis of cancers, disorders of the
immune system, angiogenesis disorders, neurological diseases and
                                                    exemplification of the present invention.
                                                                                                                                                                   disorders of the immune system; (c) angiogenesis disorders; (d) hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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18-DEC-1998;
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5; Conserv
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62.5%;
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Shi Y, Lafleur DW, Olsen
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sen HS, Florence
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ARESULT AABO 798 AID 6798 AID 6798 AID 6798 AID 6798 Clau XX Clau XX Clau XX Clau XX Clau XX Clau XX Clau XX Clau XX Mamm XX Mamm XX Mamm XX Mamm XX Mamm XX Mamm XX AID PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03-1 PR 03
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Best Local 9
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Claim 73; Page 104; 121pp; English
                                                           Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous sys and across the skin -
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                                                        and across
                                                                                                                                                              WPI; 2000-365610/31.
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30-MAR-1999;
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30-MAR-1999;
                                                                                                                                                                                                                                                                (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory disease;
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99US-0282029
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99US-0282029.
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62.5%;
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RESULT
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                                                                          The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present
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                                                                                                                                                                                                                                                                                                                                                                                                      Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous systand across the skin - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claudin-6 modulating agent; claudin-9 modulating agent; cell adhesion recognition sequence; CAR sequence; autoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-NOV-1998;
30-MAR-1999;
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5; Conservative
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                                                        has
                                                                                                                                                                                                                                                                                                                                        Page 104; 121pp;
10 AA;
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                                                     a cyclic conformation.
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99US-0282029
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Pred. No.
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3.8;
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Best Local
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             28-SEP-2000
                                     AAB06781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claudin-6/9 cyclic cell adhesion recognition sequence SEQ
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                                                            AAB06781 standard;
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30-MAR-1999;
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99US-0282029.
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                                                            peptide;
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Best Local
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                                                                                                            Claudin-6 modulating agent; claudin-9 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune inflammatory disease; cancer; graft rejection; cyclic.
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                                                             WO200026360-A1
                                                                                      Mammalia
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                                                                                                                                                                                                                                              AAB06789 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system
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30-MAR-1999;
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Thehes 5; Conserv
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The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins are cadherins, which are membrane glycoprotecins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and those peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claudin-6 modulating agent; claudin-9 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer; graft rejection; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins are cadhesion, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to feel that the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the second in the s
                                                                                                                                                                                                                                                                                                                               Claim 73; Page 104; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blaschuck OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-NOV-1998;
30-MAR-1999;
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99US-0282029.
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62.5%;
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Pred. No.
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. 4.3e+05;
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                             The present sequence is a peptide which can be used in a claudin-mediated cell adhesion modulator. The claudin group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and this peptide can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, it can also be used to facilitate drug delivery
                                                                                                                            Claim 71; Page 103; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claudin cell adhesion recognition modulating sequence SEQ ID NO:
Sequence
                                                                                                                                                    and across the skin -
                                                                                                                                                                                                   WPI; 2000-365610/31
                                                                                                                                                                                                                          Blaschuck OW,
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30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claudin modulating agent;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    facilitate drug delivery to the desired target site. The present sequence has a cyclic conformation.
                                                                                                                                                                vasopermiability,
                                                                                                                                                                          Antibody modulation of claudin-mediated cell adhesion for increasing
                                                                                                                                                                                                                                                 (ADHE-) ADHEREX TECHNOLOGIES INC
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                       the desired target site
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5; Conserv
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99US-0282029
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62.5%;
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Best Local Similarity Matches 5; Conserv

Conservative

0;

Mismatches

85.7%;

Score 30; DB 21; Pred. No. 4.3e+05;

Length 8;

Indels

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Gaps

0;

Query Match

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries
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Perfect score:
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DB
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Gapop 10.0 ,
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| | 2005 US STATE STAT | 219 |
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| ALIGNMENTS | AAM39937 AAM39937 AAB861183 AAB850968 AAB50968 AAG116747 AAG116747 AAG116747 AAG116747 AAG116747 AAG145943 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG15746 AAG14735 AAG14736 | 168 |
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PR 03-1
PR 03-1
PR 30-1
YX AD1
                                                                                                                                                                                                     Claudin-6 modulating agent; claudin-9 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease;
                                                                                                                                                                                                                                        Claudin-6/9 cell adhesion recognition sequence SEQ ID NO: 335
                                                          03-NOV-1998;
30-MAR-1999;
                                                                                                                                             WO200026360-A1.
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             Blaschuck OW,
                                                                                              03-NOV-1999;
                                                                                                                    11-MAY-2000.
                                                                                                                                                                     Mammalia
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                                  (ADHE-) ADHEREX TECHNOLOGIES INC.
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                                                          98US-0185908.
99US-0282029.
           Symonds JM,
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             Gour BJ;
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Q9X982;
Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; "NEDO human cDNA sequencing project.";
                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
HYPOTHETICAL 73.3 KDA PROTEIN.
HOmo sapiens (Human)
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Mol. Microbiol 21:77-96(1996).
EMBL; AL512667; CAC21620.1;
InterPro; IPR001753; Enoyl_COA_hydrtse.
Pfam; PF00378; ECH; 1.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.
SEQUENCE 266 AA; 28121 MW; C07F9346B82E0451 CRC64;
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Sinorhizobium.
NCBI_TaxID-382;
                                                                                                                                                      TISSUE=EMBRYO;
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Q9Z2L5;
01-MAY-1999 (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, L
01-JUN-2001 (TrEMBLrel. 17, L
TRANSKETCLASE (FRAGMENT).
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Salamon C., Sax C.M., Piatigorsky J
Salamon C., Sax C.M., Piatigorsky J
Submitted (FEB-1998) to the EMBL/Ger
EMBL; AF046917; AAC80281.1; -.
HSSP; P23254; 1TRK.
InterPro; IPR000360; Transketolase.
Pfam; PF00456; transketolase; 1.
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Mammalia; Eutheria;
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A Pang Z., Morgan J.I.;
A Pang Z., Morgan J.I.;

"Cloning and characterization of a novel precerebellin-related gen

L Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF218380; AAF32315.1; -.

JR EMBL; AF218379; AAF32314.1; -.

JR MGD; MGI:1889286; Cbin3.

DR InterPro; IPRO01073; C1q.

DR Pfan; PF00386; C1q; 1.

DR PRINTS; PR00007; COMPLEMNTC1Q.

DR SMART; SM00110; C1Q; 1.

DR PROSITE; PS01113; C1Q; 1.

SQ SEQUENCE 197 AA; 21077 MW; DBA8925C9BB11B77 CRC64;
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EMBL; APO01512; BAB05321.1; -.

InterPro; IPR002912; ACT.

InterPro; IPR002912; D_2_hydroxyacid_DH.
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Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID~10090;
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01-OCT-2000
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Pfam; PF01842; ACT; 1.
PROSITE; PS00670; D_2_HYDROXYACID_DH_2;
PROSITE; PS00671; D_2_HYDROXYACID_DH_3;
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MEDLINE-20512582; PubMed-11058132;
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Q9ADDO;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE ENOYL-COA HYDRATASE.
25CK31.11C.
Stroctory
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Q9EWW0;
01-MAR-2001
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Cerdeno A.M., Parkhill J., E
Submitted (MAR-2001) to the
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                                                                      STRAIN=A3(2);
Cerdeno A.M., Parkhill J., E
Submitted (JAN-2001) to the
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Seeger K.J., Harris D.;
                                                                                                                                                                                                         Streptomyces coelicului.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL589707; CAC33901.1;
Hypothetical protein.
SEQUENCE 243 AA; 27350 MW; 819C5DF7366DDE70 CRC64
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NCBI_TaxID=1902;
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           MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapa
                                    SEQUENCE FROM N.A. STRAIN-A3(2);
                                                                                                                                    Submitted (JAN-2001) to
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NCBI_TaxID=1902;
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MEDLINE=97000351; PubMed=8843436;
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Hopwood D.A.;
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Matches 5
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O97363;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TREMBLrel. 10, Last sequence update)
O1-MAY-1999 (TREMBLrel. 17, Last annotation update)
LIPOPOLYSACCHARIDE BINDING PROTEIN PRECURSOR.
Bombyx mori (Silk moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Dit
                                                                                                                                                                                                                                      TISSUE-HEMOCYTE;
TISSUE-HEMOCYTE;
MEDLINE-99142698; PubMed-9989592;
MEDLINE-99142698; PubMed-9989592;
MEDLINE-99142698; PubMed-9989592;
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Jain R.K., Thompson R.G., Taylor D.C., MacKenzie S.L., McHughen A.G.,

Rowland G.G., Tenaschuk D., Coffey M.;

"Isolation of the two flax stearoyl-acyl carrier protein desaturase
gene promoters by the inverse polymerase chain reaction and their
differential regulation in transgenic flax, tobacco, and canola.";

Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF
CIS DOUBLE BOND BETWAEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
                                                                                                                                                                                                  FEBS
                                                                                                                                                                                                                                  C-type lectin superfamily with two recognition domains.";
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pfam; PF00487; FA_desaturase; 1.
pROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
Transit peptide.
SEQUENCE 396 AA; 44881 MW; 565B4ZB1ZB0CFA23 CRC64;
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-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY),
-!- SIMILARITY: TO OTHER PLANTS STEAROYL-ACP DESATURASE
CYANOBACTERIA FATTY ACID DESATURASE (DESA).
EMBL; AJ006958; CAA07350.1; -.
EMBL; P22337; 1AFR.
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-:- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)

-:- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.

-:- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
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NCBI_TaxID=4006;
   MEDLINE=97454306;
Koizumi N., Morozu
                                                                                   TISSUE=HEMOCYTE;
                                                                                                                       SEQUENCE FROM N.A.
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01-OCT-2000
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
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SMART; SM00034; CLECT; 2.

PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 2.

SEQUENCE 327 AA; 37423 MW; 3B7FB3E662C78AFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu X., Kanost M.R.;
"Immulectin-2, a lipopolysaccharide-specific lectin from an insect,
"anduca sexta, is induced in response to gram-negative bacteria.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242202; AAF91316.1; ...
EMBL; AF242202; AAF91316.1; ...
InterPro; IPR001304; lectin_c.
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pfam; pF00059; lectin_c; 2.
SMART; SM00034; CLECT; 2.
PROSITE; pS00615; C_TYPE_LECTIN_1;
pROSITE; pS50041; C_TYPE_LECTIN_2;
Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Sphingiodea; Sphingidae; Sphinginae; Manduca.
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EMBL; AJ011573; CAB38429.1;
HSSP; P20693; 1HLJ.
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NCBI_TaxID=7130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=FAT BODY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ALCOHOL DEHYDROGENASE (EC 1.1.1.) CLASS III.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                    Sequence features of the regions of 1,044,062 bp covered by Elphysically assigned Pl clones.";

DNA Res. 4:291-300(1997).

-I- COPACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).

EMBL: AB006703; BAB09054.1; -.

InterPro: IPR002085; Adh_zinc.

InterPro: IPR00238; ADh_zinc.

InterPro: IPR00238; ADh_zinc.

InterPro: IPR00238; ADh_zinc.

InterPro: IPR00238; ADh_zinc.

InterPro: IPR00238; ADh_zinc.

InterPro: IPR00238; ADh_zinc; 1.

PROSITE: PS00059; ADh_ZINC; 1.
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Q9FND2;
                                                                                                                                                                                                                     Oxidoreductase; Zir
SEOUENCE 379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kotani H., Nakamura Y.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR002085; Adh_zinc.
InterPro: IPR002328; ADH_zinc.
Pfam; PF00107; adh_zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
Complete proteome; OxIdoreductase;
SEQUENCE 378 AA; 40479 MW; 439)
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-I- SIMILARITY: TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY.
EMBL; AL162756; CAB84746.1; -.
EMBL; AC102479; AAF41679.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98069011; PubMed-9405937;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana (Sequence features of the regions of 1,044,062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-3702;
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62.5%;
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Pred. No.
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Pred. No.
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Q9SBA2;
Q1-MAY-2000 (TrEMBLY
Q1-MAY-2000 (TREMBLY
Q1-JUN-2001 (TREMBLY
ACYL-|ACYL-CARRIER F
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082014;
01-NOV-1998
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Jain R.K., Thompson R.G., Taylor D.C., MacKenzie S.L., McHughen A.G.,
Rowland G.G., Tenaschuk D., Coffey M.;
"Isolation of the two flax stearcyl-acyl carrier protein desaturase
gene promoters by the inverse polymerase chain reaction and their
differential regulation in transgenic flax, tobacco, and canola.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databbases.
-I- FUNCTION: CONVERTS STEARCYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast; Fatty acid biosynthesis; Transit peptide.
SEQUENCE 396 AA; 44857 MW; 938ClCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mendel; 32621; Linus;1039;32621.
InterPro; IPRO1225; FA_desaturase.
Pfam; PF00487; FA_desaturase; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
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-I- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)

- OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.

-I- COPACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Linaceae; Linum.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ACYL-[ACYL-CARRIER PROTEIN] DESATURASE (EC 1.14.99.6) (STEAROYL-ACP
         Eukaryota; Viridiplantae;
                                                                      SAD2
                                                                                            DESATURASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ006957; CAA07349.1; -. HSSP; P22337; 1AFR.
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-i- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
-i- SIMILARITY: TO OTHER PLANTS STEAROYL-ACP DESATURASE AND CYANOBACTERIA FATTY ACID DESATURASE (DESA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                 Linum usitatissimum (Flax) (Linseed).
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PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
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62.5%;
Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                  Last sequence update)
Last annotation update)
DESATURASE (EC 1.14.99.6) (STEAROYL-ACP
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RESULT
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EMBL;
EMBL;
EMBL;
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EMBL;
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PROSITE; PS00059; ADH_ZINC; 1.

PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.

Oxidoreductase; Zinc.

SEQUENCE 377 AA; 40213 MW; C0F35E5208E438A1 CR
                                                                                                Oxidoreductase.
SEGUENCE 377 AA;
                                                                                                                     "Ascidian and amphioxus Adh genes reveal functional and molecular evolution of the ADH family expansion during vertebrate evolution Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                Canestro C., Hjelmqvist L., Albalat R.,
Gonzalez-Duarte R., Jornvall H.;
                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (Tremblrel. 17, 01-JUN-2001 (Tremblrel. 17, 01-JUN-2001 (Tremblrel. 17, ALCOHOL DEHYDROGENASE CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002085; Adh_zinc.
InterPro; IPR002328; ADH_zinc.
InterPro; IPR000531; TonB_boxC
                                                                                                                                                                              Canestro
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20507554; PubMed=11054102;
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Branchiostoma.
                                                                                                                                                                                                                                                                                                                                     Branchiostoma floridae (Florida lancelet) (Amphioxus)
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                                                                                                                                                                     Gonzalez-Duarte R.;
                                                                                                                                                                             SEQUENCE FROM N.A.
Canestro C., Albalat R.,
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7739;
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317
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AF156701; AAF73255.1;
AF156702; AAF73255.1;
AF156703; AAF73255.1;
AF156704; AAF73255.1;
AF156706; AAF73255.1;
AF156706; AAF73255.1;
AF156707; AAF73255.1;
AF156707; AAF73255.1;
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AF156698;
AF156699;
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AAF73255.1;
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                                                                                                  40191 MW;
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62.5%;
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MEDLINE-20507554; PubMed-11054102;

Canestro C., Hjelmqvist L., Albalat R., Garcia-Fernandez J.,

Gonzalez-Duarte R., Jornvall H.;

Gonzalez-Duarte R., Jornvall H.;

Gonzalez-Duarte R., Jornvall H.;

Gonzalez-Duarte R., Jornvall H.;

Gonzalez-Duarte R., Jornvall H.;

Gonzalez-Ernandez J.,

Gonzalez-Fernandez 
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Q9BJ33;
Q1-JUN-2001
Q1-JUN-2001
Q1-JUN-2001
                                                                                                                                                             MEDLINE-20222556; PubMed-10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltrwell T., Hamlin N., Holroyd
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
menigitidis 22491.";
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Q9JRB0;
Q9JRB0;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ALCOHOL DEHYDROGENASE CLASS-III (EC 1.1.1.1) (ALCOHOL DEHYDROGENASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis (serogroup
Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta su
NCBI_TaxID=65699, 491;
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01-JUN-2001 (TrembLrel. 17,
01-JUN-2001 (TrembLrel. 17,
01-JUN-2001 (TrembLrel. 17,
SEQUENCE FROM N.A.
STRAIN=MC58 / SEROGROUP
MEDLINE=20175755; PubMec
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Last annotation updat
3 (EC 1.1.1.1).
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Pred. No.
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                                             SEQUENCE FROM N.A.

MEDLINE-21173698; PubMed-11259647;

NIErman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RIESEN J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

POLOCKA I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DOBOY R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

KOlonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

"Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

EMBL, Ac005919; AAK24487.1; -.
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O1-JUN-2001 (TrEMBLrel. 17, C
O1-JUN-2001 (TrEMBLrel. 17, I
O1-JUN-2001 (TrEMBLrel. 17, I
ALCOHOL DEHYDROGENASE, CLASS
                   Complete proteome
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Bacteria; Proteobacteria;
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01-JAN-1998 (TremBlrel. 05, Last sequence update)
01-JUN-2001 (TremBlrel. 17, Last annotation update)
GLUTATHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE (E
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SEQUENCE 369 AA; 39424 MW;
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InterPro; IPR002328; Adh_zinc.
InterPro; IPR002205; Adh_binding.
Pfam; PF00107; Adh_zinc; 1.
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databbases.
-: COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
EMBL; AF154331; AAF73254.1;
InterPro; IPR002085; Adh_zinc.
InterPro; IPR002328; ADH_zinc.
InterPro; IPR002328; ADH_zinc.
InterPro; IPR00231; TonB_boxC.
Pfam; PF00107; adh_zinc.
InterPro; IPR000551; TonB_boxC.
Pfam; PF00107; adh_zinc.
InterPro; IPR000551; TonB_boxC.
SEQUENCE FROM N.A.

Canestro C., Hjelmqvist L., Albalat R., Garcia-Fernandez J., Canestro C., Hjelmqvist L., Albalat R., Garcia-Fernandez J., Gonzalez Duarte R., Jornvall H.;

"Amphioxus ADH class III gene and protein characterization: "Amphioxus ADH class III gene and protein characterization: expansion and divergence times among major living forms.";

submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                O9NJC3;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ALCOHOL DEHYDROGENASE CLASS III (EC 1.1.1.1)
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01-OCT-2000
01-OCT-2000
01-JUN-2001
                                                                                                                                                                Eukaryota; Metazoa; Branchiostoma.
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                                                                                                                                                                        Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
Eukaryota: Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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PROSITE; PSO0059; ADH_ZINC; 1.

PROSITE; PSO0430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
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Branchiostoma.
NCBI_TaxID=7739;
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Eukaryota: Metazoa: Chordata: Cephalochordata: Branchiostomidae:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Search time 112.89 Seconds (without alignments)
10.366 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 18 18 19 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | o | ъ | 4 | ω | 2 | ш | Result No. |
|------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------------------|--------|--------------------|--------------------|--------|--------|--------|--------------------------|
| 28 28 | 28 | 28 | 29 | 29 | 29 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | 30 | Score |
| 80.0 | 80.0 | 80.0 | 82.9 | 82.9 | 82.9 | 85.7 | 85.7 | 85.7 | 85.7 | 85.7 | 85.7 | 85.7 | 85.7 | 85.7 | 85.7 | 85.7 | Query Match |
| 311 643 | 243 | 197 | 540 | 327 | 313 | 396 | 396 | 379 | 378 | 377 | 377 | 377 | 377 | 369 | 369 | 369 | Query Match Length DB |
| 404 |) N | 11 | N | G | Ų | 10 | 10 | 10 | 2 | տ | ű | σ | S | 2 | N | 2 | DB. |
| Q9X982 Q9NWE0 | Q9ADD0 | Q9JHG0 | Q9KCG9 | Q9NBV9 | 097363 | Q9SBA2 | 082014 | Q9FND2 | Q9JRB0 | Q9вJ33 | Q9ВJ34 | Q9NJC3 | Q9NJD0 | Q9A5D4 | 024687 | Q59399 | ID |
| | Q9add0 streptomyce | Q9jhg0 mus musculu | Q9kcg9 bacillus ha | Q9nbv9 manduca sex | 097363 bombyx mori | Q9sba2 linum usita | | | | Q9bj33 branchiosto | | Q9njc3 branchiosto | Q9njd0 branchiosto | | _ | • | Description |

| 50 | 49 | 48 | 47 | 46 | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ა 5 | 34 | ယ | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 . | 21 | 20 |
|--------------------|--------|-------------|--------|--------|--------|--------|--------|----------|----------|--------|--------------------|--------|--------|--------|--------------------|--------|--------------------|--------|-------------------|--------|--------------------|--------|--------|--------|--------|--------|--------|-----------|--------|--------|
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| 74.3 | | 74.3 | | | | 74.3 | | • | 74.3 | • | | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 |
| 379 | 379 | 375 | 375 | 375 | 375 | 375 | 375 | 348 | 316 | 303 | 247 | 242 | 229 | 208 | 182 | 166 | 1639 | 895 | 619 | 559 | 372 | 370 | 330 | 315 | 315 | 214 | 214 | 159 | 158 | 65 |
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| Q9PLK0 | 084731 | Q9R0E4 | Q9Z2M1 | Q9Z2M2 | Q9Z2M3 | Q64673 | Q64533 | Q9GI47 | 026177 | P97157 | Q9EYE4 | Q91715 | Q9ZX28 | Q9PSS0 | P97158 | Q99KK2 | Q9P7Q7 | Q9FGN6 | Q9VA04 | Q9ESA0 | Q9RDU5 | Q9HY01 | Q9S2V4 | Q9R9L5 | Q9X983 | Q98SR2 | Q9DE12 | Q38144 | Q9н667 | Q9Z2L5 |
| Дуртко сптатупта н | | 4 geomys Kn | geomys | | geomys | | geomys | dapnnipn | | _ | Q9eye4 escherichia | | | _ | P97158 escherichia | N. | Q9p7q7 schizosacch | | Q9va04 drosopnila | | Q9rdu5 pseudomonas | | | | | ~ | | pacteriop | | 5 mus |

ALIGNMENTS

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RESTRAIN=CLINICAL ISOLATE;

RX MEDLINE=97046207; PubMed=8891129;

RX MEDLINE=97046207; PubMed=8891129;

RY Plasmid-mediated formaldehyde resistance in Escherichia coli:

RY Plasmid-mediated formaldehyde resistance in Escherichia coli:

RY characterization of resistance gene.";

RI characterization of resistance gene.";

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RY coffactor. REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).

RY COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).

RY COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).

RY COFACTOR: REQUIRES ZINC CONTAINING ALCOHOL DEHYDROGENASE FAMILY.

RY COFFACTOR: REPOLITES ACH_ZINC.

RY FERNI, PRO032085; AGH_ZINC.

RY FERNI, PRO03105; AGH_ZINC.

RY COFFACTOR: RECOLARIES ACH_ZINC.

RY PROSITE; PS00055; AGH_ZINC.

RY COFFACTOR: RECOLARIES ACH_ZINC.

RY COFFACTOR: RECOLARIES ACH_ZINC.

RY FERNI, PRO03105; AGH_ZINC.

RY COFFACTOR: RECOLARIES ACH_ZINC.

RY COFFACTOR: RECOLAR
Query Match
Best Local Similarity
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Q59399; O1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1) (FORMALDEHYDE DEHYDROGENASE)
(GLUTATHIONE)) (FORMIC DEHYDROGENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
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SEQUENCE 369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
[1]
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AA: 39089 MW;
            85.7%;
62.5%;
            Score 30;
Pred. No.
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            DB
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Query Match
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HSSP; P11766; 1TEH.

InterPro; IPR002328; ADH_zinc.

InterPro; IPR002085; Adh_zinc.

Pfam; PF00107; adh_zinc; 1.

PROSITE; PS00059; ADH_ZINC; 1.
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SEQUENCE OF 1-6.
MEDLINE::88005160; PubMed::3653405;
MEDLINE::88005160; PubMed::3653405;
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P12711;
01-OCT-1989
01-OCT-1989
30-MAY-2000
                                                                                                             METAL
METAL
                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dehydrogenases. Differences FEBS Lett. 222:99-103(1987).
                                                                          BINDING
                                                                                                                                                                                   Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                         Lapatto R.; "Model for the structure of formaldehyde dehydrogenase based" f x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE: Liver;

MEDLINE-88152004; PubMed-3278908;

Julia P., Pares X., Joernvall H.;

"Rat liver alcohol dehydrogenase of class functional consequences and relationships dehydrogenases.";
                                                                                                                                                 METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91363326; PubMed-1888714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Joernvall H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ALCOHOL DEHYDROGENASE CLASS III (EC 1.1.1.1) (ALCOHOL
2) (GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FDH) (FALDH) (ALCOHOL DEHYDROGENASE-B2).
ADH5 OR ADH2 OR ADH-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Acetylated N-terminal structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-10116;
                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: CYTOPLASMIC SINILARITY: BELONGS TO THE ZINC-COFAMILY. CLASS-III SUBFAMILY.
                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ALCOHOL + NAD(+) & ALDEHYDE CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE S-FORMYLGLUTATHIONE + NADH.

COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                          J. BIOJ. MACTOMOL. 13:73-76(1991).
FUNCTION: CLASS-III ADH IS REMARKABLY
ETHANOL, BUT IT READILY CATALYZES THE
PRIMARY ALCOHOLS AND THE OXIDATION OF
                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                   GLUTATHIONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Blochem. 172:73-83(1988).
  Similarity
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62.
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Ψ.:
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                                            ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (SECOND ATOM) (BY SIMILARITY).
ZINC (SECOND ATOM) (BY SIMILARITY).
ZINC (SECOND ATOM) (BY SIMILARITY).
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ZINC (SECOND ATOM) (BY SIMILARITY).
ZINC (SECOND ATOM) (BY SIMILARITY).
ZINC (SCOND ATOM) (BY SIMILARITY).
IMPORTANT FOR FOH ACTIVITY AND ACTIVATION BY FATTY ACIDS (BY SIMILARITY).
BY FATTY ACIDS (BY SIMILARITY).
  Score
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                                                                                                                                                                     ACETYLATION.
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Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of class III alcohol
the three enzyme cla
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  NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             three enzyme classes.";
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DB 1;
9.2;
                                                                                                                                                                                                                                                                                                                                                                         INEFFECTIVE IN OXIDIZING OXIDATION OF LONG-CHAIN S-(HYDROXYMETHYL)
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           Length 373
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                                                                                                                                                                                                                                                                                                                                                                             "Alcohol dehydrogenase of class III: consistent patterns of structural and functional conservation in relation to class I and other proteins.";
FBBS Lett. 373:212-216(1995).
-i- FUNCTION: CLASS-III ADH IS REMARKABLY INEFFECTIVE IN OXIDIZING ETHANOL, BUT IT READILY CATALYZES THE OXIDATION OF LONG-CHAIN PRIMARY ALCOHOLS AND THE OXIDATION OF S-(HYDROXYMETHYL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ALCOHOL DEHYDROGENASE CLASS III (EC 1.1.1.1) (GLUTATHI FORMALDEHYDE DEHYDROGENASE) (EC 1.2.1.1) (FDH).
Uromastyx hardwickii (Indian spiny-tailed lizard).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; EuLepidosauria; Squamata: Iguania; Acrodonta; Agamidae;
                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LOCATION: CYTOPLASMIC -i- SIMILARITY: BELONGS TO THE ZINC-CC FAMILY. CLASS-III SUBFAMILY. HSSP: P11766; 1TEH.
                                                                                                                     BINDING
                                                                                                                                                                                                                  Oxidoreductase;
                                                                                                                                                                                                                         InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zinc.
Pfam; PF00107; adh_zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
 313
                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: REQUIRES
                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: ALCOHOL
-!- CATALYTIC ACTIVITY: FORMALDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P80467;
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                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313
                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: FORMALDEHYDE
S-FORMYLGLUTATHIONE + NADH.
COFACTOR: REQUIRES ZINC FOR ITS /
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WKGTAFGG
                    wkxxafxg
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                                         Similarity 62.55; Conservative
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PS00059; AL._
PS00059; AL._
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ZINC (SECOND ATOM).
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ZINC (CAPALYTIC).
IMPORTANT FOR FDH ACTIVITY AND ACTIVATION
BY FATTY ACIDS (BY SIMILARITY).
MW; 2BB3B44A0A9FCF06 CRC64;
                                                                                                                                                                                                                  Multigene
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                                                  Score 30;
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EHYDE + GLUTATHIONE
                                         Mismatches
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                                                                                                                                                                                (CATALYTIC).
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                                                                                                                                                                                                                Acetylation
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                                                           Length 373;
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                                                                                                                                                                                                                                                                                           ALCOHOL DEHYDROGENASE
                                       Indels
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Search completed: January 14, Job time: 504 sec

2002, 07:40:38

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J. Biol. Chem. 270:10868-10877(1995).

-i- FUNCTION: CLASS-III ADH IS REMARKABLY INEFFECTIVE IN OXIDIZING ETHANOL, BUT IT READILY CATALYZES THE OXIDATION OF LONG-CHAIN ETHANOL, BUT IT READILY CATALYZES THE OXIDATION OF S-(HYDROXYMETHYL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLUTATHIONE.
-!- CATALYTIC ACTIVITY: ALCOHOL + NAD(+)
-!- CATALYTIC ACTIVITY: FORMALDEHYDE + GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zgombic-Knight M., Ang H.L., Foglio M.H., Duester G.; "Cloning of the mouse class IV alcohol dehydrogenase (retino dehydrogenase) cDNA and tissue-specific expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dehydrogenase) and an unexpressed processed pseudogene with an intact
open reading frame.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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-!- COFACTOR: REQUIRES ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95256259; PubMed=7738026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur.
                                                                                                                                                                                                                                                                                                       InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zinc.
Pfam; PF00107; adh_zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
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SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
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Pred. No. 9
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CBBBDD404F79EAFA CRC64;
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                                                                                  Length 373;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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of the enzyme.";
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MEDLINE=98151253; PubMed=
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InterPro; IPR002085; Adh_zinc.
Pfam; PF00107; adh_zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
Oxidoreductase; Zinc; NAD; Mul
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CATALYTIC ACTIVITY: ALCOHOL + NAD(+) = ALDEHYDE OR KETONE + NAD(+) = CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE + NAD(+) = S-FORMYLGJUTATHIONE + NADH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY. CLASS-III SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: CYTOPLASMIC
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PubMed=9492289;
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                                                                                                                                                                                                                   MW;
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ZINC (CATALYTIC).
ZINC (SECOND ATOM).
ZINC (CATALYTIC).
AUTOPATANT FOR FOH ACTIVITY AND ACTIVATION
BY FATTY ACIDS (BY SIMILARITY).
MW; 9C9B84FD04D91625 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yang Z.-N., Bosron W.F., Hurley T.D.;
"Structure of human chi chi alcohol dehydrogenase:
dependent formaldehyde dehydrogenase.";
J. Mol. Biol. 265:330-343(1997)
-1- FUNCTION: CLASS-III ADH IS REMARKABLY INEFFECTI
ETHANOL, BUT IT READILY CATALYZES THE OXIDATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88209465; PubMed-3365377; Kaiser R., Holmquist B., Hempel J., Vallee B.L., Joernvall H.; Kaiser R., Holmquist B., Hempel J., Vallee B.L., Joernvall H.; "Class II human liver alcohol dehydrogenase: a novel structural equidistantly related to the class I and class II enzymes."; Blochemistry 27:1132-1140(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93077045; PubMed-1446828; Hur M.W., Edenberg H.J.; "Cloning and characterization of dehydrogenase 5, formaldehyde deh Gene 121:305-311(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97170743; PubMed-9018047;
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MEDLINE-93211987; Pubme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE, AND MUTAGENESIS MEDLINE-93264427; Pubmed-8494891; Holmquist B. Moulis J.M., Engelar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Scl. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vallee B.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         BL; M30471; AAA79018.1; -.
BL; M29872; AAA51597.1; -.
BL; M81118; AAA51596.1; JOINED.
BL; M811112; AAA51596.1; JOINED.
BL; M81113; AAA51596.1; JOINED.
BL; M81114; AAA51596.1; JOINED.
BL; M81115; AAA51596.1; JOINED.
BL; M81117; AAA51596.1; JOINED.
BL; M81117; AAA51596.1; JOINED.
BL; M81117; AAA51596.1; JOINED.
BL; M81117; AAA51596.1; JOINED.
BL; M81117; AAA51596.1; JOINED.
BL; M81117; AAA51596.1; JOINED.
BL; M81117; AAA51596.1; JOINED.
BL; M81117; AAA51596.1; JOINED.
BL; M8117; AAA51596.1; JOINED.
BL; M8174; AAA51596.1; JOINED.
BL; M8174; AAA51596.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: CYTOPLASMIC.
MISCELLANEOUS: THERE ARE 7 DIFFERENT ADH'S 1
THREE BELONGS TO CLASS-I: ALPHA, BETA, AND C
PI, ONE TO CLASS-III: CHI, ONE TO CLASS-IV:
                                                                                                                                                                                                                                                                                                                                            PI, ONE TO CLASS-III: CHI, OF CLASS-V: ADH6.
SIMILARITY: BELONGS TO THE Z. FAMILY. CLASS-III SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed⇔8460164;
eg J.-O., Holmqu
                                                                                                                                                                                                                                                                                                                                                           TO THE ZINC-CONTAINING ALCOHOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holmquist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90:2491-2494(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the ADH5 gene encoding human alcohol dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF ARG-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В.,
                                                                                                                                                                                                                         moved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLUTATHIONE + NAD(+) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Estonius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INEFFECTIVE IN OXIDIZING OXIDATION OF LONG-CHAIN S-(HYDROXYMETHYL)
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, ONE TO CLASS-II:
AND ONE TO
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Best Local
                                                                                                                                                                                                                                                                                                   X_MOUSE
ADHX_MOUSE
P28474;
01-DEC-1992
01-DEC-1992
30-MAY-2000
                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-91272926; PubMed-2053480;
MEDLINE-91., Brown C.J., Carr L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
SEQUENCE
Foglio M.H., Duester G., "Characterization of the alcohol dehydrogenase (gl
                                                                                      Hur M.W., Ho W.H., Brown C.J., Goldman D., Edenberg H.J., "Molecular cloning of mouse alcohol dehydrogenase-B2 cDNA: sequences of the class III ADH genes evolve slowly even for
                                                                                                                  SEQUENCE FROM N.A. MEDLINE=93112997; PubMed=1472709;
                                                                                                                                          Adv.
                                                                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
ALCOHOL DEHYDROGENASE CLASS III (EC 1.1.1.1) (ALCOHOL DEHYDROGENASE
2) (GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE) (EC 1.2.1.1)
(FDH) (FALDH) (ALCOHOL DEHYDROGENASE-B2) (ADH-B2).
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METAL
METAL
                                                                                                                                                                    Edenberg H.J., Brown C. "Alcohol dehydrogenase
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BINDING
                                MEDLINE=96215448; PubMed=8647091;
                                                   SEQUENCE FROM N.A
                                                                               substitutions
                                                                                                                                                              chi-like ADH
                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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METAL
METAL
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                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                             ADH5 OR ADH2 OR ADH-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zinc.
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103710; -.
136490; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 5; Conser
                                                                     3:167-175(1992).
                                                                                                                                                    Med.
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                                                                                                                                                    Biol.
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                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Rodentia;
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245
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                                                                                                                                                                                                                                                                                                                                                                                                                                           85.7%;
62.5%;
                                                                                                                                                  284:253-262(1991).
 (glutathione-dependent
                                                                                                                                                                     gene
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           functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC (CATALYTIC).

IMPORTANT FOR FDH ACTIVITY AND ACTIVATION
BY EATTY ACIDS.
R->A,D: LOSS OF FDH ACTIVITY AND LOSS OF
ACTIVATION BY FATTY ACIDS.
D -> Y (IN REF. 2).
F -> L (IN REF. 2).
MW; A4EA1ABD6F0424F4 CRC64;
                                                                                                                                                                     expression
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ZINC (CATALY
ZINC (SECONE
ZINC (SECONE
ZINC (SECONE
ZINC (SECONE
ZINC (SECONE
ZINC (SECONE
ZINC (CATALY
                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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Pred. No.
                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CATALYTIC).
(CATALYTIC).
(SECOND ATOM).
(SECOND ATOM).
(SECOND ATOM).
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9.2;
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           encoding
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                                                                                                                                                                    cloning
   formaldehyde
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           mouse
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                                                                                                                                                                    of the mouse
           Class
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            III
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SETTITION TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET
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ADHX_HO
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P19854;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
ALCOHOL DEHYDROGENASE CLASS III CHAIN (EC 1.1.1.1)
ALCOHOL DEHYDROGENASE DEHYDROGENASE) (EC 1.2.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished observations (NOV-1994).

-: CATALYTIC ACTIVITY: ALCOHOL + NAD(+) = ALDEHYDE OR KETONE + NADH.

-: CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE + NAD(+) =

S-FORMYLGLUTATHIONE + NADH.

-: COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (POTENTIAL).

-: SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

-: SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY. CLASS-III SUBFAMILY.

-: CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT HAD TO BE INTRODUCED IN POSTTION 128 TO PRODUCE THIS ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions we are modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed.
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                                                                                                                                                                                         MEDIINE=90105360; PubMed=2690942; Kaiser R., Holmquist B., Vallee B.L., Joernvall H.; Kaiser R., Holmquist B., Vallee B.L., Joernvall H.; "Characteristics of mammalian class III alcohol dehydrogenases, enzyme less variable than the traditional liver enzyme of class Biochemistry 28:8432-8438(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HORSE
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                                                                                                                                                                                                                                                                                                                                                                                                                   Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
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                                                 Joernvall H.;
                                                                                                     MEDLINE-88005160;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                            "Acetylated N-terminal structures
                                                                                                                                           SEQUENCE OF 1-6.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309
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Pro; IPR002085; Adh_zinc.
PF00107; adh_zinc; 1.
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etical protein; Oxidoreductase; Zinc (CATAI)
40 40 ZINC (CATAI)
62 62 ZINC (CATAI)
92 92 ZINC (SECON)
95 95 ZINC (SECON)
106 106 ZINC (SECON)
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5; Conserv
                                                                                 T., Julia
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  Differences
                                                                                 PubMed=3653405;
a P., Kaiser R.,
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62.5%;
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among
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(C (CATALYTIC) (BY SIMILARITY).

(C (CATALYTIC) (BY SIMILARITY).

(C (SECOND ATOM) (BY SIMILARITY).

(C (SECOND ATOM) (BY SIMILARITY).

(C (SECOND ATOM) (BY SIMILARITY).

(C (SECOND ATOM) (BY SIMILARITY).

(C (CATALYTIC) (BY SIMILARITY).
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  of o
                                                                                    Holmquist B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
No.
                            class III alcohol
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RESULT 16
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PIR; $02617; $02617.
PIR; $02617; $02617.
PIR; A33419; A33419.
HSSP; P11766; 1TEH.
InterPro; IPR002328; ADH_zinc.
InterPro; IPR002328; ADH_zinc.
InterPro; IPR002085; Adh_zinc.
Pfam; PF00107; Adh_zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
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MOD_RES 1

METAL 44

METAL 66

METAL 96

METAL 102

METAL 110

METAL 111

METAL 173

BINDING 114
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01-0CT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ALCOHOL DEHYDROGENASE CLASS III CHI CHAIN (EC
DEPENDENT FORMALDEHYDE DEHYDROGENASE) (EC 1.2.
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MEDLINE-90056459; PubMed=2818582;

Sharma C.P., Fox E.A., Holmquist B., Joernvall H., Valle

"cDNA sequence of human class III alcohol dehydrogenase.

Biochem. Biophys. Res. Commun. 164:631-637(1989).
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                                                                                                                   Giri P.R., Krug J.F., Kozak C., N
Seuanez H.N., Goldman D.;
"Cloning and comparative mapping
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SEQUENCE FROM
                                                         Biochem.
                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE~90026418; PubMed=2679557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADHX_HUMAN
                                                                                     dehydrogenase cDNA.";
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S-FORMYLGLUTATHIONE + NADH.

COPACTOR: REQUIRES ZINC FOR ITS ACTIVITY'
SUBUNIT: HOMODIMER.
SUBCELLULAR TOTAL
SUBCELLULAR TOTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: CYTOPLASMIC. SIMILARITY: BELONGS TO THE ZINC-CONTAINING
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                                                         Biophys.
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62.5%;
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Pred. No. 9.2;
0; Mismatches
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INFORTANT FOR FDH ACTIVITY AND ACTIVATION
BY FATTY ACIDS (BY SIMILARITY).

491F01B0A7D43D32 CRC64;
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                                                                164:453-460(1989)
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.1.1) (FDH).
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RP SEQUENCE OF 1-47.

RA MEDILINE-92118844; PubMed-1731906;

RA GULDELL W.G., Holmquist B., Vallee B.L.;

RA FUNCTION, Characterization, and partial sequence of the glutathione-dependent formaldehyde dehydrogenase from Escherichia Coli: a class III alcohol dehydrogenase.";

Blochemiatry 31:475-481(1992).

C-1- FUNCTION: HAS HIGH FORMALDEHYDE DEHYDROGENASE ACTIVITY IN THE DIOCHMISTION FAMBLE AND CATALYZES THE OXIDATION OF NORMAL PRESENCE OF GLUTATHIONE AND CATALYZES THE OXIDATION OF NORMAL ALCOHOLS IN A REACTION THAT IS NOT GSH-DEFENDENT. IN ADDITION, CLUDING COMEGA-THIOL FATTY ACIDS, ALSO ARE SUBSTRATES.

C-1- CATALYTIC ACTIVITY: FORMALDEHYDE FORMED OR KETONE + NADH.

C-1- CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE + NADH.

C-1- CCFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (4 IONS OF ZINC PER
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Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _ECOLI STANDARD; PRT; 369 AA.
ADH3_ECOLI STANDARD; PRT; 369 AA.
P25437; P75696; Q47533;
O1-MAY-1992 (Rel. 22, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALCOHOL DEHYDROGENASE CLASS III (EC 1.1.1.1) (GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE) (EC 1.2.1.1) (FDH) (FALDH).
ADHC OR B0356.
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SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN~K12 / MG1655;
MEDLINE~97426617; PubMcd~9278503;
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STRAIN-K12 / MG16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mau B., Shao Y.;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence nce 277:1453-1474(1997).
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MEM 82
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MEM 161
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EMBL/GenBank/DDBJ
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databases.
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Best Local
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P39450;
01-FEB-1995
                                                                                                                                                                                                                                                                         _PASPI
                                                                              SEQUENCE FROM N.A.
MEDLINE=94328963; PubMed=8052160;
Kim E.H., Aoki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
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METAL
METAL
                                "The transposon-like structure of IS26-tetracycline, resistance determinant derived from transferable R ppathogen, Pasteurella piscicida.", Microbiol. Immunol. 38:31-38(1994).
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METAL
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InterPro; IPR002328; ADH_zinc.
InterPro; IPR002385; Adh_zinc.
InterPro; IPR002085; Adh_zinc.
Pfam; PF00107; adh_zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bjoinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                          Photobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
 CDENTIFICATION,
Rudd K.E., Bair
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                                                                                                                                                                                                                                                                                                                     309 WKGSAFGG
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nes 5; Conserv
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SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: CYTOPLASMIC.
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
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           CONCEPTUAL TRANSLATION
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ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (SECOND ATOM) (BY SIMILARITY).

ZINC (SECOND ATOM) (BY SIMILARITY).

ZINC (SECOND ATOM) (BY SIMILARITY).

ZINC (SECOND ATOM) (BY SIMILARITY).

ZINC (SECOND ATOM) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

H -> E (IN REF. 5).

T -> G (IN REF. 5).
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RESULT 11
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Best Local
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30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
20-AUG-2001 (Rel. 4
Strausberg |
Submitted (/
-!- FUNCTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morita K., Furuse M., Tsukita S.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00822; PMP22_Claudin; PRINTS; PR01077; CLAUDIN. PROSITE; PS01346; CLAUDIN; 1.
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InterPro; IPR000729; PMP22_C
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20-AUG-2001
                                                              "Claudin multigene family encoding four-transmembrane components of tight junction strands."; proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).
                                                                                                                                                                                                                    CLAUDIN-6.
                                                                                                                                                                                                                                                                               CLD6_MOUSE
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                                                                                                  MEDLINE=99110921; pubMed=9892664; Morita K., Furuse M., Fujimoto K.,
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FUNCTION: COMPONENT
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MEM 13 33 P

MEM 82 102 P

MEM 117 137 P
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                                                                                                                                                                                                                              39, Created)
39, Last sequence update)
40, Last annotation update)
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the EMBL/GenBank/DDBJ databases OF TIGHT JUNCTION (TJ) STRANDS.
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Pred. No.
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                  pfam; PF00822; PMP22_Claudin;
PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
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InterPro; IPR001832; Claudin6.
InterPro; IPR003925; Claudin6.
InterPro; IPR000729; PMP22_Cla
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                                                                                                                      EMBL; AJ249735; CAB56533.1; InterPro; IPR001832; Claudin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                       InterPro; IPR003925; Claudin6.
InterPro; IPR000729; PMP22_Claudin.
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CGUTACHTIONE

C-1- CATALYTIC ACTIVITY: ALCOHOL + NAD(+) - ALDEHYDE OR KETONE + NADH.

C-1- CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE + NAD(+) -

CS-FORMYLGLUTATHIONE + NADH.

C-1- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY.

C-1- SUBUNIT: HOMODIMER AND HETERODIMER WITH L CHAIN.

C-1- SUBUNIT: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE

C-1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE

C-1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE

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PROSITE; PS01346; CLAUDIN; 1.
Tight function; Transmembrane.
                                                                                                                                                                    modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Keen T.J., Inglehearn C.F.;

Keen T.J., Inglehearn C.F.;

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-I- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
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09YH91;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
CLAUDIN-LIKE PROTEIN ZF-A89.
                                                              InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Futebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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IMPORTANT FOR FOH ACTIVITY AND ACTIVATION
BY FATTY ACIDS (BY SIMILARITY).
0B9760AB77329FE3 CRC64:
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RESULT 10
CLD9_MOUSE STANDARD;
ID CLD9_MOUSE STANDARD;
AC Q920S7;
DT 30-MAY-2000 (Rel. 39, Created)
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CLD9_HUMAN
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PRINTS; PRO1077; CLAUDIN; 1.
PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
                                                                                                                                                                                                                                           EMBL; AJ130941; CAA10254.1; -.
InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                Keen T.J., Inglehearn C.F.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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GA4BB5EBF3CCABB1 CRC64;
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RESULT 6
OM25_BRUSU
ID OM25_B
AC Q45689
DT 15-DEC
DT 15-DEC
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Q45326;
15-DEC-1998
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OM25_BRUSU
Q45689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloeckaert A., Verger J.M., Grayon M., Zygmunt M.S., Grepinet O. Nucleotide sequence and expression of the gene encoding the maj Skilodalton outer membrane protein of Brucella ovis: Evidence 25-kilodalton outer membrane protein of Brucella species, due to a antigenic shift, compared with other Brucella species, due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRUNE
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                                                                                                                                                                                                                                                                                                                                                                                            deletion in the gene.";
Infect. Immun. 64:2047-2055(1996).
-!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
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Pfam; PF01389; OmpA_membrane; 1.
Antigen; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96239016; PubMed=8675306;
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(Rel. 37, Created)
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62.5%;
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Last annotation update)
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Pred.
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RESULT 7

ADHH_GADH_G
AC P81600
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DT 15-JUL
DT 15-JUL
DT 15-JUL
DT ALCOHO
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RP SEQUEN
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Infect. Immun. 64:2047-2055(1996).
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25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN PRECURSOR OMP25.
                                                      Danielsson O., Shatgat J., January Banielsson O., Shatgat J., January Bangary With anomalous alcohol dehydrogenase. Effects on the alcohol dehydrogenase exchanges at 'nc
                                                                                                                                                                                                                                                                                              P81600;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ALCOHOL DEHYDROGENASE CLASS III H CHAIN (EC 1.1.1.1) (GLUTATHIONE-
DEPENDENT FORMALDEHYDE DEHYDROGENASE) (EC 1.2.1.1) (FDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Infect. Immun. 64:204/-2023(1990).
-!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Brucellaceae; Brucella.
                                                                                                                                                                                                                              Gadus morhua (Atlantic cod).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acthopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000498; OmpA_tmem.
Pfam; PF01389; OmpA_membrane; 1
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   Biochemistry 35:14561-14568(1996).
-i- FUNCTION: CLASS-III ADH IS REMARKABLY
ETHANOL, BUT IT READILY CATALYZES THE
                                                    protein."
                                                                                                                                                                                                                                                                                                                                                                                                            ADHH_GADMO
                                                                                                                        MEDLINE=97085413; PubMed=8931553;
Danielsson O., Shafqat J., Estonius M., El-Ahmad M.,
                                                                                                                                                                                           NCBI_TaxID=8049;
                                                                                                                                                              SEQUENCE
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 FUNCTION: ETHANOL, I
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25 KDA OUTER-MEMBRANE IMMUNOGENIC
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                                                                       ous dimer patterns in the activity and qua'non-functional' sit
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   INEFFECTIVE IN OXIDIZING OXIDATION OF LONG-CHAIN
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ding the major
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MBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           de Wergifosse P., Lintermans P., Limet J.N., Cloeckbert A.; "Cloning and nucleotide sequence of the gene coding for the kilodalton outer membrane protein of Brucella abortus."; J. Bacteriol. 177:1911-1914(1995).
-!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q44664;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN PRECURSOR.
                                                                                                                                                    OM25_BRUCA STANDARD; PRT; 213 AA Q45110; Q45110; Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update 25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN P
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MEDLINE~96239016; PubMed~8675306;
Cloeckaert A., Verger J.M., Grayo
"Nucleoilde sequence and expressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95204367; PubMed-7896724;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brucella abortus
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                                                                                                  Brucellaceae;
                                                                                                              Bacteria; Proteobacteria;
                                                                                                                           Brucella canis.
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Antigen; Outer mcmbrane; Signal.
SIGNAL 1 23 POT
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                                            STRAIN RM6
                                                       SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID 36855;
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 Grayon M., Zygmunt M.S.,
pression of the gene enco
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PROTEIN.
; 2328515F1F794BC7 CRC64;
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000498; OmpA_tmem. Pfam; PF01389; OmpA_membrane; 1. Antigen; Outer membrane; Signal.
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Infect. Immun. 64:2047-2055(1996)
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                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloeckaert A., Verger J.M., Grayon M., Zygmunt M.S., Grepinet O. "Nucleotide sequence and expression of the gene encoding the maj 25-kilodalton outer membrane protein of Brucella ovis: Evidence antigenic shift, compared with other Brucella species, due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM25_BRUME STANDARD; PRT; 213 AA. Q45321; Q45321; Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 15-DEC-1998 (Rel. 37, Last annotation update) 25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRUME
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Pfam; PF01389; OmpA_membrane; 1
Antigen; Outer membrane; Signal
SIGNAL 1 23 PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-kilodalton outer membrane protein antigenic shift, compared with other deletion in the gene."; Infect. Immun. 64:2047-2055(1996).
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Bacteria; Proteobacteria;
Brucellaceae; Brucella.
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-!- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
                                                                                                               EMBL; U33003; AAB06701.1;
                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
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                                                                                       InterPro;
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25 KDA OUTER-MEMBRANE IMMUNOGENIC
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  pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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DB
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Gapop 10.0 ,
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7 uromastyx h
1 gadus morhu
paracoccus
4 rhodobacter
0 myxine glut
6 sparus aura
7 haemophilus
5 drosophila
1 octopus vul
2 pisum sativ
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homo sapien
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A;Description: catalyzes the oxidation by NAD+ of formaldehyde and glutathione to C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C;Keywords: alcohol metabolism; metalloprotein; NAD; oxidoreductase; zinc F;34-371/Domain: long-chain alcohol dehydrogenase homology <LADH> F;198-227/Region: beta-alpha-beta NAD nucleotide-binding fold F;49,71,178/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted F;101,104,107,115/Binding site: zinc, noncatalytic (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Function: <ADH>
A; Description: catalyzes the oxidation of primary and secondary alcohols to C; Function: <FDH>
                                                                                                                                                                                                                                                                                                                                                                                         formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) - rice C;Species: Oryza sativa (rice) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change C;Accession: T04164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: detoxifying enzyme (2; Note: detoxifying enzyme (2; Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homo (2; Superfamily: oxidoreductase; zinc (2; Superfamily: oxidoreductase; zinc (3; Note: dehydrogenase homology (2; Note: 2; Note: 1) (2; Note: Note: 1) (3; Note: 1) (4; Note: 1) (4; Note: 1) (5; Note: 1) (5; Note: 1) (6; Note: 1) (6; Note: 1) (7; Note: 1) (7; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; Note: 1) (8; No
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Plant Mol. Biol. 34, 843-854, 1997
A;Title: Maize glutathione-dependent formaldehyde dehydrogenase cDNA: a
A;Reference number: Z14885; MUID:97435970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Zea mays (maize)
C; Date: 24-Mar-1999 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: fdh
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A;Experimental source: cultivar Black Mexican Sweet
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A; Residues: 1-381 <FLE>
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                                                                                                                                                                                                                                                                   R;Dolferus, R.; Osterman, J.C.; Peacock, W.J.; Dennis, submitted to the EMBL Data Library, November 1996 A;Description: Cloning of the Arabidopsis and rice class
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                                                                                 A; Molecule type: DNA
A; Residues: 1-381 <DOL>
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Cross-references: EMBL:U77637; NID:q1675393; PIDN:AAB19117.1; PID:g1675394;Experimental source: subsp. Indica, var. IR36
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Pred. No. 23;
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A;Gene: AdhIII
A;Gene: AdhIII
A;Introns: 14/1; 59/3; 75/2; 184/1; 211/3; 237/1; 289/3; 343/3
A;Introns: 14/1; 59/3; 75/2; 184/1; 211/3; 237/1; 289/3; 343/3
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: NAD; oxidoreductase; zinc
C;Keywords: NAD; oxidoreductase; zinc
F;34-370/Domain: long-chain alcohol dehydrogenase homology <LAD>
F;49,71,179/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alcohol dehydrogenase (EC 1.1.1.) SFA1 - yeast (Saccharomyces cerevisiae) N,Alternate names: class III alcohol dehydrogenase; protein D1473; protein N;Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) C;Species: Saccharomyces cerevisiae C;Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 21-Jul-2000 C;Accession: S31140; S61045; S67720 R;Wehner, E.P.; Rao, E.; Brendel, M. Mol. Gen. Genet. 237, 351-358, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Thehes 5; Conserv
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                                                                                          A,Title: Molecular structure and genetic regulation A;Reference number: S31138; MUID:93247548 A;Accession: S31140
                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:274216; NID:g1431267; PIDN:CAA98742.1; PID:g1431268; A;Experimental source: strain S288C C;Comment: Class III alcohol dehydrogenases are pyrazole-insensitive, are not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-386 < POH>
A; Cross-references: EMB
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                                                                                                                                                                                                                                                                                                             A;Gene: SGD:SFA1; MIPS:YDL168w
A;Cross-references: SGD:S0002327;
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A; Residues: 1-386 < POW>
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A;Map position: 4L
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                  Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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62.5%;
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Score 30; DB Pred. No. 23; 0; Mismatches
    0;
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Pred. No.
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322

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A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-378 <PAR>
A:Cross-references: GB:AL162756; GB
A:Cross-references: serogroup A.
C:Genetics:
A:Genetics:
A:Genetics:
A:Genetics: NMB1304; NMA1518
C:Superfamily: alcohol dehydrogena:
C:Keywords: NAD: oxidoreductase; z:
F:49,71,178/Binding site: zinc, car
A;Description: catalyzes the oxidation by NAD+ of formaldehyde and glutathione to S-form C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidor F;2-379/Product: alcohol dehydrogenase Fdh #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alcohol dehydrogenase (EC 1.1.1) Fdh - fruit fly (Drosophila melanogaster)
N.Alternate names: class III alcohol dehydrogenase
N.Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1); octanol dehydrogenase
C.Species: Drosophila melanogaster
C.Accession: S51357
R.Luque, T.; Atrian, S.; Danielsson, O.; Joernvall, H.; Gonzalez-Duarte, R.
Eur. J. Biochem. 225, 985-993, 1994
A. Filtle: Structure of the Drosophila melanogaster glutathione-dependent formaldehyde deh
hydrogenase genes.
A. Reference number: S51357; MUID:95045575
A. Rocession: S51357
A. Rocession: S51357
A. Rocession: S51357
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A:Introns: 7/3; 37/3
C:Complex: homodimer
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C;Accession: F81097; B81843
R;Tettelin, H; Sanders, N.J; Heidelberg, J.; Jeffries, A.C.; Nelson, R.Tettelin, H; Sanders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Ri, M.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-379 <LUQ>
A;Residues: 1-379 <LUQ>
A;Cross-references: EMBL:U07799; NID:g538264; PIDN:AAA57187.1; PID:g538265
C;Comment: Class III alcohol dehydrogenases are pyrazole-insensitive, are
                                                                                                                                                                                           C; Function:
                                                                                                                                                                                                                                  A; Description:
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A:Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitid A:Reference number: A81775; MUID:20222556

A:Accession: B81843
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A; Residues: 1-378 <TET>
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A;Accession: F81097
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:Superfamily: alcohol dehydrogenase;
:Keywords: NAD; oxidoreductase; zinc
:49,71,178/Binding site: zinc, cataly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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nes 5; Conservative
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A, strain Z2491
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; Dougherty,
; Pizza, M.
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                                                                                                                                                                                                                                                                                                            alcohol dehydrogenase (EC 1.1.1.) FDH1 - yeast (Candida maltosa) N;Alternate names: class III alcohol dehydrogenase N;Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) C;Species: Candida maltosa C;Date: 30-Sep-193 #sequence_revision 30-Sep-1993 #text_change 1: C;Accession: JN0447 C;Accession: JN0447 R;Sasnauskas, K.; Jomantiene, R.; Januska, A.; Lebediene, E.; Lebe Gene 122, 207-211, 1992 A;Ritle: Cloning and analysis of a Candida maltosa gene which conf A;Reference number: JN0447; MUID:93083986 A;Accession: JN0447; MUID:93083986
                                                                                                        A;Cross-references: GB:M58332; NID:g170870; PIDN:AAA343444.1; PID:g170871 C;Comment: This protein confers resistance to formaldehyde in yeast C;Comment: Class III alcohol dehydrogenases are pyrazole-insensitive, ar
                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-381 <SAS>
                                                                                  C; Genetics:
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Albescription: Catalyzes the oxidation by NAD+ of formaldehyde and glutathione C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C:Keywords: alcohol metabolism; metalloproteain; NAD; oxidoreductase; zinc F:32-388/Domain: long-chain alcohol dehydrogenase homology <LADH> F:197-226/Region: beta-alpha-beta NAD nucleotide-binding fold F:47,69.177/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted F:99,102,105,113/Binding site: zinc, noncatalytic (Cys) #status predicted
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A;nection: <FDH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N:Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 16-Jun-2000
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A; Residues: 1-379 < MAR>
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E:197-226/Region: beta-alpha-beta NAD nucleotide-binding fold
E:24/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
E:48,70.177/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
E:100,103,106,114/Binding site: zinc, noncatalytic (Cys) #status predicted
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alcohol dehydrogenase (EC 1.1.1) class III - common octopus N;Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) C;Species: Octopus vulgaris (common octopus) C;Date: O7-Apr-1994 #sequence_revision 31-Dec-1995 #text_change O1-Ma C;Accession: A49662 R;Kaiser, R.; Fernandez, M.R.; Pares, X.; Jornvall, H. Proc. Natl. Acad. Sci. U.S.A. 90, 11222-11226, 1993 A;Title: Origin of the human alcohol dehydrogenase system: implicatio A;Reference number: A49662; MUID:94068576 A;Accession: A49662 A;Molecule type: protein A;Residues: 1-378 <KAIP A;Experimental source: gills, salivary glands, heart ...
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C;Species: Myxine glutinosa (Atlantic hagfish)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Feb-1999
C;Accession: S51187; S66197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, FEBS Lett. 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogena
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C;Complex: homodimer
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A; Residues: 1-17 < HJE>
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Accession: S66197
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J. Biochem. 225, 1081-1088, 1994
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probable alcohol dehydrogenase (EC C; Species: Neisseria meningitidis

1.1.1.1) class III NMA1518 [similarity] - Neisseri

RESULT F81097

14

QУ

1 wkxxafxg 8

Вþ

318 WKGSAFGG

Query Match Best Local Similarity Thes 5; Conserv

Conservative

85.7%;

Score 30; Pred. No.

DB 22;

<u>,,</u>

Length 378;

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Gaps

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A;Description: Gatalyzes the oxidation by NAD+ of formaldehyde and glutathione to C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C;Superfamily: alcohol dehydrogenase homology C;Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; F;1-378/Product: alcohol dehydrogenase class III #status experimental <MAT'> F;32-367/Domain: long-chain alcohol dehydrogenase homology <LADH> F;196-225/Region: beta-alpha-beta NAD nucleotide-binding fold F;47,69,176/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted F;47,69,176/Binding site: zinc, noncatalytic (Cys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alcohol dehydrogenase (EC 1.1.1.) HI0185 - Haemophilus influenzae (strain F N; Alternate names: class III alcohol dehydrogenase N; Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) C; Species: Haemophilus influenzae C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 11-Jun-1999 C; Accession: H64052
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C; Function: <FDH>
A;Description: catalyzes the oxidation by NAD+ of formaldehyde and glutathione to S-f C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C;Keywords: alcohol metabolism; homodimer; metalloprotein; NAD; oxidoreductase; zinc F;34-369/Domain: long-chain alcohol dehydrogenase homology <LADH> F;198-227/Region: beta-alpha-beta NAD nucleotide-binding fold F;49,71,178/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted F;101,104,107,115/Binding site: zinc, noncatalytic (Cys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                      C; Complex: homodimer
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C;Comment: Class III alcohol dehydrogenases are pyrazole-insensitive, are not very ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-378 <TIGR>
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Best Local
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                                                                                                                                                                                                                                                                                        the oxidation of primary and secondary alcohols to aldehydes
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62.5%;
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22;
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J. Protein Chem. 10, 69-73, 1991
A;Title: Human class III alcohol dehydrogenase/glutathione-dependent formaldehyde dehydr A;Reference number: A61428; MUID:91273763
A;Molecule type: protein A;Residues: 2-374 <KA2>
R;Yang, Z.N.; Hurlev m -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alcohol dehydrogenase (EC 1.1.1.1) 2 - mouse
N;Alternate names: alcohol dehydrogenase chi chain; class III alcohol dehydrogenase
N;Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1)
C;Species: Mus musculus (house mouse)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 11-Jun-1999
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 11-Jun-1999
C;Accession: A56643, A60269; S71333
R;Hur, M.W.; Ho, W.H.; Brown, C.J.; Goldman, D.; Edenberg, H.J.
DNA Seq. 3, 167-175, 1992
A:Status: preliminary
A:Molecule type: mRNA
A:ROLecule type: mRNA

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C; Functi
                                                                                                                                                                                                                                                                                                                                       DNA Seq. 3, 167-175, 1992
A:Title: Molecular cloning of mouse alcohol A:Reforence number: A56643; MUID:93112997
A:Accession: A56643
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submitted to the Brookhaven Protein Data Bank, February 1996
A;Reference number: A66716; PDB:ITEH
A;Contents: annotation; X-ray crystallography, 2.70 angstroms, residues 2-374
C;Comment: Class III alcohol dehydrogenases are pyrazole-insensitive, are not C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4921-4925
A;Introns: 4/3; 38/3; 86/1; 115/2; 188/3; 275/3; 321/1; 367/2
C;Complex: homodimer; does not form heterodimers with the class I alcohol dehydrogenases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:ADH5
A;Cross-references: GDB:118978; OMIM:103710
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A;Accession: A29983
A;Molecule type: protein
A;Residues: 2-374 <KAI>
R;Kaiser, R.; Holmquist, B.; Vallee, B.L.
J. Protein Chem. 10, 69-73, 1991
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Best Local
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5; Conserv
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A;Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes C;Function: <PDH>
A;Description: <PDH>
A;Description: catalyzes the oxidation by NAD+ of formaldehyde and glutathione to S-f C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C;Keywords: acetylated amino end; alcohol metabolism; homodimer; metalloprotein; NAD; F;2-374/Product: alcohol dehydrogenase 2 %status predicted <MAT>
F;30-365/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;194-223/Region: beta-alpha-beta NAD nucleotide-binding fold f;22/Modified site: acetylated amino end (Ala) (in mature form) #status predicted F;45,67,174/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted F;97,100,103,111/Binding site: zinc, noncatalytic (Cys) #status predicted
A;Description: catalyzes the oxidation by NAD+ of formaldehyde and glutathione to C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C;Keywords: alcohol metabolism; dimer; metalloprotein; NAD; oxidoreductase; zinc E;2-376/Product: alcohol dehydrogenase class III #status predicted <MAT> F;32-367/Domain: long-chain alcohol dehydrogenase homology <LADH> F:196-225/Region: beta-alpha-beta NAD nucleotide-binding fold E;47,69,176/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted F;99,102,105,113/Binding site: zinc, noncatalytic (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-376 <FUN>
A;Cross-references: GB:U84791; NID:g1814385;
C;Comment: Class III alcohol dehydrogenases #
                                                                                                                                                                                                                                                               A:Description: catalyzes the oxidation of primary C;Function: <FDH>
                                                                                                                                                                                                                                                                                                                               C;Complex: homodimer
C;Function: <ADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Funkenstein, B.; Jakowlew, S.B.
Gene 174, 159-164, 1996
A;Title: Molecular cloning of fish alcohol
A;Reference number: JC4967; MUID:97017142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N:Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) C:Species: Sparus aurata (gilthead sea bream) C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jun-1999 C:Accession: JC4967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JC4967
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C;Complex: homodimer; does not form heterodimers with the class I alcohol C;Function: <ADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alcohol dehydrogenase (EC 1.1.1.1) class III - gilthead sea bream
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Foglio, M.H.; Duester, G.
Eur. J. Biochem. 237, 496-504, 1996
A;Title: Characterization of the functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: adh-2
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A; Residues: 1-374 < FOG>
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A;Title: Alcohol dehydrogenase gene expression
A;Reference number: A60269; MUID:91272926
A;Accession: A60269
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62.5%;
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are pyrazole-insensitive, are
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R:Koivusalo, M., Baumann, M.; Uotila, L.

FEBS Lett. 257, 105-109, 1989

A;Title: Evidence for the identity of glutathione-dependent formaldehyde dehydrogenase & A;Reference number: S06633; MUID:90033321

A;Accession: S06633; MUID:90033321

A;Status: preliminary

A;Molecule type: protein
A;Residues: 9-25,84-95,'X',97-98,'X',187;188,189-193,'X',195-198;357-365 <KOI>
A;Experimental source: strain Wistar
C;Comment: Class III alcohol dehydrogenases are pyrazole-insensitive, are not very active.
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R;Julia, P.; Pares, X.; Joernvall, H.
Eur. J. Biochem. 172, 73-83, 1988
A;Title: Rat liver alcohol dehydrogenase of class A; Reference number: $00331; MUID:88152004
A;Accession: $00331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Complex: homodimer; does not form heterodimers with the class I alcohol dehydrogenases C:Function: <ADH>
A:Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes an C:Function: <FPH>
A:Description: catalyzes the oxidation by NAD+ of formaldehyde and glutathione to S-form C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C:Keywords: acetylated amino end: alcohol metabolism; homodimer; metalloprotein; NAD; ox F:1-373/Product: alcohol dehydrogenase 2 #status experimental <fra>
F:29-364/Domain: long-chain alcohol dehydrogenase homology <LADH>
F:193-222/Region: beta-alpha-beta NAD nucleotide-binding fold
F:14,66,173/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted
F:96,99,102,110/Binding site: zinc, noncatalytic (Cys) #status predicted
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A;Accession: S02619
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A; Residues: 1-373 < JUL>
R: Fairwell, T; Julia, P: Kaiser,
FEBS Lett. 222, 99-103, 1987
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 01-May-1998
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                                                                                                                            alcohol dehydrogenase (EC 1.1.1.1) class III - Indian spiny-tailed N;Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) C;Species: Uromastyx hardwickii (Indian spiny-tailed lizard) C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 01-C;Accession: S68061; S66194
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A; Title: Alcohol dehydrogenase of class III: A; Reference number: S68061; MUID: 96033975
                                                                 R;Hjelmqvist, L.; Shafqat, J.; Siddiqi, A.R.; Joernvall, FEBS Lett. 373, 212-216, 1995
                                                                                                                                                                                                                                                                                                          S68061
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                                         consistent
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                                             of structural and
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alcohol dehydrogenase (EC 1.1.1) 5 [validated] - human
N;Alternate names: alcohol dehydrogenase chi chain; class III alcohol dehydrogenase
N;Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1)
C;Species: Homo sapiens (man)
C;Date: 30.5ep-1991 #sequence_revision 05-Aug-1994 #text_change 15-Sep-2000
C;Date: 30.5ep-1991 #sequence_revision 05-Aug-1994 #text_change 15-Sep-2000
C;Accession: JH0789; A36739; A33428; A55397; A29983; A61428; S02618; S11077
R;Hur; M.W.; Edenberg, H.J.
Gene 121, 305-311, 1992
A;Title: Cloning and characterization of the ADH5 gene encoding human alcohol dehydro
A;Reference number: JH0789; MUID:93077045
A;Accession: JH0789; MUID:93077045
A;Cross-references: GB:M81112; GB:M81118; NID:g178128; PIDN:AAA51596.1; PID:g178130
A;Residues: 1-374 <HUR>
A;Cross-references: GB:M81112; GB:M81118; NID:g178128; PIDN:AAA51596.1; PID:g178130
A;Rosidues: Lophys Res. Commun. 164, 631-637, 1989
A;Title: CDNA sequence of human class III alcohol dehydrogenase.
A;Residues: 1-374 <SHAN
A;Residues: 1-374 <SHAN
A;Residues: 1-374 <SHAN
A;Residues: GR:MA71. NID:G178133. DIDN:AAA70018 1. DID:G178134
A;Residues: GR:MA70471. NID:G178133. DIDN:AAA70018 1. DID:G178134
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                                                                                                                                                                           A;Cross-references: GB:M30471; NID:g178133; PIDN:AAA79018.1; PID:g178134 R;Giri, P.R.; Krug, J.F.; Kozak, C.; Moretti, T.; O'Brien, S.J.; Seuanez, Blochem. Biophys. Res. Commun. 164, 453-460, 1989 A;Fitle: Cloning and comparative mapping of a human class III (chi) alcoh A;Reference number: A33428; MUID:90026418 A;Accession: A33428 MUID:90026418 A;Molecule type: mRNA A;Residues: 'MGAATPVDSPPRRPESVN',1-166,'Y',168-374 <GIR>
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A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogena:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: catalyzes the oxidation of primary and secondary alcohols to
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A;Cross-references: GB:M29872; NID:9178131
A;Note: the authors translated sequence upstream of Met-1 R;Hur, M.W.; Edenberg, H.J.
J. Biol. Chem. 270, 9002-9009, 1995
A;Title: Cell-specific function of cis-acting elements in
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NYALCETHALE Halmess Clades III accounce dehydrogenase (glutathione) (EC 1.2.1.1)

C. Species: Escherichia coli
C. Species: Escherichia coli
C. Pate: 10-Jul-1992 #sequence_revision 01-May-1998 #text_change 11-Jun-1999
C. Accession: SS7525
R. Kuemmerle, N.; Feucht, H.; Kaulfers, P.M.
submitted to the EMBL Data Library, June 1993
A. Description: Plasmid-mediated formaldehyde-resistance in E. coli: nucleotide sequence A: Reference number: S57525
A: Molecule type: DNA
A: Residues: 1-369 <KUE>
A: Residues: 1-369 <KUE>
A: Residues: 1-369 <KUE>
A: Compent: Cluss III alcohol dehydrogenases are pyrazole-insensitive, are not very active (Complex: homodiner Cluss III alcohol dehydrogenases are pyrazole-insensitive, are not very active (Complex: homodiner Cluss III alcohol dehydrogenases are pyrazole-insensitive, are not very active (Complex: homodiner Cluss III alcohol dehydrogenases are pyrazole-insensitive, are not very active (Complex: homodiner catalyzes the oxidation of primary and secondary alcohols to aldehydes are C: Function: <ADH>
A: Description: catalyzes the oxidation by NAD+ of formaldehyde and glutathione to S-form C: Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology (Complex: Complex: chain alcohol dehydrogenase homology (Complex: Complex: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alcohol dehydrogenase (EC 1.1.1.1) C - Escherichia coli (isolate VU N;Alternate names: class III alcohol dehydrogenase N;Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Doscription: catalyzes oxidation by NAD+ of formaldehyde and glutathione to S-formylgl C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C:Keywords: alcohol metabolism; homodiner; metalloprotein; NAD; oxidoreductase; zinc F:25-360/Domain: long-chain alcohol dehydrogenase homology <LADH> F:189-218/Region: beta-alpha-beta NAD nucleotide-binding fold F:40,62,169/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted F:92,95,98,106/Binding site: zinc, noncatalytic (Cys) #status predicted
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A:Residues: 1-24, X', 26-40, /E', 42-45, 'G', 47 <GUT>
A:Residues: this enzyme also has hemithiolacetal dehydrogenase activity
R:Nashimoto, H.; Saito, N.
R:Nashimoto, H.; Saito, N.
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A;Residues: 'MLPLHLL',11,'VNRWKSLKLTLHHR',26-369 <NAS>
A;Cross-references: EMBL:D85613
A;Cross-references: EMBL:D85613
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                                                    Query
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           Local
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A;Description: Catalyzes the oxidation of primary and secondary alcohols to aldehydos C;Function: cFDH>
A;Description: catalyzes the oxidation by NAD+ of formaldehyde and glutathione to S-f
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: acetylated amino end; alcohol metabolism; homodimer; metalloprotein; NAD;
F;1-373/Product: alcohol dehydrogenase chi chain #status experimental <mary
F;29-364/Domain: long-chain alcohol dehydrogenase homology <LADH>
F;193-222/Region: beta-alpha-beta NAD nucleotide-binding fold
F;14Modified site: acetylated amino end (Ser) #status experimental
F;44,66,173/Bidding site: zinc, catalytic (Cys, His, Cys) #status predicted
                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 1-373 <KAI>
C; Comment: Class III alcohol dehydrogenases are |
C; Complex: homodimer; does not form heterodimers
C; Function: <ADH>
                                                                                                                                                                                                                                                                                                                                            A; Reference number: A33419; A; Accession: A33419 A; Molecular L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alcohol dehydrogenase (EC 1.1.1.1) class III horse N:Contains: formaldehyde dehydrogenase (glutathione) C:Species: Equus caballus (domestic horse) C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85530
A;Status: preliminary
A;Molecule type: DNA
A;Residuse: 1-369 <STO>
A;Cross-references: GB:AE005174; NID:g12513195; PIDN:AAG54707.1; GSPDB:
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kaiser, R.; Holmquist, B.; Vallee, B.L.; Joernvall, H. Biochemistry 28, 8432-8438, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Kaiser, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: A33419
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C;Superfamily: alcohol dehydrogenase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iller, L.; Grotbeck, E.J.; Davis, N.W.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: G85530
R; Perna, N.T.; Plunk
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  96,99,102,110/Binding site: zinc,
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anta, E.;
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Similarity 5; Conser

62

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Score 30; Pred. No.

DB 22;

<u>,</u>

Length 373

Indels

0

Gaps

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Mismatches

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Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match
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35
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D64763
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|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-----------------|--------------------|--------------------|--------------------|
| 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 28 | 28 | 29 |
| 74.3 | | 74.3 | | | 74.3 | 74.3 | 74.3 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | • | 80.0 | 82.9 |
| 264 | 242 | 224 | 198 | 185 | 135 | 100 | 93 | 1639 | 600 | 600 | 599 | 370 | 330 | 280 | 224 | 193 | 159 | 528 | 528 | 1220 |
| 2 | Ν | ν | 2 | N | N | N | Ν | N | N | N | N | Ν | N | Ν | N | 2 | 2 | 2 | N | 2 |
| н64086 | F83629 | G85842 | G85506 | S20593 | JQ1225 | JQ0859 | H36808 | T50119 | S00561 | A28960 | A29947 | B83191 | T34972 | A39484 | A60032 | A37873 | S41178 | T45418 | G70854 | A56236 |
| glycerol facilitat | " | probable tall comp | hypothetical proce | alcohol denydrogen | Unci protein nomor | | | | prostagiandin-endo | prostagiandin endo | prostagiandin-endo | alcohol denydrogen | probable membrane | androgen-withdrawa | cerebellin-like gi | cerebettin precurs | gene 36 protein | phosphoglycerate d | probable sera proc | probable RNA helic |

ALIGNMENTS

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major 25k outer membrane protein precursor - Brucella abortus
C;Species: Brucella abortus
C;Species: Brucella abortus
C;Apecies: D3-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 08-Oct-1999
C;Accession: A56152
R;de Wergifosse, P.; Lintermans, P.; Limet, J.N.; Cloeckaert, A.
J. Bacteriol. 177, 1911-1914, 1995
A;Title: Cloning and nucleotide sequence of the gene coding for the major 25-kilodalt
A;Reference number: A56152; MUID:95204367
A;Accession: A56152
A;Accession: A56152
A;Ccossion: A56152
A;Residues: DNA
A;Residues: 1-213 <DEA>
A;Residues: 1-213 <DEA>
A;Cross-references: GB:X79284; NID:g769744; PIDN:CAA55872.1; PID:g769745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
A56152
                                                                                                                                                                                                                   RESULT 2
104763
1054763
alcohol dehydrogenase (EC 1.1.1) C - Escherichia coli
alcohol dehydrogenase class III alcohol dehydrogenase
N;Alternate names: class III alcohol dehydrogenase
N;Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 11-Jun-1999
C;Accession: D64763; A42015; S78608
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; R
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; R
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Recession: D64763
A;Cross-references: GB:AE000142; GB:U00096; NID:g1786542; PIDN:AAC73459.1; PID:g17865
A;Experimental source: strain K-12, substrain MG1655
R;Gutheil, W.G.; Holmquist, B.; Vallee, B.L.
Biochemistry 31, 475-481, 1992
                                                                                                                          A;Status: nucleic acid sequence not shown;
A;Molecule type: DNA
A;Residues: 1-369 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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Best Local Similarity
"hes 5; Conserv
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62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                      translation not shown
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7.6;
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US-08-487-744-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 396-(
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH. 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 5, Application US/08480065
Patent No. 5837479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08487744 Patent No. 6048850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Young, Donald A.
APPLICANT: Young, Donald A.
APPLICANT: O'Banion, Michael K.
APPLICANT: Winn, Virginia D.
TITLE OF INVENTION: METHODS FOR INHIBITING PROSTAGLANDIN
TITLE OF INVENTION: SYNTHESIS IN A MAMMALIAN HOST
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/480,065
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COTUZEL, LAURA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Young, Donald A.
APPLICANT: O'Banion, Michael K.
APPLICANT: Winn, Virginia D.
TITLE OF INVENTION: SCREENIN ASSAYS FOR INHIBITORS OF
TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1155 Aven
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
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                                                                                                      STREET: 1155 Ave
CITY: New York
STATE: New York
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                                                             COUNTRY: U.S.A. ZIP: 10036-2711
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                                                                                                                                                                       ADDRESSEE:
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pennie & Edmonds
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    Mismatches

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Search completed: January 14, 2002, 07:23:43 Job time: 74 sec
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Best Local Similarity
Thes 4; Conserv
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,744
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 3996-013
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-9741/88
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  LENGTH: 604 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                              531 WKPSTFGG 538
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                1 wkxxsfxg 8
                                                                                                                                                                       Conservative
                                                                                                                                                                                         74.3%;
50.0%;
                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                         Score 26; DB 3;
Pred. No. 3.6e+02;
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                                                                                                                                                                                                           Length 604;
                                                                                                                                                                         0;
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0,

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US-08-480-065-2
                          FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COCUZZI, LAULA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 3996-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 604 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/480,065
FILING DATE: 07-JUN-1995
CIASSFERICATION: ASE
  TELEFAX: (Z14) CONTROL TO N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Young, Donald A.
APPLICANT: O'Banion, Michael K.
APPLICANT: Winn, Virginia D.
TITLE OF INVENTION: SCREENIN ASSAYS FOR INHIBITORS OF
TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
NUMBER OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/487,753
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
CCLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION UMBER: 30,742
REFERENCE/DOCKET NUMBER: 3996-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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TELEFAX: 66141 F
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STATE: New York
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ID NO:
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Pred. No. 3.6e+02;
1; Mismatches 3;
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US-08-480-065-4
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Best Local Similarity 50.u
Warches 4; Conservative
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STREET: 111-
STREET: 102-
STATE: New York
CITY: New York
COUNTRY: U.S.A.
2IP: 1036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: STREM: PC-DOS/MS-DOS
COMPUTER: 104-
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TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA
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APPLICANT: O'Banion, Michael K.
APPLICANT: O'Banion, Michael K.
APPLICANT: Winn, Virginia D.
TITLE OF INVENTION: SCREENIN ASSAYS FOR INHIBITORS OF
TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown MOLECULE TYPE: protein
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 3991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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LENGTH: 604 amino acid
531 WKPSTFGG 538
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                                                                                                 1 wkxxsfxg
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                                                                                                                                                                                                                                                                  74.3%;
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Pred. No. 3.6e+02;
1; Mismatches
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                                                                                                                                                                                                         Score 26; DB 2; Le
Pred. No. 3.6e+02;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                           Length 604;
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RESULT 19 US-08-480-065-5

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Дb
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                                                                                                                                           ; MOLECULE TYPE: US-08-487-753-2
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Best Local 9
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                                                                                            Query Match
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TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                      NAME: CORUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 399
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/487,753 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: O'Banion, Michael K.
APPLICANT: Winn, Virginia D.
TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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531 WKPSTFGG 538
                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                            TELEFAX: (212)
TELEFAX: 66141 PENNIE
TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 50.0
                                                                                                                                                                            LENGTH: 604 amino acids TYPE: amino acid TOPOLOGY: unknown
                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
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                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995
N: 536
                                                                                                                                                            protein
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50.0%;
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                                                                               74.3%;
50.0%;
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                                                                 1; Mismatches
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Pred. No. 3.6e+02
                                                                               Score 26;
Pred. No.
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                                                                               3.6e+02;
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                                                                                                DB 1;
                                                                                              Length 604;
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US-08-487-753-4
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                                                                                                                                                                                                                                                                                       RESULT 16
US-08-487-753-5
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Patent No. 5807733
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                     APPLICANT: Young, DOMAND APPLICANT: O'BBRION, MICHAEL K.
APPLICANT: Winn, Virginia D.
TITLE OF INVENTION: MAMMALIAN PROSTATITLE OF INVENTION: FUSION PROTEINS
TITLE OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CORUZZI, Laura A.
REGISTRATION NUMBER: 39,742
REFERENCE/DOCKET NUMBER: 399
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: O'Banion, Michael K.
APPLICANT: Winn, Virginia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                                                                                                                                                                 531 WKPSTFGG 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/487,753 FILING DATE: 07-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 10036-2711
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                       1 wkxxsfxg 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.3%;
50.0%;
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                                                                                                                                                        MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
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Pred. No. 3.6e+02;
1; Mismatches 3
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GENERAL INFORMATION:

APPLICANT: Donohue, Timothy
APPLICANT: Barber, Robert
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: Microbial System for Formaldehyde Sensing and
TITLE OF INVENTION: Remediation
FILE REFERENCE: 960296.95505
CURRENT APPLICATION NUMBER: US/09/192,983A
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/919,953
EARLIER APPLICATION NUMBER: 08/919,953
EARLIER APPLICATION NUMBER: 08/608,241
EARLIER FILING DATE: 1997-08-29
EARLIER FILING DATE: 1996-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-919-953-2
US-09-192-983-2
                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-192-983-2
                                                  SEQ ID NO 2
LENGTH: 376
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Best Local Similarity
                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ver
          TYPE: PRT ORGANISM: Rhodobacter sphaeroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seay, NIChOLAS J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93511
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: FLORBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ZIP: 53703
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1 South Pinckney Street
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50.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/608,241
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Pred. No. 1.4e+02;
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US-08-064-271-10

; Sequence 10, Application US/08064271

; Patent No. 5543297
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LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-214-278-1
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APPLICANT: Sakano, Seij:
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFF
FILE REFERENCE: KP-8576
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity 50.0
Matches 4; Conservative
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CURRENT FILING DATE: 1999-01-26
NUMBER OF SEG ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                          SOFTWARE: Microsoft Word 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 19930506
CLASSIFICATION: 435
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System
            ATTORNEY/AGENT INFORMATION:
NAME: Panzer, Curtis C.
REGISTRATION NUMBER: 33,752
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kennedy, Brian P.
APPLICANT: Cromlish, Wanda A.
APPLICANT: Mancini, Joseph A.
APPLICANT: O'Neil, Gary
APPLICANT: Vickers, Philip J.
APPLICANT: Wong, Elizabeth
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wong, Elizabeth
TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 cDNA AND
TITLE OF INVENTION: ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 WKSLHFSG 159
                                                                                                                                                                                                               STATE: NJ
COUNTRY: US
ZIP: 07065
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CTREET: 126 Lincoln Avenue
                                                                                                                                                                                                                                                              CITY: Rahway
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NUMBER:
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                                                                                                                                             System 7
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50.0%;
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Pred. No. 1.4e+02;
Pred. No. 3;
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Pred. No. 1.4e+02;
0; Mismatches 4
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CORRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION UNMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 222
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-140-804-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-608-241-2
; Sequence 2, Application US/08608241
; Patent No. 5747328
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US-08-608-241-2
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Best Local Similarity 50.0
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09140804 Patent No. 6197930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                              TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE TITLE OF INVENTION: SENSING AND REMEDIATION
                  MOLECULE TYPE: protein
                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 WKYSTFSG 216
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CITY: Madison
                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/608,241 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 53703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: WI
                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                        LENGTH:
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                                                    amino acid
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Barber, Robert D
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                                                                          RESULT 10
US-08-919-953-2
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Best Local Similarity
"hes 4; Conservations
                         Sequence 2, Application US/08919953; Patent No. 5837481; GENERAL INFORMATION:
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBII
TITLE OF INVENTION: SENSING
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Seay, NICHOLAS J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 WKGSAFGG 323
                                                                                                                                        316 WKGSAFGG 323
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STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: CLASSIFICATION: 435
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Barber, Robert
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50.0%;
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Pred. No. 1.4e+02;
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CURRENT APPLICATION NUMBER: US/09/222,817
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: JP 10-3751
EEARLIER FILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: JP 10-353521
EARLIER APPLICATION NUMBER: JP 10-353521
NUMBER OF SEQ ID NOS: 18
SOFTMARE: PATENTIN Ver. 2.0
SEQ ID NO 14
LENGTH: 530
; TWPE: PRT; OKGANISM: Brevibacterium flavum US-09-222-817-14
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Best Local Similarity
Trohes 5; Conserve
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LENGTH: 345
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-222-786-2
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                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/09222817 Patent No. 6037154 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MIKEO SUGA, MASAKAZU SUGIMOTO, TSUYOSHI OSUMI, TSUYOSHI NAKAMATSU, TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION
FILE REFERENCE: OP813
CURRENT APPLICATION NUMBER: US/09/222,817
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER APPLICATION NUMBER: JP 10-35521
EARLIER APPLICATION NUMBER: JP 10-353521
EARLIER APPLICATION NUMBER: JP 10-353521
UNMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTING DATE: 1998-12-11
NUMBER: PATENTING DATE: 198-12-11
NUMBER: PATENTING DATE: 198-12-11
SOFTWARE: PATENTING DATE: 2.0
SEQ ID NO 12
LENGTH: 530
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Best Local Similarity 62.0
""" hes 5; Conservative
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                                                                                                                                                                                                                                               APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU, TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION FILE REFERENCE: OP813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1998-12-11 NUMBER OF SEQ ID NOS: 14 SOFTWARE: Patentin Ver. 2.0
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; Sequence 12, Application US/09222786A

; Patent No. 6258573
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Best Local Similarity
** 6 Conserve
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                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 530
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU,
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION
FILE REFERENCE: OP812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: METHOD OF PRODUCING L-SERINE BY FERMENTATION
FITTLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION
FILE REFERENCE: OP812
CURRENT APPLICATION NUMBER: US/09/222,786A
CURRENT FILING DATE: 1998-12-30
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER FILING DATE: 1998-12-11
NUMBER: OF SEQ ID NOS: 14
COPTUMBER: DATE: 1998-12-11
NUMBER: OF SEQ ID NOS: 14
                                    Matches
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SEQ ID NO 12
LENGTH: 530
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Best Local :
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number of hits satisfying chosen parameters:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
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US-09-227-786-2
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US-09-227-786-14
US-09-140-804-7
US-08-608-241-2
US-08-919-953-2
US-08-919-953-2
US-08-919-953-2
US-08-064-271-10
US-08-064-271-10
US-08-487-753-5
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ALIGNMENTS

Sequence 2, Application US/09222786A Patent No. 6258573 GENERAL INFORMATION: APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyo TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE FILE REFERENCE: OP812 CURRENT APPLICATION NUMBER: US/09/222,786A CURRENT APPLICATION NUMBER: 1998-12-30 ; ORGANISM: Corynebacterium glutamicum US-09-222-817-2 GENERAL INFORMATION: APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuy TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION FILE REFERENCE: OP813 CURRENT APPLICATION NUMBER: US/09/222,817 CURRENT FILING DATE: 1998-12-30 EARLIER APPLICATION NUMBER: UP 10-3751 EARLIER FILING DATE: 1998-01-12 EARLIER FILING DATE: 1998-01-12 EARLIER APPLICATION NUMBER: JP 10-353521 EARLIER APPLICATION NUMBER: JP 10-353521 EARLIER FILING DATE: 1998-12-11 RESULT 1 US-09-222-817-2 RESULT 2 US-09-222-786-2 ; Sequence 2, Application ; Patent No. 6037154 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2 Matches Query Match Best Local CURRENT APPLICATION NUMBER: US/09/222,786A CURRENT FILING DATE: 1998-12-30 EARLIER APPLICATION NUMBER: JP 10-3751 EARLIER FILING DATE: 1998-01-12 EARLIER APPLICATION NUMBER: JP 10-353513 NUMBER OF SEQ ID NOS: 18 TYPE: PRT LENGTH: 345 132 WKRSSFNG 139 Local Similarity nes 5; Conserv 1 wkxxsfxg 8 Conservative 85.7%; 62.5%; US/09222817 Score 30; Pred. No. Mismatches DB . 31; TSUYOShi OSUMI, TSUYOShi NAKAMATSU ERINE BY FERMENTATION ω •• ω Length 345; Indels Tsuyoshi NAKAMATSU, 0, Gaps 0;

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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0693036.

19-CCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM8642-AAM42213) with nootropic, inmunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathles and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
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cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiavascular; antianaemic; antiaggregant; haemostatic; vulnerary; antidiabetic; osteopathic; dermatological; antiallergic; antiastimatic; antidiabetic; cytostatic; neuroprotective; antidepressant; noctropic; antidiabetic; cytostatic; neuroprotective; antidepressant; noctropic; antidiaparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, autoimmunity, genetic diseases, haematopoietic disorders, and protein and fungal infections.

anaemia, platelet disorders,

thrombocytopaenia,

AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic;

Claim 20; Page 278; 1217pp; English

the

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RESULT 1
AAM25829
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Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma; thorambonitic antiparkinsonian; asthma; antiparkinsonian; asthma; cardiac disease; haematopoletic disorder; platelet disorder; asthma;
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21-JAN-2000;
25-APR-2000;
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                                     Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 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N-PSDB; AAH99770.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                            immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activing inhibin activity, chemotractic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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03-AUG-2000;
14-SEP-2000;
                                                                        09-AUG-2001
                                                                                                   AAE04281;
Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic di
                                          Exeman gene 10 encoded secreted protein fragment,
                                                                                                                          AAE04281 standard; Protein; 113
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Zhao
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                                                                                                                                                                                                                                                                                                                                               specification.
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N-PSDB; AAI59563.
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09-JUL-2000;
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                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                     1 wkxxsfxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                           wkqssyag 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                           The sequence data
                                                                                                                                                                                                                                             4,
                                                                                                                                                                                                                                                                                                                                                                        isorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                     (first entry)
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2000US-0598042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodrich R,
                                                                                                                                                                                                                                                           80.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                         for this patent did
                                                                                                                                                                                                                                               Score 28; DB Pred. No. 71; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                       not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qian XB,
Yang Y,
 haematopoietic disorder;
                                                                                                                                                                                                                                                                        Length 83
                                          SEQ ID
                                                                                                                                                                                                                                                Indels
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Zhang J;
                                          NO: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D,
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AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,

callergies, neurological disorders (e.g., Alzheimer's disease,

Parkinson's disease), cognitive disorders, schizophrenia, asthma,

cskin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,

cardiovascular disorders, anglogenic disorders, kidney disorders,

cardiovascular disorders, pregnancy-related disorders, endocrine

disorders, and infections. The proteins can also be used to aid wound

bealing and epithelial cell proliferation, to prevent skin ageing due to

sunburn, to maintain organs before transplantation, for supporting cell

culture of primary tissues, to regenerate tissues, to identify their

cognate ligands or binding partners, and in chemotaxis, and can be used

as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in

alleviating symptoms associated with the disorders mentioned above, and

in diagnostic immunoassave e g radioimmunoassave renzyme linked
                                                               in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a humn secreted protein fragment referred to in the disclosure of the inv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, hamatopoletic disorders, diseases of the immune system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or therapy. Pathological conditions can be diagnosed by determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04240-Tepresent human secreted protein fragments or variants.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 502; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune system disorder; AIDS; autoimmune disease; rheumatoid arthrit inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsia; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-NOV-2000; 2000WO-US31162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endocrine disorder; infection; wound hea cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-NOV-1999; 99US-0166415; 30-JUN-2000; 2000US-0215136.
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113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Komatsoulis GA, Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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L-amino acids"
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/note= "Xaa equ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΚP,
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Query Match Best Local Similarity

50 50 . 0%

Score Pred.

28; No.

DB 95;

22;

Length 113;

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AC AAY3
XX
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Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and induspostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human constructed protein fragment referred to in the disclosure of the invention.
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                                                                                                                                                                                                                                                              Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-NOV-1999; 99US-0166415.
30-JUN-2000; 2000US-0215136.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 39; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-2001
                      AAY32938;
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                              AAY32938 standard; Protein;
                                                                                                    15
                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                              56
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                   80.0%;
50.0%;
                                                                                                                                                                                                                                              Score 28; DB Pred. No. 49; 1; Mismatches
                                                                                                                                                                                                                                                                 DB
49;
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                                                                                                                                                                                                                                                                                   Length 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the human cerebellin-2 of the invention. The cerebellin-2 protein may be administered to treat or prevent neurological disorders associated with the inappropriate expression of cerebellin-2 proteins and disruption of the synapse function. These disorders include Parkinson's disease, Alzheimer's disease, affective disorders (both bipolar and unipolar disorders), schizophrenia, olivopontocerebellar atrophy, Shy-Dager syndrome and other disorders caused by disruption of synapse function. Cerebellin-2 may also be used as an antigen in the production of vaccines and antibodies specific for the protein and in assays to identify agonists and other antagonists of cerebellin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated cerebellin-2 related polypeptides useful for treating neurological disorders such as Parkinson's Alzheimer's disease and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barnes MR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cerebellin-2 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-527473/44.
N-PSDB; AAZ11193.
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23-FEB-1998;
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              peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                        AAM40407
                                                                                                                                                                                                                                                                                                       AAM40407 standard; Protein; 83 AA
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                                                                                                                                                          polypeptide SEQ ID NO 3552.
                                                                                                            nootropic; immunosuppressant; cytostatic; gene therapy;
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98GB-0003786.
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50.0%;
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Pred. No.
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62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC AAC97991 to AAC98763 encode the human colon cancer associated proteins, CC called human colon cancer antigens, given in AAB53234 to AAB54006. The CC human colon cancer antigens can have cytostatic, cardioactive, muscular; CC encurprotective, immunomodulatory, gynaecological, gastrointestinal, CC vulnerary, nephrotropic, antiinfective and antibacterial activities, and CC can be used in gene therapy. The colon cancer antigen polynucleotides, CC proteins and antibadies to the proteins are useful for the prevention, CC treatment and diagnosis of colon disorders, such as colon cancer. The CC polynucleotides may be used in diagnostics and research, such as for CC chromosome identification, and as hybridisation probes. The proteins CC may also be used to prevent diseases such as neural disorders, immune CC gastrointestinal disorders, wounds, renal disorders, infectious CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and CC AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream requiatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostat
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY12227 standard; Protein; 55 AA.
                            thrombolytic;
                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                      18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                   AAY12227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 1990; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC98643.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || || || |
| 60 wklxsflg 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                   (first entry
                                                                                                                                                                                                                                      secreted protein SEQ ID NO: 540
                         anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
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75.0%;
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Pred. No.
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Matches
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                                                                                                                            nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, haematopoiesis regulating activity, receptor/ligand activity, anti-inflammatory activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide into a membrane, or importing a polypeptide into
                                                                                                                                                                                                                                                                                                                                           human secreted proteins, and encode the proteins given in AAV01602 ar AAV11994 to AAV12260, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene
                                                                                        Sequence
                                                                                                                           a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acids encoding human secreted proteins - obtained cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 34; Page 601; 622pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1998;
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Local Similarity
nes 4; Conserv
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-IB01238
                   80.0%;
50.0%;
                   Score 28; DB
Pred. No. 48;
   Mismatches
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                                  Length 55;
   Indels
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RESULT
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Human gene 10 encoded secreted protein fragment,

SEQ

ID NO:150.

09-AUG-2001 (first entry)

AAE04286 standard;

peptide;

56

rarkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene the

pregnancy-related disorder; gene therapy;

disorder;

infection;

Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma;

Length 530;

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RESULT 1
AAG91161
ID AAG9
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AC AAG9
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AC AAG9
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XX
                                                                                                                                                                                                       RESULT 10
AAY22647
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Best Local :
                                                                                                                                                                                                                          organism is used for large-scale fermentation of L-scrine for amino acid mixtures which are used in pharmaceuticals, Chemicals and cosmetics. The present sequence represents a mutant 3-PGDH protein, also known as serA, and is used in the course of the invention.
                                                                                                                                                                                                                                                                 The specification describes a coryneform bacterium which is able produce L-serine. The activity of at least one phosphoserine phosphoserine transaminase is enhanced in the organism. The
                                                                                                                                                                                                                                                                                                                                                                                     Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-1998;
12-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP931833-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brevibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphoserine transaminase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynetorm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant 3-PGDH protein, also known as serA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY22647;
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                                                                                                                                                                                                                                                                                                                                                                                              Hibino W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-1999
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                             Example 5; Page 25-27; 33pp; English.
                                                                                                                                                                                                                                                                                                                                 New coryneform bacterial strain useful
                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                  (AJIN ) AJINOMOTO CO INC
             26-SEP-2001
                                 AAG91161;
                                                      AAG91161 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 wkrssfng 139
                                                                                                         132 wkrssfng 139
                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                      1999-397161/34
DB; AAX81849.
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                                                                                                                                                   Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacterium; L-serine production; phosphoserine phosphatase;
lne transaminase; large-scale fermentation; 3-PGDH; serA.
                                                                                                                                                                                                       530
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                                                                                                                                                   Conservative
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             (first
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98JP-0003751.
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                                                       Protein;
             entry)
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62.5%;
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Pred. No. 1.6e+02;
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                                                                                                                                                              DB 20;
1.6e+02;
                                                                                                                                                                                                                                                                                                                                  producing L-serine
                                                                                                                                                                                                                                                                                                                                                                                                Suga
                                                                                                                                                                       Length 530;
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AAB53886
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Matches 5
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                       mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. The are useful for identifying the mutation point of a gene derived from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identify mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coryneform bacterium; amino acid organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C glutamicum protein fragment SEQ ID NO: 4915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2000;
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09-MAR-2001
                                                                                                                                                        AAB53886 standard;
                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                               AAB53886
                                                                                                                                                                                                                                                                                                                                                           European
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DB; AAH66380.
                                                                            colon cancer antigen protein sequence SEQ ID NO:1426
                                                                                                                                                                                                                                                                       Similarity 62.
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                           Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                                                                                                    530
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2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mizoguchi H, An
Senoh A, Ikeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000EP-0127688
                                                 cancer; colon cancer antigen; diagnosis; detection;
                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                    AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO: 4915; 246pp + Sequence Listing; English
                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                    85.7%;
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da M, Ozaki A;
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                Length 530;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analysing
                                           vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yokoi
                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Η,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C (3-PGDH) of Brevibacterium flavum AJ13327, a mutant strain obtained by chemical mutagenesis of B. flavum AT23327, a mutant strain obtained by chemical mutagenesis of B. flavum ATCC 14067. This mutant cenzyme has Lys at position 325 replacing the Glu residue of the wild-type enzyme (see AAV31649). The invention provides a method of producing L-serine, potentially on an industrial scale, using a coryneform bacterium having resistance to azaserine or beta-(2-thionyl)-DL-alanine, and L-serine productivity. Such bacteria produce a 3-PGDH in which feedback inhibition by L-serine is desensitised. An example is the mutant 3-PGDH produced by B. flavum AJ13327. A claimed method of producing L-serine comprises cultivating a coryneform bacterium having L-serine productivity, or a beta-(2-thionyl)-DL-alanine and having L-serine productivity, or a coryneform bacterium which harbours recombinant DNA coding for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
          Claim
                                                                       N-PSDB;
                                                                                                           Sugimoto M;
                                                                                                                                                                                                                                                                                        Brevibacterium
                                                                                                                                                                                                                                                                                                               D-3-phosphoglycerate dehydrogenase; serA gene;
                                                                                                                                                                                                                                                                                                                                    Brevibacterium flavum wild-type D-3-phosphoglycerate dehydrogenase
                                New coryneform bacterium, useful for production of L-serine pharmaceuticals, chemicals and cosmetics
                                                                                    WPI;
                                                                                                                        Hibino W,
                                                                                                                                               (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                         11-DEC-1998;
12-JAN-1998;
                                                                                                                                                                                                              12-JAN-1999;
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                                                                                                                                                                                                                                                                EP943687-A2
                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                           AAY31649;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAY31649 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutant 3-PGDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Page 23-25; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New coryneform bacterium, useful for production pharmaceuticals, chemicals and cosmetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 wkrssfng 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 wkxxsfxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                       1999-510578/43
DB; AAX87796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1999-510578/43.
DB; AAX87797.
         ۵.
     Page 19-20; 27pp; English.
                                                                                                                      Ito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    530 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                       ,
                                                                                                                                                                       98JP-0353513.
98JP-0003751.
                                                                                                                                                                                                                                                                                        flavum
                                                                                                                                                                                                              99EP-0100324
                                                                                                                       Nakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.7%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                     530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30;
Pred. No.
                                                                                                                      Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                       Osumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.6e+02;
ches 3;
                                                                                                                      Ή
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                      Suga
                                                                                                                                                                                                                                                                                                               3-PGDH; L-serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of L-serine
                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
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RESULT
AAY22646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                       The specification describes a coryneform bacterium which is able to produce L-serine. The activity of at least one phosphoserine phospha and phosphoserine transaminase is enhanced in the organism. The organism is used for large-scale fermentation of L-serine for amino acid mixtures which are used in pharmaceuticals, chemicals and cosmetics. The present sequence represents 3-PGDH protein, also known cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents wild-type D-3-phosphoglycerate dehydrogenase (3-PGDH) of Brevibacterium flavum ATCC 14067. The invention provides a method of producing L-serine, potentially on an industrial scale, using a coryneform bacterium having resistance to azaserine or beta-(2-thienyl)-DL-alanine and L-serine productivity. Such bacteria produce a 3-PGDH in which feedback inhibition by L-serine is desensitised. An example is the mutant 3-PGDH (see AAV31650) produced by B. flavum AJI3327, which has the glutamic acid residue at amino acid position 325 replaced by lysine. A claimed method of producing L-serine comprises cultivating a coryneform bacterium having resistance to azaserine or beta-(2-thienyl)-DL-alanine and having L-serine productivity, or a coryneform bacterium which harbours recombinant DNA coding for the mutant 3-PGDH.
                          as serA,
                                                                                                                                          Example 5; Page 21-22; 33pp; English.
                                                                                                                                                                       New coryneform bacterial strain useful
                                                                                                                                                                                                                    WPI; 1999-397161/34
                                                                                                                                                                                                                                                Sugimoto M;
                                                                                                                                                                                                                                                              Hibino W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coryneform bacterium; L-serine production; phosphoserine phosphatase; phosphoserine transaminase; large-scale fermentation; 3-PGDH; serA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wild type 3-PGDH protein, also known as serA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY22646;
                                                                                                                                                                                                      N-PSDB; AAX81848
                                                                                                                                                                                                                                                                                            (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                         11-DEC-1998;
12-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brevibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY22646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 wkrssfng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 wkxxsfxg
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                        and is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                              Ito M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
                        present sequence represents 3-PGDH protein, s used in the course of the invention.
                                                                                                                                                                                                                                                                                                                        98JP-0353521
98JP-0003751
                                                                                                                                                                                                                                                                                                                                                                                                                                                             flavum
                                                                                                                                                                                                                                                                                                                                                                     99EP-0100325
                                                                                                                                                                                                                                                                Nakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB
Pred. No. 1.6e
0; Mismatches
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                                                                                                                                                                                                                                                                Ţ,
                                                                                                                                                                                                                                                              Osumi
                                                                                                                                                                       for
                                                                                                                                                                                                                                                              Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
1.6e+02;
                                                                                                                                                                     producing L-serine
                                                                                                                                                                                                                                                            Suga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
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                                                     chemicals and
                                     also known
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                                                                                               phosphatase
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530 AA;

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RESULT
AAY2645
ID AAY2
XX
AC AAY2
XZ
DT 02-5
XX
DE 3-PC
XX
KW COT)
KW Phos
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AAY31651
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                                                                                                                                                                                                                                                                                                                                                                                   DЪ
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the N-terminal portion of the D-3-phosphoglycerate dehydrogenase (3-PGDH) of Corynebacterium glutamicum strain K82 (FERM BP-2444), as deduced from the nucleotide sequence of PCR-amplified K82 DNA (see AAX87798). PCF primers (see AAX87799 and AAX87800) based on the amplified K82 DNA used in the amplification of Brevibacterium flavum 3-PGDH sera gene sequences. The invention provides a method of producing L-serine, potentially on an industrial scale, using a coryneform bacterium having resistance to azaserine or beate-(2-thienyl)-DL-alanine and L-serine productivity. Such bacteria produce is 3-PGDH (see AAX31650) in which feedback inhibition by L-serine is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New coryneform bacterium, useful for production pharmaceuticals, chemicals and cosmetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-510578/43.
N-PSDB; AAX87798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-3-phosphoglycerate dehydrogenase; serA gene; 3-PGDH; L-serine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum D-3-phosphoglycerate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1999
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  Coryneform bacterium; L-serine production; phosphoserine phosphatase; phosphoserine transaminase; large-scale fermentation; 3-PGDH; serA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 13-14; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugimoto M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hibino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AJIN ) AJINOMOTO CO INC.
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12-JAN-1998;
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                                                                                                                                        02-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                3-PGDH protein, also known as
                                                                                                                                                                                           AAY22645;
                                                                                                                                                                                                                                                AAY22645 standard; Protein; 345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             desensitised.
                                                                                                                                                                                                                                                                                                                                                                                   132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             1 wkxxsfxg 8
                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                   wkrssfng 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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98JP-0003751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.7%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB Pred. No. 1.1e 0; Mismatches
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                                                                                      serA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suga
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AAX31650
ID AAY3
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AC AAY3
AC AAY3
AC Brev
XX Brev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             produce L-serine. The activity of at least one phosphoserine and phosphoserine transaminase is enhanced in the organism. The organism is used for large-scale fermentation of L-serine for organism is used for large-scale fermentation of L-serine for organism is used for large-scale fermentation of L-serine for organism.
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Hibino W,
Sugimoto M;
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Fan P, Feng P, Ferrie AM, Fischer CL, Florence C;
Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW;
Li Y, Moore PA, NI J, Olsen HS, Rosen CA, Ruben SM;
Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
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97US-0048971.
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CC useful for preventing, treating or ameliorating medical conditions e.g.

Cby protein or gene therapy. Pathological conditions can be also

CC diagnosed by determining the amount of the new polypeptides in a sample

CC or by determining the presence of mutations in the new polypucleotides.

CC Specific uses are described for each of the polynucleotides, based on

CC which tissues they are most highly expressed in, and include developing

CC products for the diagnosis or treatment of cancer, neurodegenerative

CC disorders, developmental abnormalities and foetal deficiencies, blood

CC disorders, tumours, leukemias, diseases of the immune system, autoimmune

CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,

CC such as osteoporosis, arthritis or malignancies, diseases of testes.

CC lung or thymus, digestive/endocrine disorders, infections and AIDS. The

CC polypeptides are also useful for identifying their binding partners.

CC The present sequence represents human secreted protein (see descriptor

CC line for gene number and cone identification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleic acid sequences (AAV84411 to AAV84633) encoding human secreted proteins (AAW88534 to AAW88756). The secreted protein gene sequences are deposited with the ATCC under deposit numbers ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010, 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host cells comprising recombinant vectors containing the nucleic acid sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful for are
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Sequence
      206
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Query Match Best Local Similarity

88.6%;

Score 31; Pred. No.

DB 41; 20;

Length 206,

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254 wklisftg 261

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wkxxsfxg

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Matches Query Match Best Local

Local Similarity 62. nes 5; Conservative

85.7%;

Score 30; DB Pred. No. 94; 0; Mismatches

22; ω,

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RESULT
AAG90500
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                                                            sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
Sequence
                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; SEQ ID NO: 4254; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
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301 AA;
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Senoh A, Ikeda
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2000JP-0280988.
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da M, Ozaki A;
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20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
02-DEC-1999;
                                                                                                                                                                             The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
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 AAW88747 standard; Protein; 206 AA.
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                                                                                                                                                                                                                                                                                                    Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene
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Pan J, Paoni NF, Roy MA, S
Watanabe CK, Williams PM, V
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05-JAN-2000;
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99WO-US20111.
99US-0162506.
99WO-US28313.
99WO-US28551.
99WO-US30095.
2000WO-US00219.
                                                                                                    Conservative
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99US-0144758
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Pred. No.
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97US-0048875.
97US-0048878.
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97US-0048894.
97US-0048990.
97US-0048916.
97US-0048970.
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97US-0048970.
97US-0057645.

97US-0057651.

97US-0057662.

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97US-0057768.

97US-0057763.

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97US-0057771.
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                                                                                                                                              AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                   Claim
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N-PSDB; AAA37102.
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                                      Conservative
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13-SEP-1998
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18-SEP-1998
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| 7 | 30 | 85.7 | 530 | 20 | AAY31650 | Brevibacterium fla |
| 8 | 30 | 85.7 | 530 | 20 | AAY31649 | Brevibacterium fla |
| 9 | 30 | 85.7 | 530 | 20 | AAY22646 | Wild type 3-PGDH p |
| 10 | 30 | 85.7 | 530 | 20 | AAY22647 | Mutant 3-PGDH prot |
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| | | | diagnosis; screening. | |

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Matches 4; Conservative
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STRAIN-BOLIVIA A;

MEDLINE-98062136; PubMed-9400964;

MEDLINE-98062136; PubMed-9400964;

MEDLINE-9806218; Ramirez P.;

"Variability of geographically distinct isolates of maize rayado fino virus in Latin America.";

J. Gen. Virol. 78:0-0(0).

EMBL; U97717; AAB96562.1; -.

InterPro; IPR000574; Tymo_coat.

Pfam; PF00983; Tymo_coat; 1...

Coat protein.

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SEQUENCE 177 AA; 18661 MW; E91A97A26A575EC1 CRC64;
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O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
COAT PROTEIN (FRAGMENT).
maize rayado fino virus.
Viruses; ssrNA positive-strand viruses, no DNA stage; Marafivirus.
NCBI_TaxID=59749;
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A Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

A Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,

A Bowman C.L., White O., Nierman W.C., Fraser C.M.;

"Arabidopsis thallana chromosome III P1 MZB10 genomic sequence.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; ACO10871; AAF07825.1; -.

R EMBL; ACO10871; AAD56319.1; -.

R InterPro; IPR000210; BTB_POZ.

R InterPro; IPR000210; BTB_POZ.

R InterPro; IPR000131; K_tetra; 1.

R Pfam; PF02214; K_tetra; 1.

R PROSITE; PS00037; MYB_1; UNKNOWN_1.
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InterPro; IPR000212; UvrD-helicase.
Pfam; PF005580; UvrD-helicase; 1.
PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_1.
SEQUENCE 1083 AA; 117442 MW; A531F5FBA85EB748 CRC64;
                                                                                                                                                                                                                                         Griffin T.J. IV, Parsons L., Leschziner A.E., DeVost J., Derbyshire K.M., Grindley N.D.F.;
"In vitro transposition of Tn552: a tool for DNA sequencing
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINE-MC2155 (NB2);
MEDLINE-99412429; PubMcd-10481025;
                                                                                                                                                                                                                                                                                                                                                                                                          RECB.
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                                                                                                                                                                                                                              mutagenesis.";
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                                                                                                                                                                                     EMBL; AF157643; AAD46808.1; HSSP; P56255; 2PJR.
                                                                                                                                                                                                               Nucleic Acids Res. 27:3859-3865(1999).
                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID-1772;
                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium smogmatis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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            1 wkxxsfxg 8
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E 460 AA; '
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                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49278 MW;
                                                   80.0%;
50.0%;
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                                      Score 28; DB
Pred. No. 4.3e
1; Mismatches
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Pred. No. 1.8e
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                                 DB 2; 1.~
4.3e+02;
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                                                                   Length 1083;
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                                       Indels
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Best Local S
Matches 4
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DNA Res. 7:131-135(2000).

EMBL; AB028611; BAB01838.1;

InterPro; IPR001410; DEAD.

InterPro; IPR002464; DEAH_ATP_helicase.

InterPro; IPR003029; S1.

InterPro; IPR003029; S1.

Pfam; PF00575; S1; 1.

SMART; SM00487; DEXDC; 1.

SMART; SM00490; HELICC; 1.

SMART; SM00316; S1; 1.
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Q9QDK6;
Q9QDK6;
Q1-MAY-2000 (TrEMBLrel. 13, C
Q1-MAY-2000 (TrEMBLrel. 13, I
Q1-JUN-2001 (TrEMBLrel. 17, I
COAT PROTEIN (FRAGMENT).
malze rayado fino virus.
Viruses; ssrnn positive-stran
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Q9LRV0;
Q9LRV0;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 17, Last sequence update)
Q1-QUN-2001 (TrEMBLrel. 17, Last annotation update)
PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE-LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
BUKATYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosi
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Submitted (SEP-1999) to the EMBL; AF186177; AAD56416.1;
                                                                  Hammond R.W., Bedendo I.P.;
"Molecular confirmation of maize rayado fino virus
corn streak virus and its present association with
                                                                                                                              STRAIN-BRAZIL Hammond R.W.,
                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, NCBI_TaxID=59749;
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                                                       in Brazil.";
                                                                                                                                                                                      SEQUENCE FROM
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17;
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Pred. No. 4.7e+02;
1; Mismatches 3;
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Best Local
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                                                                                                             Q9B0E2;
01-JUN-2001
01-JUN-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biondi E.G., Fancelli S., Bazzicalupo M.; "ISRm10: a new insertion sequence of Sinorhizobium meliloti: nucleotide sequence and geographic distribution."; FEMS Microbiol. Lett. 181:171-176(1999). EMBL; AF143444; AAD37358.1; -. InterPro; IPR001584; Rve.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSym.
Bacteria; Proteobacteria; alpha subdivision;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) TRANSPOSASE HOMOLOG.
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01-MAY-2000
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                                                                  Staphylococcus aureus
                                                                                                                                                                                                       Q9B0E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                         NCBI_TaxID=130478
                                                Viruses
                                                                                           PORTAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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50.0%;
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                                                                                                             sequence update)
annotation update)
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1.2e+02;
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(C) Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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(N C) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Core eudicots; Rose eurosids II; Barassicales; Brassicaceae; Arabidopsis.
(N C) C Eukaryota; Viridiplantae; Streptophyta; Core eudicots; Rose eurosids II; Barassicales; Brassicaceae; Arabidopsis.
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EMBL, AC002392; AAB71967.1; -.

R Mendel; 26469; Arath; 3328; 26469.

R InterPro; IFR001392; Adap_comp_sub.

R Pfam; PF00928; Adap_comp_sub; 1.

R PFINTS; PS00928; Adap_comp_sub; 1.

R PRINTS; PS00991; CLAT_ADAPTOR_M_1; 1.

R PROSITE; PS00991; CLAT_ADAPTOR_M_2; 1.

O SEQUENCE 428 AA; 49032 MW; 1C3C18CF06919C4F CRC64;
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB045978; BAB21733.1;
EMBL; AB045978; BAB21733.1;
SEQUENCE 412 AA; 47728 MW; 0E36224385DC8A35 CRC64;
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01-JUN-2001 (TIEMBLIEL. 17, Last annotation updat
PUTATIVE CLATHRIN COAT ASSEMBLY PROTEIN.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Q9ET38;
01-MAR-2001 (TrEMBLrel. 10
01-MAR-2001 (TrEMBLrel. 11
01-JUN-2001 (TrEMBLrel. 11
CLAUDIN-19 (FRAGMENT).
STRAIN-ICR;
Kluchl Y., Worlta K., Furuse M., Tsukita S.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; Ar249889; AAF98323.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coat protein.
NON_TER
SEQUENCE 177
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Pfem; pr00386; Clq; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; ClQ; 1.
SMART; SM001113; ClQ; UNKNOWN_1.
PROSITE; PS01113; ClQ; UNKNOWN_1.
SEQUENCE 158 AA; 17625 MW; 47DB10EDD6DC9760 CRC64;
                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hammond R.W., Kogel R., Ramirez P.;

"Variability of geographically distinct isolates virus in Latin America.";

J. Gen. Virol. 78:0-0(0).

EMBL: U97723; AAB96558.1;

EMBL: U97723; AAB96558.1;
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                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000574; Tymo_coat. Pfam; PF00983; Tymo_coat; 1.
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MEDLINE=98062136; PubMed=9400964;
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Rodentia;
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19102 MW;
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Pred. No.
                                                                                                                                                                                                                                                                        Craniata; Vertebrata; | Sciurognathi; Muridae;
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01-NOV-1999
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  Rhizobium
Bacteria;
                                      ORFAB
                                                                                               Q9x983
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20036896; PubMed-10567266; Minte O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nalson M.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalawski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Makarova K.S., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
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SEQUENCE
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InterPro; IPR007729; pmp22_Claudin.
Pfam; pr00822; pmp22_Claudin; 1.
PRINTS; PR01077; CLAUDIN; UNKNOWN_1.
PROSITE; PS01346; CLAUDIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                Science 286:1571-1577(1999).
EMBL; AE002085; AAF12100.1;
TIGR; DR2562; -.
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Bacteria; Thermus/Deinococcus
NCBI_TaxID=1299;
[1]
                                                                                                                                                                                                                                                               Transferase; Methyltransferase; Ubiquinone; Complete proteome SEQUENCE 206 AA; 22186 MW; 6F63E1369E12D870 CRC64;
                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus radiodurans \ensuremath{\text{R1."}};
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01-JUN-2001 (TremBLrel. 17, Last annotation update)
3-DEMETHYLUBIQUINONE-9 3-METHYLTRANSFERASE, PUTATIVE
                         ISRM10-2.
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InterPro; IPR000051; SAM_bind.
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Proteobacteria; alpha subdivision;
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01-NOV-1999
01-NOV-1999
01-MAR-2001
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SMART; SM00270; LRK; 16.
SMART; SM00220; STKC; 1.
SMART; SM002219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
FROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
ATP-binding; Kinase; Transferase.
SEQUENCE 895 AA; 98906 MW; 18CD89626834CD06
                                                                                                                                                 Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Embryc Spermatophyta; Magnoliophyta; eudicotyledons; Saxifragales; Daphniphyllaceae; Daphniphyllum. NCBI_TaxID=132526;
                                                                                                                                                                                                                                                                                                                                                                                                       O9G147 PRELIMINARY; PRT; 348 AA.
09G147;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MATURASE K (FRAGMENT).
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                                                                    SEQUENCE FROM N.A. Fishbein M., Hibsch-Jetter C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martinez-Abarca F., "Bacterial group II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=382; [1]
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                                       *Phylogeny of Saxifragales
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Best Local
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aeolicus.";
Nature 392:353-358(1998).
EMBL; AEO00769; AACO7799.1; -.
Hypothetical protein; Complete
PROMENCE 392 AA; 45252 MW;
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 45.3 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Len
Deckert G., Werbeek N., Snead M.A., Keller M., Aujay M
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium
                                                                                                                                 Q9H667 PRELIMINARY; PRT; 158 AA.
Q9H667;
Q9H667;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CDNA: FLJ22569 FIS, CLONE HSIO2142.
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SEQUENCE FROM N.A.
TISSUE-HUMAN SMALL INTESTINE;
TISSUE-HUMAN SMALL INTESTINE;
Watanabe K., Kumagai A., Itakura S., Yamazal
Suzuki Y., Obayashi M., Nishi T., Shibahara
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
                                                                                     Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aquifex aeolicus.
Bacteria; Aquificales;
                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=63363;
                                                                                                                                                                                                                                                        127
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                                                                                                                                                                                                                                                                                                      Similarity 62.5; Conservative
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5; Conser
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348 AA;
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41584 MW;
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62.5%;
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62.5%;
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Pred.
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                                                                                                                                                                                                                                                                                                      ed. No. 92;
Mismatches
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4F9F8BB04BB5989C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                          Yamazaki M
ibahara T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aquifex
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                 им.,
т., Tanaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aujay M.,
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                                        Tashiro
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Best Local
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MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lowis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09VA04;
01-WAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
CG15560 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Ptorygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ephydroidea; Dro
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9VA04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9ADDO;
O1-JUN-2001 (TrEMBLrel. 17, Cr.
O1-JUN-2001 (TrEMBLrel. 17, La.
O1-JUN-2001 (TrEMBLrel. 17, La.
HYPOTHETICAL 27.3 KDA PROTEIN.
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Saunders D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN: A3(2);
Cerdeno A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCBAC5H2.06C.
Stroptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redenbach M., Kieser H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97000351; PubMed-8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ADD0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein.
243 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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, Parkhill J., Ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harris
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e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB Pred. No. 20; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravita S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Welssenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Kibms R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Welssenbach J.,
RA Hilliams S.M., Shong W., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Jengy X.H., Zhong F.N., Zhong W., Zhong S., Zhu X., Smith H.O.,
RA Cibbs RA, Myers E.W., Rubin G.M., Venter J.C.;
RY The genome sequence of Drosophila melanogaster.";
C. While Account A. Stupski M.P., Smith H.O.,
RA Kang S., Shong S., Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                  O9FGN6 PRELIMINARY; PRT; 895 AA.
O9FGN6;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 17, Last sequence update
O1-JUN-2001 (TrEMBLrel. 17, Last annotation upda
RECEPTOR PROTEIN KINASE-LIKE.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryoph
Eukaryota; Viridiplantae; Streptophyta; Embryoph
Spermatophyta; Magnoliophyta; eudicotyledons; cc
eurosids [I] Brassicales; Brassicaceae; Arabidop
InterPro; IPRO(InterPro; IPRO(Pfam; PF00560;
            Submitted (APR-1999) to the EMBL/GenBank/DDBJ EMBL; AB025621; BAB09746.1; ... InterPro; IPR001919; Euk_pkinase. InterPro; IPR001611; LRR. InterPro; IPR003592; LRR_out. InterPro; IPR003299; Ser_thr_kin_actsite. InterPro; IPR001245; Tyr_kin.
                                                                                                                                                                                   Tabata S.;
                                                                                                                                                                                                    Kaneko T., Katoh T.,
                                                                                                                                                                                                                         STRAIN-COLUMBIA;
                                                                                                                                                         "Structural analysis of Arabidopsis thaliana
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303
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CE 619 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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                                                                                                                                                                                                    Sato
                                                                                                                                                                                               S., Nakamura
                                                                                                                                                                                                                                                                                                  Arabidopsis
                                                                                                                                                                                                                                                                                                                                      Embryophyta;
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                                                                                                                                                            chromosome
                                                                                                                                         databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ψ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                               Y., Kotani H.,
                                                                                                                                                                                                                                                                                                                        eudicots;
                                                                                                                                                                                                                                                                                                                                    Tracheophyta;
                                                                                                                                                            5. XI.";
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Title:
Perfect score:
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                            Database
                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries
                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                                                                                                                                                                                                                                       Sequence:
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length: 2000000000
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Gapop 10.0 ,
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35
                                                                                                                                                                                                                                                                                 473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                       January 14, 2002, 07:39:41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                       wkxxsfxg
    sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacteria:*
                                                                    sp_organelle:*
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sp_mammal:*
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                                                                                                                                                                                                                                                                                                                                                                                 Search time 112.89 Seconds (without alignments)
10.366 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | ω | 2 | 1 | Result No. |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|-------------------|--------------------|--------------------|--------------------------|
| 27 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 29 | 29 | 29 | 30 | 30 | 31 | 31 | Score |
| 77.1 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 82.9 | 82.9 | 82.9 | 85.7 | 85.7 | 88.6 | 88.6 | Query Match I |
| 175 | 1168 | 1083 | 460 | 428 | 412 | 315 | 315 | 206 | 193 | 177 | 158 | 392 | 348 | 311 | 895 | 619 | 243 | 197 | Query Match Length DB |
| 12 | 10 | 2 | 10 | 10 | 9 | N | N | N | 11 | 12 | 4 | N | œ | N | 10 | G | N | 11 | H |
| Q9QDK6 | Q9LRV0 | Q9RPH6 | Q9S7R7 | 022715 | Q9B0E2 | Q9R9L5 | Q9X983 | Q9RRD0 | Q9ET38 | 041989 | Q9н667 | 067832 | Q9GI47 | Q9X982 | Q9FGN6 | Q9VA04 | Q9ADD0 | Q9JHG0 | ID |
| Q9qdk6 maize rayad | Q9lrv0 arabidopsis | Q9rph6 mycobacteri | Q9s7r7 arabidopsis | 022715 arabidopsis | Q9b0e2 staphylococ | Q9r9l5 rhizobium m | | | Q9et38 mus musculu | O41989 maize rayad | Q9h667 homo sapien | O67832 aquifex aeo | | | Q9fgn6 arabidopsis | Q9va04 drosophila | Q9add0 streptomyce | Q9jhg0 mus musculu | Description |

| 50 2 | ν | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | | 2 | 2 | | | | | | 2 | N N | ผ | 2 | 2 | | N | | | |
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| | 7 77.1 | | | 7 77.1 | 7 77.1 | | 77. | | 7 77.1 | | | | 7 77.1 | | | 77 | 7 77.1 | 7 77.1 | 7 77.1 | 77. | | 7 77.1 | | 77. | 77. | 77.1 | 77. | 77.1 | 77.1 | 77.1 |
| 441 | 432 | 415 | 396 | 396 | 379 | 379 | 379 | 379 | 378 | 377 | 377 | 377 | 377 | 369 | 369 | 369 | 177 | 177 | 177 | 177 | 177 | 177 | 177 | 177 | 177 | 177 | 177 | 177 | 177 | 177 |
| 10 | σı | 2 | 10 | 10 | 10 | N | N | Ν | ν | Ŋ | υ | σı | σı | N | N | 2 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 |
| Q9SLB4 | Q9NFP2 | Q9Z739 | Q9SBA2 | 082014 | Q9FND2 | Q9K1T9 | Q9PLK0 | 084731 | Q9JRBO | Q9вJ33 | Q9BJ34 | Q9NJC3 | Q9NJD0 | Q9A5D4 | 024687 | Q59399 | Q9QDK4 | Q9QDK5 | 041996 | 041995 | 041994 | 041993 | 041992 | 041991 | 041990 | 041988 | 041987 | 041986 | 041985 | 041983 |
| Q9slb4 arabidopsis | Q9nfp2 plasmodium | Q9z739 chlamydia p | N | | | C | | | neisseria | | | branchios | | | 024687 anabaena az | Q59399 escherichia | maize | maize | maize | maize | 4 maize | maize raya | O41992 maize rayad | maize raya | maize | 8 maize | 7 maize | Ø | 5 maize | 3 maize |

ALIGNMENTS

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                     QY
                                                           Query Match
Best Local 9
                                               Matches
                                                                                                                                                                                                                                                                                                                                                              Q9JHG0 PRELIMINARY;
Q9JHG0;
01-OCT-2000 (TrEMBLrel. I
01-OCT-2000 (TrEMBLrel. I
01-JUN-2001 (TrEMBLrel. I
                                                                                                          SEQUENCE FROM N.A.;
Pang Z., Morgan J.I.;
"Cloning and characterization of a novel precerebellin-related gene.";
"Cloning and characterization of a novel precerebellin-related gene.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF218380; AAF32315.1; -.

EMBL; AF218379; AAF32314.1; -.

MGD; MGI:1889286; Cbln3.
InterPro; IPRO01073; C1q.
Pfam; PF00386; C1q; 1.
PRINTS; PR000007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                      CBLN3.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
184 WKYSSFSG 191
                                               Local Similarity
                      1 wkxxsfxg 8
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                           88.6%;
                                                                                                                                                                                                                                                                                                                                                                  15,
15,
                                                Score 31; DB Pred. No. 16; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                 0;
                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    197
                                                                        DB 11; Length 197;
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                                                   Indels
                                                 0;
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                                                   0;
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Search completed: January 14, 2002, 07:40:37 Job time: 503 sec

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                                                                                                        POTENTIAL.
PERIPLASMIC (POTENTIAL).
MATAL LIGAND TO THE BACTERIOCHLOROPHYLL
MAGNESIUM (POTENTIAL).
55A4C306748E3D9A CRC64;
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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                                                                                                                                                                                                                                               .;
0
InterPro; IPR000066; LHC.
PROSITE; PS00968; ANTENNA_COMP_ALPHA; 1.
PROSITE; PS00968; ANTENNA_COMP_ALPHA; 1.
Antenna complex; Light-harvesting polypeptide; Transmembrane;
Magnesium; Bacteriochlorophyll; Inner membrane.

1 3 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 77.1%; Score 27; DB 1; Length 208; Similarity 50.0%; Pred. No. 36; 4; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                             Score 27; DB 1; Length 65;
Pred. No. 12;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keen T.J., Inglehearn C.F.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. 6A4BB5EBF3CCAB81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CLAUDIN-LIKE PROTEIN ZF-A89.
                                                                                                                                                                                                                                                                                                                                                                                    208 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ011789; CAA09777.1;
InterPro; IPR001832; Claudin.
InterPro; IPR000729; PWE22_Claudin.
Pfam; PF00822; PME22_Claudin; 1.
PRINTS; PR01077; CLAUDIN.
Troft junction; Transmembrane.
TRANSMEM 8 28 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 P
22205 MW;
                                                                                                                                                                                                                77.1%;
50.0%;
                                                                                                                                                                     7688 MW;
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Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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208 AA;
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Best Local Similarity
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                                                                                                                                                                     65 AA;
                                                                                                                                                                                                                                                                                                            58 WKRTSYDG 65
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35
29
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Q9YH91;
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QY Dp

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N-LINKED (GLCNAC. ..).
ASPIRIN-ACETYLATED SERINE.
R -> H.
R -> D.
R -> D.
R -> D.
R -> D.
R -> O. K.
M -> I.
Y -> F. ABOLISHES CYCLOOXYGENASE ACTIVITY.
MSR -> MV (IN REF. 3).
GYSGPNOTIPEINTWENTTLEPSPSFIH ->
GYSGPNOTIPEINTWENTTLEPSPSFIH ->
AIPAPTAPSRRYCPGSGRLCGPAPLSST (IN REF. 1).
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(IN REF. 1).
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15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE PRE-WRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryocts, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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STAINACY. COLLUMBIA;
MEDLINE-97086699; Pubmed-8932388;
Quigley F., Dao P., Cottet A., Mache R.;
"Sequence analysis of an 81 kb contig from Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 57;
1; Mismatches 3; Indels
                                                                                                          PROSTAGLANDIN G/H SYNTHASE 1
                   Oxidoreductase; Dioxygenase; Peroxidase; Glycoprotein;
Prostaglandin biosynthesis; Heme; Iron; Signal; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> L (IN REF. 3).
-> S (IN REF. 2).
-> E (IN REF. 4).
1B76E659BB44353A CRC64;
                                                                                                                                                                                                                                  DISTAL HISTIDINE.
CYCLOOXYGENASE.
PROXIMAL HEME LIGAND.
                                                   | CGF Like domain; Diosyntherists; Heme; Lich; Signal; FGSF Like domain; 3D-structure; Transmembrane. | SIGNAL | 1 24 | PROSTAGLANDIN G/H SY TRANSMEM | 1 24 | PROSTAGLANDIN G/H SY TRANSMEM | 1 2 | PROSTAGLANDIN G/H SY TRANSMEM | 1 2 | PROSTAGLANDIN G/H SY TRANSMEM | 1 2 | PROSTAGLANDIN G/H SY TRANSMEM | 1 2 | PROSTAGLANDIN G/H SY TRANSMEM | 1 2 | PROSTAGLANDIN G/H SY TRANSMEM | 1 2 | PROSTAGLANDIN G/H SY TRANSMEM | 1 2 | PROSTAGLANDIN G/H SY TRANSMEM | 1 2 | PROSTAGLANDIN G/H SY TRANSMEM | 1 2 | PROSTAGLANDIN G/H SY TRANSMEM | 1 2 | PROSTAGLANGE. | PROMINT | 1 2 | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PROSTAGLANGE. | PRO
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PS01186; EGF_2; FALSE_NEG
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50.0%;
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193
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Best Local Similarity
Matches 4; Conser
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Q38953;
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DDX8_ARATH
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eur. J. Blochem. 205:917-925(1992).

-!- FUNCTION: ANTENNA COMPLEXES ARE LIGHT-HARVESTING SYSTEMS, WHICH TRANSFER THE EXCITATION ENERGY TO THE REACTION CENTERS.

-!- SUBUNIT: THE CORE COMPLEX IS FORMED BY DIFFERENT ALPHA AND BETA CHAINS, BINDING BACTERIOCHLOROPHYLL MOLECULES, AND ARRANGED MOST PROBABLY IN TETRAMBRIC STRUCTURES DISPOSED AROUND THE REACTION CENTER. THE NON-PIGMENTED GAMMA CHAINS MAY CONSTITUTE ADDITIONAL COMPONENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Halorhodospira.
NCBI_TaxID=1052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
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01-FEB-1994 (Rel. 28, Last sequence update)
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Wagner-Huber R., Brunisholz R.A., Bissig I., Frank G., Suter F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
Hypothetical protein; mRNA processing; mRNA splicing; Helicase;
ATP-binding; Nuclear protein.
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Pred. No. 1e+02;
1; Mismatches 3; Indels
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SUBFAMILY. DDX8/PRP22 ORTHOLOG. SIMILARITY: CONTAINS 1 'S1 MOTIF' DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL).
DEAH BOX.
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EMBL, X97970; CAA66613.1; -.
InterPro; IPR001410; DEAD.
InterPro; IPR001464; DEAH_ATP_helcse.
InterPro; IPR001650; Hellcase_C.
InterPro; IPR003029; S1.
Pfam; PP00575; S1; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
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50.0%;
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Best Local Similarity
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| 955 WKAKNFSG 962
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P80103;
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SITE
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AC 010-FEB DT 01-FEB DT 01-FEB DT 01-FEB DE LIGHT-
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20-AUG-2001 (Rel. 40, Last annotation update)
PROSTAGLANDIN G/H SYNTHAASE 1 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE
-1) (COX-1) (PROSTAGLANDIN-ENDOPENOXIDE SYNTHASE 1) (PROSTAGLANDIN HZ
SYNTHASE 1) (PGH SYNTHASE 1) (PGHS-1) (PHS 1).
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MEDLINE=90203007; PubMed=2108169;
Dewitt D.L., El-Harith E.A., Kraemer S.A., Andrews M.J., Yao E.F.,
Armstrong R.L., Smith W.L.;
"The aspirin and heme-binding sites of ovine and murine prostaglandin endoperoxide synthases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dewitt D.L., Smith W.L.;
"Primary structure of prostaglandin G/H synthase from sheep vesicular gland determined from the complementary DNA sequence.";
Proc. Natl. Acad. Sci. U.S.A. 85:1412-1416(1988).
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Merlie J., Fagan D., Mudd J., Needleman P.;
"Isolation and characterization of the complementary DNA for sheep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88196421; PubMed=3129310;
Yokoyama C., Takai T., Tanabe T.;
"Primary structure of sheep prostaglandin endoperoxide synthase deduced from cDNA sequence.";
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Isolation and covalent structure of the aspirin-modified,
active-site region of prostaglandin synthetase.";
Biochemistry 22:4672-4675(1983).
                                                                                                                                                                                                             DB 1; Length 475;
                                                                                                                                                                                                                                                 3; Indels
                                   M -> I (IN REF. 1).
D -> H (IN REF. 1).
N -> K (IN REF. 1).
P -> R (IN REF. 1).
I -> M (IN REF. 1).
MISSING (IN REF. 1).
W; CGB11153B845921C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                       600 AA.
                                                                                                                                                                                                                               Pred. No. 46;
0; Mismatches
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                                                                                                                                                                                                             Score 28;
   CLAT_ADAPTOR_M_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (cyclooxygenase).";
J. Biol. Chem. 263:3550-3553(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 523-544.
MEDLINE=84024608; PubMed=6414516;
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MEDLINE=88144447; PubMed=3125548;
                                                                                                                                                        MM.
                       Phosphorylation.
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                                                                                                                                                                                                             80.0%;
62.5%;
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222
433
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475 AA;
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                                                                                                                                                                                                               Query Match
Best Local Similarity
PROSITE; PS00991;
                                                                                                                                                                                                                                                                                                                            382 WKIRSFPG 389
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                       Coated pits;
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P05979;
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                                                                                                                                                                                                                                                                                                                                                        CARBOHYDRATE-LINKAGE SITES.
MEDLINE=93352648; PubMed=8349699;
Otto J.C., Dewlit D.L., Smith W.L.;
N-glycosylation of prostaglandine endoperoxide synthases-1 and -2 and their orientations in the endoplasmic reticulum.";
J. Biol. Chem. 268:18234-18242(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94166877; PubMed-8121489; Picot D., Loll P.J., Garavito R.M.; "The X-ray crystal structure of the membrane protein prostaglandin H2 synthases" "I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) = PROSTAGLANDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
MEDLINE=96022982; Pubmed=755725;
LO11 P.1., Picot D., Garavito R.M.;
"The structural basis of aspirin activity inferred from the crystal structure of inactivated prostaglandin H2 synthase.";
Nat. Struct. Biol. 2.337-643(1995).
-! FUNCTION: MAY PLAS MAPPORTANT ROLE IN REGULATING OR PROMOTING CELL PROLIFERRATION IN SOME NORMAL AND NEOPLASTICALLY TRANSFORMED
                                                                              ACTIVE SITE TYR-385.
MEDLINE-91056037; PUDMed-2122967;
Shimokawa T., Kulmacz R.J., Dewitt D.L., Smith W.L.;
"Tyrosine 385 of prostaglandin endoperoxide synthase is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. ENDOPLASMIC RETICULUM MEMBRANE AND MICROSOMAL MEMBRANE.
MISCELLAND FOR THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- MISCELLANEOUS: THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INELAMMATORY DRUGS SUCH AS ASPIRIN.
-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i- SIMILARITY: BELONGS TO THE PROSTAGLANDIN G/H SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H_2 + A + H(2)O.
-!- PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
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PIR; A28960; A28960.
PIR; A28947; A29947.
PIR; S00561; S00561.
PDB; IPRH; 31-MAR-95.
PDB; IPGE; I1-JAN-97.
PDB; IPGE; I1-JAN-97.
PDB; IPGE; I1-JAN-97.
PDB; IPGE; I1-JAN-97.
PDB; IPGE; I1-JAN-97.
PDB; IPGE; I1-JAN-97.
PDB; IPGE; I1-JAN-97.
PDB; IPGE; I1-JAN-97.
PDB; IPGE; I1-JAN-97.
PDB; IPGE; I1-JAN-97.
PDB; IPGE; IPGE; IPGE; IPGE; INCREPTO; IPR000561; SGF-II&E.
INCREPTO; IPR001536; PEGF-II&E.
INCREPTO; IPR001536; PEGF-II&E.
PRINTS; PR00457; ANPEROXIDASE.
                                                                                                                                                                                                                                            cyclooxygenase catalysis.";
J. Biol. Chem. 265:20073-20076(1990).
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Biol. Chem. 265:5192-5198(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, J03599, AAA31576.1; -. EMBL, M18243; AAA31511.1; -. EMBL, Y00750; CAA68719.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 367:243-249(1994).
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          IMPORTANT FOR FOH ACTIVITY AND ACTIVATION BY FATTY ACIDS (BY SIMILARITY).

0B9760AB77329FE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 93:15086-15091(1996).
-1- FUNCTION: SYNTHESIZES SELENOPHOSPHATE FROM SELENIDE AND ATP.
-1- CATALYTIC ACTIVITY: ATP + SELENIDE + H(2)O = AMP + SELENOPHOSPHATE
                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MaY-2000 (Rel. 39, Last annotation update)
SELENIDE, WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2)
(SELENIUM DONOR PROTEIN 2).
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of a novel selD homolog from eukaryotes, bacteria, and archaea: is there an autoregulatory mechanism in selenocysteine metabolism?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guimaraes M.J., Peterson D., Vicari A., Cocks B.G., Copeland N.G., Gilbert D.J., Jenkins N.A., Ferrick D.A., Kastelein R., Bazan J.F., Zlotnik A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENCODED BY THE OPAL CODON, UGA.
-1. SIMILARITY: BELONGS TO THE SELENOPHOSPHATE SYNTHETASE 1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96017645; Pubmed-7588067; Guimaraes M.V., Grimaldi J.C., Lee F., McClanahan T.; A new approach to the study of haematopoietic development in the yolk sac and embryoid bodies.";
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_raxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE ACTIVE-SITE SELENOCYSTEINE IS
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                                                                    DB 1; Length 375; 37;
                                                                                           3; Indels
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ATP (POTENTIAL).
                                                                                                                                                                                             452 AA.
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                                                                    28;
No. 3
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MGD; MGI:108388; Sps2.

DR InterPro; IPR000728; AIRS_related.

VW Transferase; Selenium; Sele--
T ACT_SITE 63

SE_CYS

SITE
                                                                    Score Pred.
                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                Development 121:3335-3346(1995).
                                  39669 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1 - COFACTOR: SELENOCYSTEINE.
                                                                  80.0%;
50.0%;
                                                                                        4; Conservative
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 175
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                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                 375 AA;
                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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P97364;
                                 SEQUENCE
                                                                  Query Match
          BINDING
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SPS2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                OLOCT-1993 (Rel. 25, Created)
OL-OCT-1996 (Rel. 34, Last sequence update)
OL-OCT-1996 (Rel. 34, Last annotation update)
OL-OCT-1996 (Rel. 34, Last annotation update)
CLATHRIN COAT ASSEMBLY PROTEIN AP54 (CLATHRIN COAT ASSOCIATED PROTEIN
AP54) (GOLGI ADAPTOR AP-1 54 KDA PROTEIN) (HA1 54 KDA SUBUNIT)
(CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).
SAPMI OR YAP54 OR YPL259C OR P0394.
Saccharomyces cerevisiae (Baker's syeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The medium chains of the mammalian clathrin-associated proteins have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungl; Ascomycota; Saccharomycotlna; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
BEDLINE-92104180; Pubmed=1761056;
Nakayama Y., Goebl M., O'Brine G.B., Lemmon S., Pingchang C.E.,
Kirchhausen T.;
                                                                                                                                                       ö
                                                                                                              Length 452;
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Messenguy F., Dubois E., Vierendeels F., Scherens B.; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                      POLY-ALA.
9DA6F7250CFE80E4 CRC64;
                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                475 AA
                                                                                                          DB
44;
                                                                                                                                                       Mismatches
                                                                                                          Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD; S0006180; APM1.
InterPro; IPR001392; Adap_comp_sub.
Pfam: PF00928; Adap_comp_sub. 1.
PRIWTS; PR00314; CLATHRINADPT.
PROSITE; PS00990; CLAT_ADAPTOR_M_1; 1.
    POLY-ALA
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a homolog in yeast.";
Eur. J. Biochem. 202:569-574(1991).
9 PC
440 PC
47786 MW;
                                                                                                          80.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X60288; CAA42828.1; -. EMBL; Z73615; CAA97989.1; -. PIR; S17028; S17028.
                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                STANDARD;
2
433
452 AA;
                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                           1 wkxxsfxg
                                                                                                                                                                                                                                      52 WRLTSFSG
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Q00776;
                    DOMAIN
SEQUENCE
                                                                                                                                                     Matches
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TRANSMEM
TRANSMEM
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METAL
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METAL
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ADHH_GADMO
                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                       0;
                    Mada C., Ohtani H.;

"Molecular cloning of rat cerebellin-like protein cDNA which encodes a movel membrane-associated glycoprotein.";

"A novel membrane-associated glycoprotein.";

"E nain Res. Mol. Brain Res. 9:71-77(1991).

"I. FUNCTION: PROBABLY INVOLVED IN SYNAPTIC FUNCTIONS IN THE CNS.

"I- FUNCTION: PROBABLY INVOLVED IN SYNAPTIC FUNCTIONS IN THE CNS.

"I- SUBCELLIALIAR LOCATION: MEMBRANE-ASSOCIATED.

"I- ALTERNATIVE PRODUCTS: TISSUE SPECIFIC ALTERNATIVE SPLICING OCCURS.

"I- SINGLARITY: CONTAINS. 1 CLQ DOMAIN.

"II SEGUE SPECIFICITY: BRAIN, ADRENAL GLAND AND SPLEEN.

"I- SINGLARITY: CONTAINS I CLQ DOMAIN.

"IN FACOSTICE PRODUCTS: COMPLEMNTCLQ.

"SRART: SMOOIL9; CLQ; 1.

"SNART: SMOOIL9; CLQ; 1.

"TRANSEMENT STATES A POTENTIAL.

"TRANSEMENT STATES A POTENTIAL.

"TRANSEMENT STATES A POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P., Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
A8C3ED240CEA53A7 CRC64;
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0
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                                                                                                                                                                                                                                                                                                                                                 80.0%; Score 28; DB 1; Length 224; 50.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reinecker H.-C., Sakaguchi T., Golden H.M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                          CEREBELLIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 AA
                                                                                                                                                                                                                                                  EXTRACELLULAR. C1Q.
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
              MEDLINE=91203483; PubMed=1850079;
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                  50
86
86
53
110
224 AA;
                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                                        211 WKYSTFSG 218
                                                                                                                                                                                                                                                                                                                                                                                                  1 wkxxsfxg 8
  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLD2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLAUDIN-2.
                                                                                                                                                                                                                                                                          SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth.";
                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                 DOMAIN
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CLD2_HUMAN
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-:- CATALYTIC ACTIVITY: ALCOHOL + NAD(+) = ALDEHYDE OR KETONE + NADH.
-:- CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE + NAD(+) = S-FORMYLGALUTATHIONE + NADH.
-:- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY.
-:- SUBUNIT: HOMODIMER AND HETERODIMER WITH L CHAIN.
-:- SUBUNIT: HOMODIMER AND HETERODIMER WITH L CHAIN.
-:- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY. CLASS-III SUBFAMILY.
InterPro: IPR002328; ADM_Zinc.
InterPro: JPR002085; AdM_Zinc.
PROM: PF00107; adm_Zinc: JPR002085; Adm_Zinc.
PROM: PF00107; adm_Zinc: JPR002085; Adm_Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Danielsson O., Shifqat J., Estonius M., El-Ahmad M., Joernvall H.; Danielsson O., Shifqat J., Estonius M., El-Ahmad M., Joernvall H.; "Isozyme multiplicity with anomalous dimer patterns in a class III alcohol dehydrogenase. Effects on the activity and quaternary structure of residue exchanges at 'non-functional' sites in a native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.";
Biochemistry 35:14561-14568(1996).
Biochemistry Biochemistry Biochemistry Biochemistry Biochemistry Biochemistry Biochemistry Biochemistry Biochemistry Biochemistry Biochemistry Catalyzes The Oxidation OF Long-CHAIN FIHARY ALCOHOLS AND THE OXIDATION OF S-(HYDROXYMETHYL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ALCOHOL DEHYDROGENASE CLASS III H CHAIN (EC 1.1.1.1) (GLUTATHIONE-
DEPENDENT FORMALDEHYDE DEHYDROGENASE) (EC 1.2.1.1) (FDH).
Gadus morhua (Atlantic cod).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 1; Length 230;
Pred. No. 24;
1; Mismatches 3; Indels
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MOD_RES 1 1 ACETYLATION.
METAL 46 46 ZINC (CATALYTIC).
                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
52CA642D4A62B70D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SECOND ATOM).
(SECOND ATOM).
(SECOND ATOM).
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ZINC (CATALYTIC).
ZINC (SECOND ATOM).
ZINC (SECOND ATOM).
ZINC (SECOND ATOM).
ZINC (SECOND ATOM).
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                        POTENTIAL.
                                                 EMBL, AF250558; AAF98151.1; -.
EMBL, AF177340; AAG17984.1; -.
INTERPO; IPR001823; Claudin.
INTERPO; IPR000729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin.
INTERPOSETE; PS01346; CLAUDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97085413; PubMed=8931553;
                                                                                                                                                                                                                              Tight junction; Transmembrane.
TRANSMEM 8 28 E
                                                                                                                                                                                                                                                                                                                                                                       24548 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
68
98
101
1104
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117 1
163 1
230 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 WKTSSYVG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 wkxxsfxg 8
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Р81600;
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81

74 WKAGAFAG 1 wkxxsfxg

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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
NCBI_TaxID~29460;
                                                                                                                                                    POTENTIAL.
25 KDA OUTER-MEMBRANE IMMUNOGENIC
PROTEIN.
                                                                                                                                                                                                                                                                   .
0
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                                                                                                                                                                                                                                      Score 28; DB 1; Length 213; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 1; Length 213; Pred. No. 22;
                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                             59003CF46F6D0ED3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49EEE0F47B784F87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                            213 AA
                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
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                                                                                                        InterPro; IPR000498; OmpA_tmem. Pfam; PF01389; OmpA_membrane; 1. Antigen; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000498; OmpA_tmem. Pfam; PF01389; OmpA_membrane; 1. Antigen; Outer membrane; Signal.
                                                                                                                                                                                            213 AA; 23185 MW;
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                                                                                                                                                                                                                                    50.08;
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ilarity 50.0%;
Conservative 1
                                                                                           EMBL; U33003; AAB06701.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U39359; AAB36694.1; -
                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                      23
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brucella neotomae
                                                                                                                                                                                                                                                                                            1 wkxxsfxg 8
                                                                                                                                                                                                                                                                                                                      74 WKAGAFAG 81
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                                                                                                                                                                                                                                                                                                                                                                                          OM25_BRUNE
                                                                                                                                                                                            SEQUENCE
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Best Local S
Matches 4
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloeckaert A., Verger J.M., Grayon M., Zygmunt M.S., Grepinet O.; "Nucleotide sequence and expression of the gene encoding the major 25-Kilodalton outer membrane protein of Brucella ovis: Evidence for antiqenic shift, compared with other Brucella species, due to a deletion in the gene.";
Infect. Immun. 64:2047-2055[1996].
-: SUBCELLULAR LOCATION: OUTER MEMBRANE.
-: SUBCELLULAR LOCATION: OUTER MEMBRANE.
                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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25 KDA OUTER-MEMBRANE IMMUNOGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.0%; Score 28; DB 1; Length 213; 50.0%; Pred. No. 22; 3; Indels iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN.
55F33CF46F6D0ED3 CRC64;
                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NUC-2001 (Rel. 40, Last annotation update)
CEREBELLIN-LIKE GLYCOPROTEIN.
      213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 AA.
      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96239016; PubMed-8675306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U39397; AAB36695.1; -.
InterPro; IPR000498; OmpA_tmem.
Pfam; PF01389; OmpA_membrane; 1.
Antigen; Outer membrane; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 AA; 23151 MW;
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      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                              Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=29461;
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                                                                                                                                                                                                                               Brucella suis.
OM25_BRUSU
Q45689;
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MEDLINE=95204367; PubMed=7896724;
MEDLINE=95204367; PubMed=7896724;
MeDLINE=95204367; PubMed=7896724;
"Clonding and nuclectide sequence of the gene coding for the major 25-
kilodalton outer membrane protein of Brucella abortus.";
J. Bacteriol. 177:1911-1914(1995).
-! SUBCELLUIAR LOCATION: OUTER MEMBRANE.
-! SIBCLELUIAR LOCATION: OUTER MEMBRANE.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
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             25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 28; DB 1; Length 213; 50.0%; Pred. No. 22; ive 1; Mismatches 3; Indels
                                                                                  Length 201
                                                                                                                  3; Indels
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                                           85A4897489A0935B CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-01998 (Rel. 37, Last annotation update)
25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN PRECURSOR.
                                                                                     DB 1;
21;
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Last annotation update)
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                                                                                                                  1; Mismatches
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Pred. No.
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InterPro; IPR000498; OmpA_tmem.
Pfam; PF01389; OmpA_membrane; 1.
Antigen; Outer membrane; Signal.
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(Rel. 37, Last anno
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Best Local Similarity
Matches 4; Conserv
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Q45110;
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"Nucleotide sequence and expression of the gene encoding the major 25-kilodatton outer membrane protein of Brucella ovis: Evidence for antigenic shift, compared with other Brucella species, due to a deletion in the gene.";
Infect. Immun. 64:2047-2055(1996).
-:- SUBCELIULAR LOCATION: OUTER MEMBRANE.
-:- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
                                                                                                                                                                     Cloeckaert A., Verger J.M., Grayon M., Zygmunt M.S., Grepinet O.; "Nucleotide sequence and expression of the gene encoding the major 25-kilodalton outer membrane protein of Brucella ovis: Evidence for antigenic shift, compared with other Brucella species, due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
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D7E40E247A39B9DF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 28; DB 1; Length 213; 50.0%; Pred. No. 22;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN PRECURSOR.
                                                                                                                                                                                                                                           deletion in the gene.";
Infect. Immun. 64:2047:2055(1996).
-i- SUBCELLULE LECCATION: OUTER MEMBRANE.
-i- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                          STRAIN=RM6/66;
MEDLINE=96239016; PubMed=8675306;
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PP01389; OmpA_membrane; 1.
Antigen; Outer membrane; Signal.
SIGNAL
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                      NCBI_TaxID=36855;
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                                  Brucella canis.
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Q45321;
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-1 FUNCTION: CEREBELLIN EXERTS NEUROMODULATORY FUNCTIONS. DIRECTLY STIMULATES NOREPILIN EXERTS NEUROSCIATE CYCLASE/PKA-DEPENDENT SIGNALING PATHWAY: AND INDIRECTLY ENHANCES ADRENOCORTICAL SECRETION IN VIVO, THROUGH A PARACRINE MECHANISM INVOLVING MEDULLARY CATECHOLAMINE RELEASE (BY SIMILARITY).

-1 TISSUE SPECIFICITY: IN THE PURK MJE CELLS POSTSYNAPTIC STRUCTURES.
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain; MEDLINE-95182808; PubMed-7877445; Kavety B., Jenkins N.A., Fletcher C.F., Copeland N.G., Morgan J.I.; "Genomic structure and mapping of precerebellin and a precerebellin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Pred. No. 20;
1; Mismatches 3; Indels
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OBST17: 09QVT5; P28655;
01-DEC-1992 (Rel. 24, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CERBBELLIN PRECURSOR (PRECEREBELLIN) (BRAIN PROTEIN D3).
                                                                                                                                                                  N-LINKED (GLCNAC. . .) (PC
N-LINKED (GLCNAC. . .) (PC
N-LINKED (GLCNAC. . .) (PC
D542FC7987E401A5 CRC64;
         Pfam; PP00386; C1q; 1. PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1. SMOSITE; PS01113; C1Q; 1. Synaptosome; Glycoprotein; Membrane; Signal.
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Brain Res. Mol. Brain Res. 63:98-104(1998).
                                                                                                                        CEREBELLIN
                                                                                             POTENTIAL.
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MEDLINE-99058013; PubMed-9838062;
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50.0%;
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Best Local Similarity
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CERB_MOUSE
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Nucleotide sequence and expression of the gene encoding the major
25-kilodalton outer membrane protein of Brucella ovis: Evidence for
antigenic shift, compared with other Brucella species, due to a
deletion in the gene.";
Infect. Immun. 64.2047-2055(1996).
I. SUBCELLULAR LOCATION: OUTER MEMBRANE.
I. SUBCELLULAR LOCATION: OTHE OMP25 / ROPB FAMILY. HAS A C-TERMINAL
DELETION COMPARED TO THAT OF OTHER BRUCELLA SPECIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Brucellaceae; Brucella.
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 193;
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A23C796C7D11BE5F CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-01998 (Rel. 37, Last annotation update)
25 KDA OUTER-MEMBRANE IMMNNOGENIC PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 1;
Pred. No. 20;
L; Mismatches
                                                                                                                                                                                                                             POTENTIAL.
BY SIMILARITY.
CEREBELLIN.
BY SIMILARITY.
                                                                                                                                                                                                                Membrane; Signal.
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                                                                           EMBL; AF164680; AAD47280.1; -.
EMBL; X64448; CAA43688.1; ALT_SEQ.
PIR; S16862.
MGD: MGI: 88281; Cbln1.
InterPro; IPR001073; Clq.
Pfan; PF00386; Clq.; 1.
SMART; SM00110; ClQ. 1.
PROSITE; PS01113; ClQ. 1.
SYNARCSORNE; ClyCoprotein; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96239016; PubMed-8675306;
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50.0%;
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00139; RECEPTOR_TYR_KIN_II; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein; ATP-binding; Phosphorylation; Proto-oncogene; Signal.
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkinase.
InterPro; IPR00177; FN_III.
InterPro; IPR001033; Ld_roptor_rep.
InterPro; IPR002011; Rcptor_tyr_kin_II.
InterPro; IPR001245; Tyr_kin.
Pfam; PF00041; fn3; 7.
Pfam; PF00069; pkinase; 1.
SMART; SM00106; FN3; 5.
SMART; SM00119; LY; 2.
                               or send an email to license@isb-sib.ch)
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                 entitles requires a license agreement
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                                                                         EMBL; M13599; AAA60277.1; EMBL; M13599; AAA60277.1; JOINED. EMBL; M13591; AAA60277.1; JOINED. EMBL; M13592; AAA60277.1; JOINED. EMBL; M13593; AAA60277.1; JOINED. EMBL; M13594; AAA60277.1; JOINED. EMBL; M13595; AAA60277.1; JOINED. EMBL; M13596; AAA60277.1; JOINED. EMBL; M13596; AAA60277.1; JOINED. EMBL; M13598; AAA60277.1; JOINED. EMBL; M13598; AAA60277.1; JOINED. EMBL; M13598; AAA36280.1; ALT_TERM. PIR; A25223; TVUURS. PIR; A24421; TVUURT. HSSP; P11362; 1FGI.
                                                                  EMBL; M34353; AAA60278.1;
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J. Neurochem. 53:886-889(1989).

J. Neurochem. 53:886-889(1989).

J. Neurochem. 53:886-889(1989).

J. Neurochem. 53:886-889(1989).

S. TIMULATES NOREPINEPHRIP RELEASE VIA THE ADENYLATE CYCLASE/PRA-STRUNCHES NOREPINEPHRIP RELEASE VIA THE ADENYLATE CYCLASE/PRA-DEPRINGENT SIGNALING PATHWAY: AND INDIRECTLY ENHANCES ADRENOCRTICAL SECRETION IN VIVO, THROUGH A PARACRINE MECHANISM CONTENTIOR MEDILLARY CAPTECHOLANINE RELEASE.

- INVOLVING MEDULLARY CAPTECHOLANINE RELEASE.

- SUBCELLULAR LOCATION: PRECERBELLIN MIGHT BE BOUND TO, OR ASSOCIATED WITH, A MEMBRANE.

- I- SUBCELLULAR TATES. LOW AT BIRTH, THE CERBELLIN CONCENTRATION INCREASES BETWEEN DAY 5 AND 15, AND REACHES PEAK VALUES BETWEEN DAY 21 AND 56.

- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEDLINE-91126057; PubMed=1704129; Warde Y., Oberdick J., Molinar-Rode R., Morgan J.I.; Urade Y., Oberdick J., Molinar-Rode R., Morgan J.I.; Proceacebellin is a cerebellum-specific protein with similarity to the globular domain of complement Clq B chain."; Proc. Natl. Acad. Sci. U.S.A. 88:1069-1073(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 57-72.
TISSUE-Cerebellum;
TISSUE-Cerebellum;
Yiangou Y., Burnet P., Nikou G., Chrysanthou B.J., Bloom S.R.;
"Purification and characterisation of cerebellins from human and
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N -> D (IN REF. 2 AND 3).
EDGDVICLNSDDIM -> KFDSSEFSSFRCTVN
                                 (POTENTIAL)
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                                                                                                                                                                                                Length 2347;
                                                                                                                                             E14F3DFD410C1D2A CRC64;
                                                                                                                                                                                                Score 29; DB 1;
Pred. No. 1.2e+02;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                  CERB_HUMAN STANDARD; PRT; 193 AA. P23435; P02682; 01-NOV-1991 (Rel. 20, Created) 01-NOV-1991 (Rel. 20, Last sequence update) 00-MUS-2001 (Rel. 40, Last annotation update) CEREBELLIN PRECURSOR (PRECEREBELLIN).
                                                                                                                                (IN REF
                                                                                                                                               263956 MW;
                                                                                                                                                                                                   82.9%;
50.0%;
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PIR; PL0124; PL0124.
MIM; 600432; -.
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Godson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLINE-98295987; PubMed-9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elglmeler K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davles R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Stalton J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the blology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-PHOSPHOHYDROXYPYRUVATE + NADH.
-1- PATHWAY: FIRST COMMITTED STEP IN THE "PHOSPHORYLATED" PATHWAY OF L-SERINE BIOSYNTHESIS.
-1- SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID
              PROSITE; PS00065; D_2_HYDROXYACID_DH_1; 1.
PROSITE; PS00670; D_2_HYDROXYACID_DH_2; 1.
PROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.
Serine blosynthesis; Oxidoreductase; NAD; Complete protecome.
ACT_SITE 232 232 SUBSITENTE-BINDING (BY SIMILARITY).
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                                                                                                                                                                                                               Score 31; DB 1; Length 528;
Pred. No. 11;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PGDH).
SERA OR RV2996C OR MT3074 OR MTV012.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: 3-PHOSPHOGLYCERATE + NAD(+) =
                                                                                                                BY SIMILARITY.
BY SIMILARITY.
1A6DC60F9FB71222 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                528 AA
                                                                                                                                                    528 AA; 54469 MW;
                                                                                                                                                                                                               88.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                              232
261
279
  PF01842; ACT: 1.
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Best Local Similarity
Local 5; Conserve
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053243;
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90280463; PubMed=2352949;
Birchmeler C., O'Neill K., Riggs M., Wigler M.;
Characterization of ROSI CDNA from a human glioblastoma cell line.";
Proc. Natl. Acad. Sci. U.S.A. 87:4799-4803(1990).
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KROS_HUMAN STANDARD; PRT; 2347 AA.
P08922; Q15368;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ROS PRECURSOR (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEDLINE-87064611; PubMed-3023956; Matsushime H., Wang L.-H., Shibuya M.; Matsushime H., Wang L.-H., Shibuya M.; Muman c-ros-1 gene homologous to the v-ros sequence of UR2 sarcoma virus encodes for a transmembrane receptorilke molecule."; Moi. Cell. Biol. 6:3000-3004(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN,
-!- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
PROTEIN KINASES. SEVENLESS SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87064625; PubMed-3785223;
Birchmeter C., Birnbaum D., Wattches G., Fasano O., Wigler M.;
Characterization of an activated human ros gene.";
Mol. Cell. Biol. 6:3109-3116(1986).
-1- FUNCTION: THIS IS A PROBABLY A CELL GROWTH OR DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                          PROSITE: PS00065; D_2_HYDROXYACID_DH_1; 1.
PROSITE: PS00670; D_2_HYDROXYACID_DH_2; 1.
PROSITE: PS00671; D_2_HYDROXYACID_DH_2; 1.
Serine biosynthesis; Oxidoreductase; NAD; Complete proteome.
ACT_SITE 232 232 SUBSTRATE-BINDING (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                          Score 31; DB 1; Length 528;
                                                                                                                                                                                                                                                                                                                                                                          Indels
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0; Mismatches
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BY SIMILARITY
                                            TIGR; MT3074;

TUBERCULIST; RV2996c;
INTEPPRO; IPR002912; ACT.
INTEPPRO; IPR002162; D_2_bydroxyacid_DH.
INTEPPRO; IPR000205; NAD_binding.
Pfam; PF00389; 2 Hadd_DH; 1.
Pfam; PF01842; ACT; 1.
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                                                                                                                                                                                                                                                                                       54554 MW;
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              AL021287; CAA16081.1;
AE007127; AAK47403.1;
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Best Local Similarity 62.5
Matches 5; Conservative
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                                          MT3074;
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SEQUENCE
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KROS_HUMAN
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7.778 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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35
1 wkxxsfxg 8
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

100059

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | 16 mycob | 053243 mycobacteri | omou ? | | _ | brucella | | | | | _ | | | | | Q00776 saccharomyc | | - | - | Q9yh91 brachydanio | _ | P56745 rattus norv | | | ~ | _ | | paste | P19854 equus cabal | | 8474 | 9053 oryctol | P12711 rattus norv |
|-----------|----------------|----------|--------------------|--------------|------|------|----------|--------------|------|------|------|------|------|--------------|------|------|--------------------|------|------|------|--------------------|------|--------------------|--------------|------|------|------|------|-------|--------------------|------|------|--------------|--------------------|
| SUMMARIES | 3 ID | SER | L SERA_MYCTU | L KROS_HUMAN | _ | | | 1 OM25_BRUAB | OM2 | OM25 | OM25 | | CERL | L CLD2_HUMAN | | | | | | | | | | 1 CLD9_HUMAN | | | • | | - | | | | ADHX | • |
| | Length DB | 528 | | | | | | | | | | | | | | | | | | | | | | 217 | | | | | | | | | | |
| đ | Query Match | 88 | 98.8 | 82.9 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 80.0 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 |
| | Score | l I | 31 | 29 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 |
| | Result No. | 1 | 7 | 3 | 4 | 2 | 9 | 7 | 8 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 |

| P80467 uromastyx h P81601 gadus morhu P45382 paracoccus P72324 rhodobacter P80360 myxine glut P79896 sparus aura P44557 heemophilus P46415 drosophila P81431 octopus vul P80572 pisum sativ Q96533 arabidopsis P93629 zea mays (m P3436 oryza sativ Q06099 candida mal Q17335 caenorhabdi P32771 saccharomyc | A A | 8 (Rel. 36, Last Sequence update) 1 (Rel. 40, Last annotation update) 1621.08 MLCB637.25. 1109 Para MLCB637.25. 110m leprae. Firmicutes; Actinobacteria; Actinobacteridae; trales; Corynebacterineae; Mycobacterium. | RE SEQUENCE FROM N.A. RX MEDLINE—21128732; PubMed=11234002; RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., RA Wingall K., Basham D., Brown D., Chillingworth T., Connor R., RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., RA Murphy L., Oliver K., Quail M.A., Rajandream MA., Rutherford K.M., RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., | us."; E + NAD(+) = "PHOSPHORYLATED" PATHWAY PECIFIC 2-HYDROXYACID | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its cuse by non-profit institutions as long as its content is in no way condified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). R FMBL: 299263: CAB16440.1: - | |
|--|--|--|--|--|---|---|
| ADHX_UROHA ADHY_GADMO FADH_PARDE ADHI_RHOSH ADHX_SPAAU ADHX_SPAAU ADHX_DROME ADHX_DROME ADHX_OCTVU ADHX_ARATH ADHX_ARATH ADHX_ARASH ADHX_ARASH ADHX_ARASH ADHX_ARASH ADHX_CANMA ADHX_CANMA ADHX_CAEEL FADH_CANMA ADHX_CAEEL FADH_YEAST STAD_LINUS | ALIGNMENTS PRT; 528 P | 15-JUL-1998 (NEI. 36, Last Sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) D-3-PHOSPHOGINCERATE DEHYDROGENASE (EC 1.1.1.95) SERA OR MLIGOS OR MLCBG37.25. Mycobacterium leprae. Bacteria; Firmicutes; Actinobacteria; Actinobacte Actinomycetales; Corynebacterineae; Mycobacteriac (1) | 234002; rrhinl J., Jame rrnier T., Church m D., Chillingy hoy S., Feltwel Hels K., Lacroli M.A., Rajandre i S., Simmonds h | leprosy bacilludosphoglyceratie + Nabh. S. S. STEP IN THE 'S. THE D-ISOMER SI | ppyright. It is e of Bioinforme of Bioinforme in Institute. Thurstings as long is not removed agreement (See @isb-sib.ch). | droxyacid_DH. |
| 373 1 375 1 375 1 375 1 375 1 375 1 376 1 376 1 378 1 378 1 378 1 381 1 1 381 1 1 386 1 39 | STANDARD; 31. 36, Creat | 1. 36, Last bl. 40, Last DERATE DEHYDR OR M.CB637.2 Leprae. Icutes, Actin s; Corynebact | N.A. 12; Pubmed=11 Imeier K., Pa Honore N., Ga Honore N., Tay | decay in the 7-1011(2001). ACTIVITY: 3-PYDROXYPYRUVATIRST COMMITTEE BIOSYNTHESI: BELONGS TO ASES FAMILY. | Tentry is cowlss Institution ioinformatics rofit instit his statement res a license il to license | CAC30645.1; 1CCN. 2; - 02912; ACT. 02162; D_2_hy 00205; NAD_bi 2-Hacid_bi; |
| 72222222222222222222222222222222222222 | 1 YCLE ERA_MYCLE 33116; 5-JUL-1998 (Re | 5-JUL-1998 (R 0-AUG-2001 (R 3-PHOSPHOGLY TRA OR ML1692 FRA OR ML1692 FRA OR ML1692 FIRM acteria: Firm ctinomycetale CBI_TaxID=176 | TRAINING FROM ITERING IN TRAINING IN TRAIN | altell book acture 409:100 1- CATALYTIC 3-PHOSPHOH 1- PATHWAX: F 0F L-SERIN 1- SIMILARITY DEHYDROGEN | this SWISS-PRO etween the S he European B se by non-p codified and t ntities requi r send an ema | WBL; AL583923 ISSP; P01542; eproma; Mil69 nterPro; IPRO nterPro; IPRO nterPro; IPRO interPro; IPRO fam; PF00389; |
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A; Description: catalyzes the oxidation of primary and secondary alcohols to aldeh a; Function: <FDH>
A; Description: catalyzes the oxidation by NAD+ of formaldehyde and glutathlone to A; Description: catalyzes the oxidation by NAD+ of formaldehyde and glutathlone to C; Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C; Keywords: acetylated amino end: alcohol metabolism; homodimer; metalloprotein; F; 1-373/Product: alcohol dehydrogenase pertuge experimental Amary
F; 193-222/Region: beta-alpha-beta NAD nucleotide-binding fold F; 34, 66, 173/Rinding site: zinc, catalytic (Cys, His, Cys) #status predicted F; 96, 99, 102, 110/Binding site: zinc, noncatalytic (Cys) #status predicted
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C; Function: <ADH>
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alcohol dehydrogenase (EC 1.1.1.1) class III - horse
N;Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1)
C;Species: Bugus caballus (domestic horse)
C;Species: Bugus caballus (domestic horse)
C;Species: Bugus caballus (domestic horse)
C;Accession: A33419
R;Kalser, R; Holmquist, B.; Vallee, B.L.; Joernvall, H.
Biochemistry 28, 8432-8438, 1989
A;Title: Characterists of mammalian class III alcohol dehydrogenases, an enzyme less valices commer: A33419
A;Rolecule type: protein
A;Reference number: A33419; MUID:90105360
A;Residues: 1-373 ckAl>
C;Comment: Class III alcohol dehydrogenases are pyrazole-insensitive, are not very active complex: homodimer; does not form heterodimers with the class I alcohol dehydrogenases
C;Complex: homodimer; does not form heterodimers with the class I alcohol dehydrogenase
C;Complex: homodimer; does not form heterodimers with the class I alcohol dehydrogenase
C;Function: catalyzes the oxidation of primary and secondary alcohols to some cropic complex: homodimer; alcohol dehydrogenase; long-chain alcohol dehydrogenase homology c;Reywords: acetylated amino end; alcohol metabolism; homodimer; alcohol dehydrogenase chi chain #status experimental characterial sacetylated amino end (SCS) #status experimental
F;193-222/Region: beta-alpha-beta NAD nucleotide-binding fold
F;193-222/Region: beta-alpha-beta NAD nucleotide-binding fold
F;193-222/Region: beta-alpha-beta NAD nucleotide-binding fold
F;193-222/Region: beta-alpha beta NaD nucleotide binding fold
F;146,69;173/Binding site: zinc, noncatalytic (Cys, His, Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Molecule Type: protein A; Residues: 9-25; 84-95, 7x', 97-98, 7x', 187;188,189-193, 7x', 195-198;357-365 < KOI> A; Experimental Source: strain Wistar C; Comment: Class III alcohol dehydrogenases are pyrazole-insensitive, are not very active G; Genetics: A; Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: ADH-2 C; Complex: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A Gene: A 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R; Residues: 1-373 < JUL>
R; Residues: 1-373 < JUL>
R; Fairwell, T.: Julia, P.: Kaiser, R.; Holmquist, B.; Pares, X.; Vallee, B.L.; Joernvall FEBS Lett. 222, 99-103, 1987
A; Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Different A; Reference number: $02617; MUID: 88005160
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A. Molecule type: protein
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B. Molecule to the identity of glutathione-dependent formaldehyde dehydrogenase
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C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
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A;Molecule type: protein
A;Residues: 1-373 <HJES-
R;Hdiquyist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson
FEBS Lett. 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogen.
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77.1%; Score 27; DB 1; Length 373; 50.0%; Pred. No. 1.2e+02; ive 1; Mismatches 3; Indels
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A; Description: catalyzes the oxidation of primary and secondary alcohols to aldehy. C; Function: <PDH> alone catalyzes the oxidation by NAD+ of formaldehyde and glutathione to the propertianity alcohol dehydrogenase; long-chain alcohol dehydrogenase homology C; Superfamily, alcohol metabolism; homodimer; metalloprotein; NAD; oxidoreductase; zir F; 25-360/Domain: long-chain alcohol dehydrogenase homology CiADH> F; 189-218/Region: beta-alpha alcohol dehydrogenase homology CiADH> F; 189-218/Region: beta-alpha alcohol dehydrogenase homology CiADH> F; 189-218/Region: beta-alpha alcohol dehydrogenase homology CiADH> F; 189-218/Region: beta-alpha incomparative (Cys, His, Cys) #status predicted F; 92, 95, 98, 106/Binding site: zinc, noncatalytic (Cys) #status predicted
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A; Residues: 1-369 (KM2)
A; Residues: 1-369 (KM2)
A; Cross-references: EMBL:x73835; NID:g887430; PIDN:CAA52057.1; PID:g887431
A; Experimental source: clinical isolate
C; Comment: class III alcohol dehydrogenases are pyrazole-insensitive, are not very
C; Complex: homodimer
C; Function: CADH>
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A;Gene: adhC
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: G85530
R;Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, 11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                  alcohol dehydrogenase (EC 1.1.1.1) C - Escherichia coli (isolate VU 3685) N;Alternate names: class III alcohol dehydrogenase (N;Conteains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 10-Jul-1992 #sequence_revision 01-May-1998 #text_change 11-Jun-1999
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                                                                                                                                                                                                           R;Kucmmerle, N.; Feucht, H.; Kaulfers, P.M.
submitted to the EMBL Data Library, June 1993
A;Description: Plasmid-mediated formaldehyde-resistance in E.
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Pred, No. 1.2e+02;
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Pred. No. 1.2e+02;
1; Mismatches 3;
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A; Accession: S57525
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Best Local Similarity
Matches 4; Conserv
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F; 189-218/Region: beta-alpha-beta NAD nucleotide-binding fold (F; 189-216/Psinding site: zinc, catalytic (Cys, His, Cys) #status predicted (F; 92,95,98,106/Psinding site: zinc, noncatalytic (Cys) #status predicted
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C;Comment: Class III alcohol dehydrogenases are pyrazole-insensitive, are not very activ
                                                                                                                                                                                                                                                                                                                                                                                                     NyAlternate names: class III alcohol dehydrogenase (glutathione) (EC 1.2.1.1)
N.Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1)
S.Specias: Escherichia coli
C.Specias: Escherichia coli
C.Specias: Escherichia coli
C.Saccassion: D64763; A42015; S78608
C.Accession: D64762; A42015; S78608
C.Accession: D64762; AMUD: 97426617
A.Reference number: A64720; MUID: 97426617
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A;Residues: 1-24, X',26-40,'E',42-45,'G',47 <GUT>
A;Note: this enzyme also has hemithiolacetal dehydrogenase activity
R;Nashimoto, H.; Saito, N.
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Pred. No. 1.2e+02;
1; Mismatches 3; Indels
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                                                                              Length
F;1/Modified site: N-formylmethionine #status experimental
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A;Residues: 'MLPLHLL',11,'VNRWKSLKLTLHHR',26-369 <NAS>
A;Cross-references: EMBL:D85613
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                                                                     DB 7
                                                                                                                                     1; Mismatches
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                                                                              Score 27;
Pred. No.
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C:Superfamily: probable membrane protein YMR119w
C:Keywords: transmembrane protein
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G:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Dec-1999
G:Accession: S62919; S62920
R:Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
  A; Experimental source: cultivar Columbia; C; Genetics:
                A;Cross-references: EMBL;AL035656; GSPDB:GN00062; ATSP:T9A14.170 A;Experimental source: cultivar Columbia; BAC clone T9A14
                                                      A; Molecule type: DNA
A; Residues: 1-700 <BEV>
                                                                                                                                      R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson submitted to the Protein Sequence Database,
                                                                                                                                                                              hypothetical protein T9A14.170 - Arabidopsis thaliana C:Speciles: Arabidopsis thaliana (mouse-ear cress) C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999 C:Accession: T06088
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F;153-169/Domain: transmembrane
F;211-227/Domain: transmembrane
F;275-291/Domain: transmembrane
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submitted to the Protein Sequence Database,
A;Reference number: $62920
A;Accession: $62920
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A; Residues: 103-669 <AND>
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N;Alternate names: hypothetical protein N2874
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A; Residues: 1-370 <DOI>
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Pred. No. 85;
1; Mismatches
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Database, April 1996
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A:Status: preliminary; translated A:Molecule type: DNA A:Residues: 1-1289 <NAR>
                                                                                                                                                                                                                                                                                                    R;Narva, K.E.; Payne, J.M.; Schwab, G.E.; Hickle, L.A.; Galasan, T.; Sick, A.J. submitted to the EMBL Data Library, July 1999
A;Description: Novel Bacillus thuringiensis microbes active against nematodes, and
                                                                                                                                                                                                                                                                                                                                                                            parasporal crystal protein cry5Abl - Bacillus thuringiensis (fragment)
C;Species: Bacillus thuringiensis
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
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T18212
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A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete A:Rittle: Complete genome sequence of Treponema pallidum, the syphilis spirochete A:Reference number: A71250; MUID:98332770
A:Accession: H71338
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                 A;Gene: CryVA(b)
C;Keywords: delta-endotoxin
                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: T18212
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-
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C;Superfamily: syphilis spirochete conserved hypothetical protein
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Q4ATE2 AllK protein - human adenovirus 2
Q5Species: Mastadenovirus 12 (human adenovirus 2)
A; Mote: host Homo sapiens (man)
C; Date: 02-Apr-1982 *sequence_revision 02-Apr-1982 *text_change 04-Mar-1994
C; Accession: A03807
Q4A02.1991
A; Metrisse, J; Rigolet, M.; Dupont de Dinechin, S.; Galibert, F.
Nucleic Acids Res. 9, 4023-4042, 1991
A; Title: Nucleotide sequence of adenovirus 2 DNA fragment encoding for the carboxylic re
A; Reference number: A93733; MUID:82059444
A; Residues: 1-116 <HER>
A; Molecule type: DNA
A; Residues: 1-116 <HER>
A; Note: this protein was assigned by correlating EM data and S1 digestion studies
C; Genetics:
C; Genetics:
A; Map position: 95.0-97.0
C; Superfamily: adenovirus early E4 11K protein
C; Keywords: early protein

Query Match
Best Local Similarity 50.0%; Pred. No. 32;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 wrxxsyxg 8
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Search completed: January 14, 2002, 07:37:29
Job time: 899 sec
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XFP_LACLA
LHA2_ECTHL
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Query Match Best Local S Matches

Similarity 62.5; Conservative

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Arnold D.A., Kowalczykowski S.C.;
"Facilitated loading of RecA protein
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Nucleic Acids Res. 14:8573-8582(1986)
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EMBL; ACCOUNTS; CAAC5859.1; -.
EMBL; X04582; CAAC38257.1; -.
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PIR; A2532; NCECX5.
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Pfam; PF00580; UVrD-helicase; Ford
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CLAUDIN-1 (SENESCENCE-ASSOCIATED EPITHELIAL MEMBRANE PROTEIN).
CLDN1 OR CLD1 OR SEMP1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                         Mitic L.M., Anderson J.M.;
"Human claudin-1 isolated from Caco-2 mRNA.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ
                                                                                                           with somatic cell hybrids.";
Cytogenet. Cell Genet. 88:217-217(2000)
-!- FUNCTION: COMPONENT OF TIGHT JUNCTI
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                                                                                                                                                                                                                                                                                                                            epithelial cells,
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Swisshelm K.L., Machl A., Planitzer S.,
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             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                            FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PRO SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
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InterPro; IPR001506; Astacin.
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EMBL; AF11556; AAD22962.1; -.
EMBL; AF134160; AAF61393.1; -.
MIM; 603718; -.
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STRAIN-BRISTOL N2;
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PROSITE; PS00022; EGF_1; 1.
PROSITE; PS010186; EGF_2; FALSE_NEG.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Signal; EGF-11ke domain; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
SMART;
SMART;
                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                            Cauliflower mosaic virus (strain PV147) (CaMV). Viruses; Retroid viruses; Caulimovirus. NCBI_TaxID=10647;
                                                                                                                                                                                                                                                                                                          VAT_CAMVP STANDARD;
P19818;
O1-FEB-1991 (Rel. 17, Created)
O1-FEB-1991 (Rel. 17, Last seq
15-JUL-1999 (Rel. 38, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
                                                                                                                                             cauliflower mosaic virus strains.";
FEBS Lett. 181:223-228(1985).
-!- FUNCTION: THIS PROTEIN IS INVOL
                                                                                                                                                                                Modjtahedi N., Volovitch M., Mazzolini L., Yot P.; "Comparison of the predicted secondary structure of aphid transmission factor for transmissible and non-transmissible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
EMBL; M37581; AAA96697.1; -. SEQUENCE 159 AA; 17843 MW;
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SM00209; TSP1; 1.
SM00235; ZnMC; 1.
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ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

                                                                                                                                             IS INVOLVED IN VIRUS TRANSMISSION.
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Query Match Best Local

Matches

Similarity 5; Conser

Conservative

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Mismatches

Indels

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83.3%;

Score 30; Pred. No.

σ DB 1;

Length 159;

g Qy

61

68

WEXXSYXG

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MEDLINE=97251358; PubMed=9097040; Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Misi T., Mizobuchi K., Mori H., Mori T., Motomura Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takada J., Takamoto K., Wada C., Yamamoto Y., Horiuchi T., Ta 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map. DNA Res. 3:379-392(1996).
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"The ZnuABC high affinity zinc uptake Escherichia coli.";
Mol. Microbiol. 28:1199-1210(1998).
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Mau B., Shao Y.;
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MEDLINE=95075659; PubMed=7984428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA repair and recombination."; Bacteriol. 170:4322-4329(1988).
(PROBABLE).
SIMILARITY: BELONGS
PROTEINS. STRONG, TO
                                                                                    SUBCELLULAR LOCATION: INTEGRAL
                                                                                                                                     FUNCTION: INVOLVED
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                                                                                                                              Gu J.R., Wan D.F., Zhao X.T.,
Qin W.X., Huang Y., Qiu X.K.,
                                                                                                                                                                                                                                                   Homo sapiens (Human
Eukaryota; Metazoa;
                                                             growth."
                                                                                                           "Novel human cDN
                                                                                                                                                    SEQUENCE FROM N.A.
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InterPro; IPR001872; Lipo_sig_PTase
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Sakaguchi T., Golden н.m.,
nnn) to the EMBL/GenBank/DDBJ databases.
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Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg

Belcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
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                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Pfam; PF01593; Amino_oxidase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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TIGR; MT3259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21235186; PubMed=11337471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XFP OR PTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TubercuList; Rv3170;
                                                                               PROSITE; PS00187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 WRASGYSG 319
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nes 4; Conser
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                                                                                                              AE006381; AAK05600.1; -
Flavoprotein;
E 822 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454 AA;
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   TPP_ENZYMES; FALSE_NEG. in; Thiamine pyrophospha; 93363 MW; C686D569D3
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49136 MW;
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; 6C1AEB97FB2F435F CRC64;
   pyrophosphate; Complete proteome
C686D569D3E8E22F CRC64;
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RESULT 10
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ID LHA2_ECTHL
AC P80103;
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RA WAGNET DOMAIN
FOR SUBCELL
DR PIR; S23164
DR INTERPRO; J
DR INTERPRO; J
DR INTERPRO; J
DR PROSITE; PS
KW Magnesium;
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Best Local
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                                                                                                                                  LT 11
_SULAC
                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
1%-JUL-1998 (Rel. 36, Last annotation update)
0UINOL OXIDASE POLYPEPTIDE II (EC 1.9.3.-) (CYTOCHROME
                                                                                                  QOX2_SULAC P39479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The primary structure of the antenna polypeptides of Ectothiorhodospira halochloris and Ectothiorhodospira halochloris and Ectothiorhodospira halophila. Four core-type antenna polypeptides in E. halochloris and E. halophila."; Eur. J. Biochem. 205:917-925(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (EHS-ALPHA-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S23164; S23164.
InterPro; IPR002361; Antenna_comp_alpha.
InterPro; IPR000066; LHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=DSM 1059;
MEDLINE=92249336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ectothiorhodospira halochloris.
Bacteria; Proteobacteria; gamma
     SOXA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00556; LHC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ANTENNA PIGMENT PROTEIN,
                    (OXIDASE AA(3) SUBUNIT
                                                                                                                                                                                                 58
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                                                                                                                                                                                                                              1 wrxxsyxg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFER THE EXCITATION ENERGY TO THE REACTION CENTERS.
SUBUNIT: THE CORE COMPLEX IS FORMED BY DIFFERENT ALPHA AND BETA
CHAINS, BIDDING BACTERIOCHLOROPHYLL MOLECULES, AND ARRANGED
MOST PROBABLY IN TETRAMERIC STRUCTURES DISPOSED AROUND THE
REACTION CENTER. THE NON-PIGMENTED GAMMA CHAINS MAY CONSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDITIONAL COMPONENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                        complex; Light-harvesting polypeptide; Transmembrane;
um; Bacteriochlorophyll; Inner membrane.
                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                   STANDARD;
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Brunisholz R.A., Bissig I.,
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55A4C306748E3D9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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Q9Z1L1;
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use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                                         Keen T.J., Inglehearn C.F.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "An archaebacterial terminal oxidase combines core st mitochondrial respiratory complexes.";
EMBO J. 11:805-812(1992).
-I- FUNCTION: THE TERMINAL OXIDASE IS THE COMPONENT O. CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO W.
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX.
-I- FUNCTION: SUBUNIT 2 TRANSFERS THE ELECTRONS FROM QUINOL TO THE BIMETALLIC CENTER OF THE CATALYTIC FORMED BY HEME A3 AND CU(B).
                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 33909
MEDLINE=92192013;
                                                     the European Bioinformatics Institute.
                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                                                                      CLDN7
                                                                                                                                                                                                                                                                                 CLAUDIN-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X62643; CAA44509.1; -. PIR; S21041; S21041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
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Archaea; Crenarchaeota; Su
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Metazoa; Chor
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PubMed=1372250
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Rodentia;
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                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                              MEDLINE-98311639; PubMed-9647647; Fujimoto K., Tsukita S.; Furuse M., Fujita K., Hilradi T., Fujimoto K., Tsukita S.; "Claudin-1 and -2; novel integral membrane proteins localizing tight junctions with no sequence similarity to occludin."; J. Cell Biol. 141:1539-1550(1998).
                                                                                                      PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE:98311639;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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088551;
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095471;
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Interpro; IPR001832; Claudin.
Interpro; IPR000729; pMP22_Claudin.
pfam; PF00822; PMP22_Claudin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gregory M., Dufresne J., Cyr D.G.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
       Eukaryota; Metazoa;
Mammalia; Eutheria;
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Best Local :
                                          between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as Ins gas its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             MEDLINE-99110921; PubMed-9892664;
MORITA K., Furuse M., Fujimoto K., Tsukita S.;
"Claudin multigene family encoding four-transmembrane domain components of tight junction strands.";
Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).
Proc. Natl. Acad. Sci. U.S.A. 96:711-710N (TU) STRANDS.
-!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TU) STRANDS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM TRANSMEM
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PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane
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TISSUE=Colon adenocarcinoma;
Keen T.J.;
EMBL; AF087825; AAD09760.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=99110921;
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Mammalia; Eutheria; Rodentia;
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InterPro; IPR000729; PMP22_Cl
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                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
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20-AUG-2001
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SMEM 82
SMEM 118
SMEM 161
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(Rel. 39, Last sequence (Rel. 40, Last annotation)
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Last annotation update)
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RESULT 17
SPS2_MOUSE
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Best Local :
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p97364;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SELENIDE MATER DIRKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE (SELENIUM DONOR PROTEIN 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
TRANSMEM
SEQUENCE
                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                Lee F., McClanahan T.; "A new approach to the study of haematopoietic development in the yolk sac and embryoid bodies."; Development 121:3335-3346(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Mutazoa; Chordata;
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InterPro; IPR000729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
            EMBL; U43285;
                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 -i- FUNCTION: SYNTHESIZES SELENOPHOSPHATE FROM SELENIDE AND
-i- CATALYTIC ACTIVITY: ATP + SELENIDE + H(2)O = AMP + SELEN
                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 93:15086-15091(1996)
                                                                                                                                                                                                                                                          metabolism?";
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                                                                                                                                                                                                                                                                                                   Zlotnik A.;
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Gilbert D.J., Jenkins
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MEDLINE=96017645; PubMed=7588067;
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                                                                                                                                                                                                                                                                                     "Identification of a novel selD homolog
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211 AA;
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              AAC53024.1;
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enkins N.A., F
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MGD; MGI:108388; Sps2.

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SE_CYS
SITE
                                                                                                                                                                                                                                                                  Kwon S.-T., Terada I., Matsuzawa H., Ohta T.;
"Nucleotide sequence of the gene for aqualysin I (a thermophilic alkaline serine protease) of Thermus aquaticus YT-1 and characteristics of the deduced primary structure of the enzyme.";
Eur. J. Biochem. 173:491-497(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 128-170. MEDLINE::88151937; PubMed::3162211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Unique precursor structure of an extracellular protease, aqual; I, with NH2- and COOH-terminal pro-sequences and its processing Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-90216674: PubMed-2182621;
Terada I., Kwon S.-T., Miyata Y., Matsuzawa H., Ohta T.;
"Unique precursor structure of an extracellular protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermus aquaticus.
Bacteria; Thermus/Deinococcus group; Thermus
NCBI_TaxID:271;
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01-NOV-1995
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P08594;
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                                      SUBCELLULAR LOCATION: SECRETED.

DEVELOPMENTAL STAGE: SECRETED FROM THE EARLY STATIONARY PHASE UNTIL THE TIME THE CELLS CEASE TO GROW.

PTM: THE N- AND C-TERMINAL PRO-SEQUENCES ARE REMOVED THROUGH THE PROTEOLYTIC ACTIVITY OF AQUALYSIN I ITSELF, IN THAT ORDER. THE C-TERMINAL PRO-SEQUENCE IS REQUIRED FOR TRANSLOCATION OF THE PROTEASES ACROSS THE OUTER MEMBRANE.

PTM: TWO DISULFIDE BONDS ARE PRESENT.
                     SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                 THE OPTIMAL TEMPERATURE FOR ITS DEGREES CELSIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chem. 265:6576-6581(1990).
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(Rel.
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9DA6F7250CFE80E4 CRC64;
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YNAB_YEAST

ID YNAB_YEAST STANDARD; PRT; 669 AA.

AC P53983;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL 76.7 KDA PROTEIN IN SPO1-SIS1 INTERGENIC REGION.

GN YNLOOSC OR N2874.
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                       SEQUENCE OF 371-669 FROM N.A.

Doignon F., Crouzet M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                        SEQUENCE OF 1-102 FROM N.A.
Andre B., Iraqui Houssaini I., Urrestarazu L.A., Vissers
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00773; SUBTILISIN.
PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D90108; BAA14135.1; -. EMBL; X07734; CAA30559.1; -. PIR; S00620; S00620. PIR; A35742; A35741. HSSP; P06873; 3PRK.
EMBL; 271284; CAA95868.1;
                                                                                                                                                                                                                                                                                                        Saccharomycetales;
NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
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Pred. No. 54;
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Best Local Similarity
                                           EMBL; AB012603; BAA31937.1;
Interpro; IPR002202; HMG-CoA_red.
Interpro; IPR000731; HMGCR_patched_5TM.
Pfam; PF00368; HMG-CoA_red; 1.
PRINTS; PR00071; HMGCOARDTASE.
PROSITE; PS00066; HMG_COA_REDUCTASE_1; 1.
PROSITE; PS00318; HMG_COA_REDUCTASE_3; 1.
PROSITE; PS00192; HMG_COA_REDUCTASE_3; 1.
PROSITE; PS00195; HMG_COA_REDUCTASE_4; 1.
PROSITE; PS50055; HMG_COA_REDUCTASE_4; 1.
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MEDLINE-98320604; PubMed-9647847;

MEDLINE-98320604; Fraser P.D., Miura Y., Saito T., Misawa N.;

Shimada H., Kondo K., Fraser P.D., Miura Y., Saito T., Misawa N.;

Shimada H., Kondo K., Fraser P.D., Miura Y., Saito T., Misawa N.;

Increased carotenoid production by the food yeast Candida utilis

through metabolic engineering of the isoprenoid pathway.";

Appl. Environ. Microbiol. 64:2676-2680(1998).

-i- FUNCTION: INVOLVED IN THE CONTROL OF CHOLESTEROL BIOSYNTHESIS.

IS THE RATE-LIMITING ENZYME OF THE STEROL BIOSYNTHESIS.

-i- CATALYTIC ACTIVITY: (R)-MEVALONATE + COA + 2 NADP(+) = (S)-3-

HYDROXY-3-METHYLGLUTARYL-COA + 2 NADPH.

-i- PATHWAY: CHOLESTEROL BIOSYNTHESIS.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           074164;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE
                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Oxidoreductase; Glycoprotein; Endoplasmic reticulum; Transmembrane; Cholesterol biosynthesis; NADP.

DOMAII: 1 442 MEMBRANE-BOUND.
                                                                                                                                                                                                                                                                                                                                     RETICULUM.
-!- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pichia jadinii (Yeast) (Candida utilis).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REDUCTASE).
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1: sp_archea:*
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5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
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36
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(c) 1993 - 2000 Compugen Ltd
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10.366 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 80 | 7 | σ | υ | 4 | w | N | | No. | Pogni i t |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------|-----------|
| 28 | 28 | 28 | 29 | 29 | 29 | 29 | 29 | 29 | 29 | 29 | 29 | 30 | 30 | 31 | 32 | 32 | 32 | 32 | Score | |
| 77.8 | 77.8 | 77.8 | 80.6 | | | 80.6 | | 80.6 | 80.6 | 80.6 | 80.6 | 83.3 | 83.3 | 86.1 | 88.9 | 88.9 | 88.9 | 88.9 | Match | Ollery |
| 206 | 197 | 157 | 1083 | 822 | 648 | 519 | 497 | 479 | 479 | 217 | 193 | 613 | 274 | 278 | 1208 | 65 | 65 | 65 | Match Length | |
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| Q9RRD0 | Q9FHV6 | 095978 | Q9RPH6 | O9CFH4 | 049559 | Q9RKB5 | Q9BRR6 | | | | Q9ET38 | | | _ | Q9KPP6 | Q9RDI7 | Q9RDI8 | Q9RDQ2 | ID | |
| Q9rrd0 deinococcus | Q9fhv6 arabidopsis | O95978 homo sapien | Q9rph6 mycobacteri | Q9cfh4 lactococcus | O49559 arabidopsis | Q9rkb5 streptomyce | Q9brr6 homo sapien | Q9jh75 sugarcane y | Q9qqn6 sugarcane y | 097402 phaedon coc | Q9et38 mus musculu | Q9a956 caulobacter | Q9sw79 triticum ae | O58458 pyrococcus | Q9kpp6 v1brio chol | Q9rdi7 streptomyce | Q9rdi8 streptomyce | Q9rdq2 streptomyce | Description | |

| 50 | 49 | 48 | 47 | 46 | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
|--------------------|--------------------|--------------------|---------|--------------------|--------|--------|-------------------|--------|------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------|------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|--------------------|-------------------|--------------------|--------------------|--------------------|------------------|
| 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 |
| 75.0 | 75.0 | | | | | | | | | | | | | | | | | | | | | | | | 77.8 | | | 77.8 | 77.8 | 77.8 |
| 323 | 303 | 270 | 266 | 262 | 261 | 260 | 246 | 241 | 199 | 175 | 169 | 159 | 159 | 159 | 159 | 158 | 154 | 154 | 115 | 99 | 68 | 64 | 7107 | 988 | 700 | 432 | 366 | 272 | 213 | 211 |
| Ν | 10 | ഗ | 10 | N | N | N | ហ | N | 10 | œ | N | 12 | 12 | 12 | 12 | N | | | | 12 | N | 12 | | | | σ | N | 10 | ហ | 4 |
| Q9HTT5 | 064761 | 045906 | Q9AWX0 | Q9HT72 | Q9CP25 | Q9KQB7 | 044142 | Q913C4 | Q9FVV5 | 079714 | 007698 | Q9WI33 | Q83166 | Q66159 | Q83179 | Q9CCU7 | Q9JSM8 | Q9K199 | Q64840 | Q83162 | Q9KKD6 | Q83157 | Q9V4F7 | 083345 | Q9T0J6 | Q9NFP2 | Q9AAC7 | Q9LTU2 | Q9NAQ9 | ONAB60 |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q9htt5 pseudomonas | O64761 arabidopsis | O45906 caenorhabdi | \circ | Q9ht72 pseudomonas | | | 044142 caenorhabd | | Q9fvv5 arabidops | 079714 rhea americ | 007698 mycobacteri | Q9wi33 cauliflower | | Q66159 cauliflower | | ∍ | Q9jsm8 neisseria | Q9k199 neisseria m | Q64840 human adeno | Q83162 cauliflower | Q9kkd6 streptomyce | Q83157 cauliflower | Q9v4f7 drosophila | | Q9t0j6 arabidopsis | Q9nfp2 plasmodium | Q9aac7 caulobacter | Q9ltu2 arabidopsis | Q9naq9 caenorhabdi | Q9bvn0 homo sapi |
| 86 | 818 | d L | tiv | as | la | 2 | d1 | as | SIS | 10 | ri | wer | wer | wer | wer | ri | 3 | 9 | eno | wer | ce | wer | æ | ď | sis | 3 | er | 818 | di | en |

ALIGNMENTS

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Q9RDQ2

PRELIMINARY; PRT; 65 AA.

AC Q9RDQ2;
DT Q1-MAY-2000 (TrEMBLrel. 13, Created)
DT Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 7.1 KDA PROTEIN.
Seeger K.J., Harris D.;
Submitted (JAN-2000) to the
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SEQUENCE FROM N.A.
                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBI_TaxID-1902;
                                                                                                                                                                                                  Streptomyces coelicolor.
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Redenbach M., Kieser H.M., Denapaite D., Eichner A.,
Redenbach H., Kieser H.M., Denapaite D., Eichner A.,
Kinashi H., Hopwood D.A.;
Rinashi H., Hopwood D.A.;
Raset of ordered cosmids and a detailed genetic and
"A set of ordered cosmids and a detailed genetic and
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Moll. Microbiol. 21:77-96(1996).
EMBL, AL135519; CAB66277.1; -.
                                                    STRAIN=A3(2);
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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ACBI_TaxID=1902;
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(TrEMBLrel. 13, Last sequence update)
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7.0 KDA PROTEIN.
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Best Local
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Q9KPP6;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
EXODEOXYRIBONUCLEASE V, 1
                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.E., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.I.

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Seller

Ermolaeva M.D., Vanathevan J., Bass S., Qin H., Dragoi I., Seller

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White (
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter
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SEQUENCE FROM I
STRAIN=A3(2);
Thomson N.R., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the 8 Mb Streptomyces coelicolor Mol. Microbiol. 21:77-96(1996).
EMBL; AL136519; CAB66278.1; -.
Hypothetical protein.
SEQUENCE 65 AA; 7127 MW; 4C9A
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Redenbach M., Kieser H.M., Denapaite D., BELLING.

Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic a

"A set of ordered cosmids and a detailed genetic a
                                                                                                                                                      Nature 406:477-483(2000).
EMBL; AE004302; AAF95464.1;
TIGR; VC2320; -.
                                                                                                       SEQUENCE
                                                                                                               Complete proteome
                                                                                                                            Pfam; PF00580; UvrD-helicase;
                                                                                                                                                  TIGR; VC2320;
                                                                                                                                                                                       cholerae.
                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae
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MEDLINE=97000351; PubMed=8843436;
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SEQUENCE FROM N.A.
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906
                                                                                                                                                                                                              Fraser C.M.;
                                                                                                                                        InterPro;
                                                                                                                                                                                                DNA sequence of both chromosomes of the cholera pathogen Vibrio
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                                                                                                      1208 AA;
                                             Conservative
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Last annotation updat
KDA SUBUNIT.
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Pred. No.
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                                             Mismatches
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RESULT 058458

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Matches 5; Conserv
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Best Local
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"Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTEKNALIYE (Wheat).
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracne
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae;
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058458;
                                                                                                                                                                                                        Zhang O., Wiskich J.T.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF174004; AAD51707.1;
InterPro; IPR002680; AOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-MACHETE; TISSUE-CHLORAMPHENICOL-TREATED SEEDLINGS; Zhang Q., Mischis L., Wiskich J.T.; "Respiratory Responses of pea and wheat seedlings to chic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ALTERNATIVE OXIDASE (FRAGMENT).
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Hypothetical protein; Complete proteome.
SEQUENCE 278 AA; 31004 MW; EE783D23A4E28FA1
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 31.0 KDA PROTEIN PH0727.
                                                                                                                                     SEQUENCE
                                                                                                                                                             Pfam; PF01786; AOX;
                                                                                                                                                                                                                                                                                                                   STRAIN MACHETE;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                        NON_TER
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                                                                                                                                   274 AA; 31794 MW;
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                             83.3%;
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                             Score 30; DB Pred. No. 58;
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Pred. No.
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Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.

A Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whit:

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

R TIGR; CC1138; T.
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Best Local
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                                                                                                Kiuchi Y., Morita K., Furuse M., Tsuki
Submitted (MAR-2000) to the EMBL/GenBai
EMBL; AF249889; AAF9823.1; -
InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claudin.
InterPro; IPR000729; PMP22_Claudin; 1.
Pfam; PF00822; PMP22_Claudin; 1.
PRINTS; PR01077; CLAUDIN; UNKNOWN_1.
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Q9ET38;
Q9ET38;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
CLAUDIN-19 (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 1:
01-JUN-2001 (TrEMBLrel. 1:
01-JUN-2001 (TrEMBLrel. 1:
TONB-DEPENDENT RECEPTOR, 1
                                     NON_TER
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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193 AA;
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Rodentia;
   20299 MW;
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putATIVE.
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Last sequence up
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Pred. No. 1
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   2F2D82DB5FCF0D7F CRC64;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 13,
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O97402;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 11, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
XYLANASE PRECURSOR (EC 3.2.1.8).
Phaedon cochleariae (Mustard beetle).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Phytophaga; Chrysomeloidea; Chrysomelidae;
                                                                                                                                                                                                                                                                                        viruses; ssrNA positive-strand viruses, Unassigned Luteoviridae
                      Moonan F., Molina J.J., Mirkov T.E.;
"Sugarcane yellow leaf virus is a new virus with a genon Polerovirus, Luteovirus, and Enamovirus properties.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF157029; AAD45687.1; -.
InterPro; IPR000893; Luteo_ORF6.
InterPro; IPR002929; PLRV_ORF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR001137; Glyco_hydro_11.

Pfam; PF00457; Glyco_hydro_11; 1.

PRINTS; PR00911; GLYCOSYL_HYDROL_F11_1; 1.

PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.

PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

Signal; Xylan degradation; Hydrolase; Glycosidase.

SIGNAL 1 17 POTENTIAL.
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Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; Y17908; CAA76932.1; -.
HSSP; P36217; 1XYO.
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STRAIN=CV. CP65-357;

X MEDILINE-20318675; PubMed=10859394;

X MEDILINE-20318675; PubMed=10859394;

X MEDILINE-20318675; PubMed=10859394;

X MEDILINE-20318675; PubMed=10859394;

X Smith G.R., Borg Z., Lockhart B.E.L., Braithwaite K.S.,

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PRINTS; PR0910; LVIRUSORF6.
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SEQUENCE 479 AA; 51676 MW;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence upda
01-JUN-2001 (TrEMBLrel. 17, Last annotation up
PUTATIVE APHID TRANSMISSION FACTOR (FRAGMENT).
sugarcane yellow leaf virus.
Viruse; ssRNA positive-strand viruses, no DNA
Unassigned Luceoviridae.
                                                                                                        SIMILAR TO RIKEN CDNA 2610017G09
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NCBI_TaxID=9606;
                         Mammalia;
                                                     Eukaryota; Metazoa;
                                                                                 Homo sapiens (Human)
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No. 1.7e+02;
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PRINTS; PRO0368; FADPNR.
PRINTS; PRO03068; FADPNR.
PRINTS; PRO0411; PNDRDTASEI.
PRINTS; PRO0469; PNDRDTASEII.
PADD; Flavoproteth; Monooxygenas
SEQUENCE 519 AA; 56673 MW;
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Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Streptomycetaceae; St
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC006112; AAH06112.1; -.
SEQUENCE 497 AA; 54088 MW; B758E977CDA88F8F CRC64;
                                                                                                                                                                  InterPro; IPR000759; Adrndx_reductase.
InterPro; IPR000137; FAD_pyr_redox.
InterPro; IPR000360; FMO.
InterPro; IPR000205; NAD_binding.
InterPro; IPR000103; Pyr_Idine_redox_2.
InterPro; IPR001100; pyr_redox.
Pfam; PF00743; FMO-like; 1.
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TISSUE-KIDNEY ADENOCARCINOMA;
                                                                                                                                                                                                                                                   the 8 mb Streptomyces coelicolor A3(2) mol. Microbiol. 21:77-96(1996). mol. COPACTOR: FAD (BY SIMILARITY). EMBL; AL132674; CAB59668.1; -.
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                                                                                                                                                                                                                                                                                                              Redenbach M., Kieser H.M., Denapaite D., Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                   STRAIN-A3(2)
                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1999)
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Thomson N.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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Seeger K.J.,
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                                                                                                                                                                                                                                                                                        "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
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                                                                                  Monooxygenase; Oxidoreductase. 56673 MW; 4031FB54427A57B4 CRC64;
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Last annotation update)
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                       Score 29; DB 2; Lo
Pred. No. 1.8e+02;
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01-JUN-2001
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O49559;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 73 5 KDA PROTEIN.
F7J7.120 OR AT4G21180.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyjedons; core eudicots; Rosid;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bevan M., Murphy G., Drost L., Hall C., Hudson S., Ridle Bancroft I., Mewes H.W., Mayer K., Schueller C.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AEC
Complete
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EMBL; AL161554; CAB79118.1; --
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Pfam; PF00226; DnaJ; 1.
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                                               Genome Res.
                                                                                                             Bolotin A., Wincker P.,
Weissenbach J., Ehrlich
                                                                                                                                                            STRAIN-IL1403;
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         Lactococcus lactis (subsp. lactis) (Streptococcus Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                                                  "The complete genome lactis.";
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                       AE006381; AAK05600.1;
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S.D., Sorokin A.;
quence of the lactic
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he EMBL/GenBank/DDBJ
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A Derbyshire K.M., Grindley N.D.F.;
I "In vitro transposition of Tn552: a tool for DNA sequencing
mutagenesis.";
Nucleic Acids Res. 27.3859-3865(1999).
EAMBL; AF157643; AAD46808.1; -
REMBL; AF157643; AAD46808.1; -
R HSSP; P56255; 2PJR.
R InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
R InterPro; IPR000212; UvrD-helicase.
R Pfams, PF00580; UvrD-helicase.
R PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
SEQUENCE 1083 AA; 117442 MW; A531F5FBA85EB748 CRC64;
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095978, 01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2001 (TrEMBLrel. 17,
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01-MAY-2000
01-MAY-2000
                  TISSUE-PERIPHERAL BLOOD;
JOX A., Zander T., Kueppers R., Irsch J., Kanzler H.,
Bohlen H., Diehl V., Wolf J.;
"Absence of immunoglobulin in Hodgkin-Reed Sternberg
Patient with mixed cellularity Hodgkin's disease is a
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                             VH1.
Homo sapiens (Human).
Chordata;
                                                                                                                                                                                                                                                                                     U1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VH1 PROTEIN PRECURSOR (FRAGMENT).
  somatic, mutations
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_TaxID=9606;
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STRAIN=MC2155 (NB2);
MEDLINE=99412429; PubMed=10481025;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID-1772;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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Pred. No. 3.9e
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Catarrhini;
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3e+02;
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3.9e+02;
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01-MAY-2000
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Q9FHV6;
01-MAR-2001
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                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
3-DEMETHYLUBIQUINONE-9 3-METHYLTRANSFERASE, PUTAT
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STRAIN=COLUMBIA;
MEDLINE=99397451; PubMed=10470850;
MEDLINE=99397451; PubMed=10470850;
NCBI_TaxID=1299;
[1]
                  Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus
                                         DR2562.
                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis Sequence features of the regions of P1 and TAC clones."; DNA Res. 6:183-195(1999).
EMBL; AB017068; BAB11363.1; -. SEQUENCE 197 AA; 23374 MW; 2080B
                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                    Kaneko T., Katoh T., Sato
Miyajima N., Tabata S.;
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMPLARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
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MRILLE O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Eisen J.A., Heidelberg J.F., Nelson W.C., Richardson D.L.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Mcffat K.S., Qlin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.M.;
"Genome sequence of the radioresistant bacterium Deinococcus
radiodurans Rl.";
Science 286:1571-1577(1999).
EMBL; AE002085; AAF12100.1; -.
TICR; DR2562; -.
                                                                                                                                                                                                                                         TISSUE~CHORIOCARCINOMA;
Strausborg R.;
Stabmitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001055; AAH01055.1; -.
SEQUENCE 211 AA; 22420 MW; 7E97DB08D3D902F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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InterPro; IPR000051; SAM_bind.
Transferase; Methyltransferase; Ubiquinone; Complete proteome.
SEQUENCE 206 AA; 22186 MW; 6F63E1369E12D870 CRC64;
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Pred. No. 1.2e+02;
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ALIGNMENTS

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       Blaschuck OW,
                                      03-NOV-1998;
30-MAR-1999;
                                                                03-NOV-1999;
                                                                                11-MAY-2000
                                                                                                WO200026360-A1
                                                                                                                 Mammalia
                                                                                                                                        Claudin-2 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer;
                                                                                                                                                                                  28-SEP-2000
                                                                                                                                                                                                   AAB06521;
                                                                                                                                                                                                                   AAB06521 standard;
                      (ADHE-) ADHEREX TECHNOLOGIES INC
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                                                                                                                                 rejection
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      Symonds JM, Gour BJ;
                                      98US-0185908.
99US-0282029.
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The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-2 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery
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                                                                                                                                                                                                                                                                                                                                        Claim 49; Page 98; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-NOV-1998;
30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claudin-2 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin - 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99US-0282029
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                                                                                                                 The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-2 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                 Sequence
                                                                                                          conformation.
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                                                                                                                                                                                                                                                   and across the skin
                                                                                                                                                                                                                                                              vasopermiability,
                                                                                                                                                                                                                                                                                                WPI; 2000-365610/31
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30-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence; autoimmune disease; inflammatory disease;
                                     Similarity
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99US-0282029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                    88.9%;
62.5%;
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                                    Score 32; |
Pred. No. 1
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Pred. No. 4.3e+05;
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                         Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claudin-2 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer; graft rejection; cyclic.
Claudin-2 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer; graft rejection; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 49; Page 98; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous sys and across the skin - \,
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30-MAR-1999;
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                                                    Claudin-2 cyclic cell adhesion
                                                                                 28-SEP-2000 (first entry)
                                                                                                              AAB06548;
                                                                                                                                         AAB06548 standard;
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99US-0282029.
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                                                                                                                                       peptide; 10
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Pred. No. 1.2;
0; Mismatches
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                                                      recognition sequence SEQ ID NO:
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Best Local :
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                                                                                                                                                                    CAR sequence; aut graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous sys and across the skin \cdot
                                  03-NOV-1998;
30-MAR-1999;
                                                                       03-NOV-1999;
                                                                                                                                                                                            Claudin-2 modulating agent; cell adhesion recognition sequence;
                                                                                                                                                                                                                    Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO:
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                                                                                                                                                                                                                                                                                            AAB06557 standard;
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                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                    autoimmune disease; inflammatory disease; on; cyclic.
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99US-0282029.
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                                   98US-0185908
99US-0282029
                                                                       99WO-CA01029
                                                                                                                                                                                                                                                                                           peptide;
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Pred. No. 1.2;
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RESULT
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 The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-2 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides
                                                                                                                                                                                                                                                                                                                                                                                                                       CAR
                                                                        Claim 49;
                                                                                                   vasopermiability, for delivering drugs and across the {\operatorname{skin}} -
                                                                                                                 Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous sys
                                                                                                                                                            WPI; 2000-365610/31.
                                                                                                                                                                                          Blaschuck OW,
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30-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system
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                                                                                                                                                                                                                                                                                                                                                                              Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                       graft rejection; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claudin-2 modulating agent; cell adhesion recognition sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                      sequence; autoimmune disease; inflammatory disease;
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                                                                        98;
                                                                                                                                                                                       Symonds JM,
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99US-0282029.
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RESULT
AAB06426
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2;
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N-PSDB; AAZ89137.
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                                                                                                                                                                                                                                                                                                                                                                                       230 AA;
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AAB06426;

AAB06426 standard; peptide;

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                                                                                                                                                                                                                                                                                                                                                                                                                Claudin-1 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                              Claim 39; Page 96; 121pp; English.
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30-MAR-1999;
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       11-MAY-2000
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                                             Mammalia
                                                             graft rejection;
                                                                               Claudin-1 modulating agent; cell adhesion recognition sequence;
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                                                                                                                     28-SEP-2000
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                                                                      sequence; autoimmune disease; inflammatory disease;
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99US-0282029.
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                                                              cyclic.
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Pred. No. 4.3e+05;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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30-MAR-1999;
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30-MAR-1999;
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                                                                                                                                                                                                                                          Mammalia.
                                                                                                                                                                                                                                                                                                         Claudin-1 modulating agent; cell adhesion recognition sequence;
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WPI; 2000-365610/31
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                                                                                                                                                                                                                                                                      sequence; autoimmune disease; inflammatory disease; cancer; ft rejection.
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99US-0282029
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99US-0282029.
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62.5%;
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Pred. No. 4.3e+05;
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vasopermiability, for delivering drugs to tumors and the nervous system and across the skin $\dot{}$

Antibody modulation of claudin-mediated cell adhesion for increasing

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                                       The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-1 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                                                                                                                                                    Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin \cdot
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                                                                                                                                                                                       Claim 43; Page 96; 121pp; English.
                                                                                                                                                                                                                                                                                    WPI; 2000-365610/31
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4.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                03-NOV-1998;
30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claudin-1 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claudin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200026360-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB06491 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                        (ADHE-) ADHEREX TECHNOLOGIES INC
                                                Local Similarity hes 5; Conser
   N
                        1 wrxxsyxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 wrxxsyxg 8
wriysyag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wriysyag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 5; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyclic cell adhesion recognition sequence
                                                                                                          10 AA;
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                  Symonds
                                                                                                                                                                                                                                                                                                                                                                                                98US-0185908.
99US-0282029.
                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-CA01029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cyclic.
                                                            86.1%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.1%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                  JM,
                                                                                                                                                                                                                                                                                                                                                  Gour BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 2
Pred. No. 1.9;
0; Mismatches
                                                            Pred.
                                                                       Score 31;
                                                 Mismatches
                                                            NO.
                                                            DB
1.9;
                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                ω,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ψ
                                                                       Length 10;
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                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:
                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                        system
                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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AAB06503
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                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Watches 5; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the use of peptides as claudin-mediated coll adhesion modulators. The claudin-1 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAR sequence; autoimmune disease; graft rejection; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claudin-1 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-NOV-1998;
30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO: 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB0 8497;
                                                                                                             Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 43; Page 97; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-365610/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-2000 (first entry)
            WO200026360-A1
                                      Mammalla
                                                             graft
                                                                                       Claudin-1 modulating agent; cell adhesion recognition sequence;
                                                                                                                                       28-SEP-2000 (first entry)
                                                                                                                                                                                        AAB06503 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                       1 wrxxsyxg 8
|| || || |
2 wriysyag 9
                                                              rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                            ξ,
                                                                         autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Symonds JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0185908
99US-0282029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-CA01029
                                                              cyclic.
                                                                                                                                                                                                                                                                                                                        86.1%;
                                                                                                                                                                                                                                                                                                            Score 31; DB Pred. No. 1.9; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gour BJ
                                                                           inflammatory disease;
                                                                                                                                                                                                                                                                                                                         DB
1.9;
                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                     Length 10
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                             0
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RESULT :
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Best Local Similarity
"hehes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-1 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-NOV-1998;
30-MAR-1999;
                    WPI; 2000-365610/31.
                                         Blaschuck OW,
                                                                                    03-NOV-1998;
30-MAR-1999;
                                                                                                                    03-NOV-1999;
                                                                                                                                           11-MAY-2000.
                                                                                                                                                                WO200026360-A1
                                                                                                                                                                                       Mammalia
                                                                                                                                                                                                          graft rejection; cyclic.
                                                                                                                                                                                                                      Claudin-1 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer;
                                                                                                                                                                                                                                                                                                  AAB06509;
                                                                                                                                                                                                                                                                                                                        AAB06509 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 43; Page 97; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-365610/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blaschuck OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-2000
                                                                                                                                                                                                                                                                            28-SEP-2000
                                                              (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                             2 wriysyag 9
                                                                                                                                                                                                                                                                                                                                                                                                  1 wrxxsyxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Symonds JM,
                                         Symonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0185908
99US-0282029
                                                                                    98US-0185908
99US-0282029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-CA01029
                                                                                                                     99WO-CA01029
                                                                                                                                                                                                                                                                                                                                                                                                                                  86.1%;
                                          JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gour BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                         Gour BJ
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Antibody modulation of claudin-mediated cell adhesion for increasing

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RESULT
AAY38421
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                             07-JAN-1998;
07-JAN-1998;
07-JAN-1998;
07-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-1 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                      Claim 11; Page 195; 227pp; English.
                                                                                                                                        Brewer LA,
Olsen HS,
                                                                   New isolated human genes and the secreted
                                                                                               N-PSDB; AAZ06254
                                                                                                             WPI; 1999-444190/37
                                                                                                                                                                                  (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                06-JAN-1999;
                                                                                                                                                                                                                                                                                                             15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                            endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein encoded by gene No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY38421 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vasopermiability, for delivering drugs to tumors and the nervous system and across the {\tt skin} -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wriysyag 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Page 97; 121pp; English.
                                                                                                                                        Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AA;
                                                                                                                                                     Duan RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                           98US-0070704.
98US-0070657.
98US-0070658.
98US-0070692.
                                                                                                                                                                                                                                                                                 99WO-US00108
                                                                                                                                                                                  SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.1%;
                                                                                                                                        Ruben
                                                                                                                                                     Ebner
                                                                                                                                      R,
SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                      Lafleur DW,
Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                 polypeptides they encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.
                                                                                                                                                      Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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This sequence represents a secreted human protein encoded by clone detailed in the descriptor line. The gene can be used

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Best Local Similarity
5; Conser
          31-MAR-1998;
31-MAR-1998;
01-APR-1998;
                                           30-MAR-1998;
31-MAR-1998;
31-MAR-1998;
                                                                          26-MAR-1998;
27-MAR-1998;
27-MAR-1998;
27-MAR-1998;
27-MAR-1998;
27-MAR-1998;
30-MAR-1998;
                                                                                                                                                                                                               11-MAR-1998;
12-MAR-1998;
13-MAR-1998;
17-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAZ06210) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 36 novel genes and their fragments (nucleic acid sequences: AAZ06219-Z06263; amino acid sequences AAY38386-Y38498) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypucleotides. Specific uses are described for each of the 36 polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                        20-MAR-1998
25-MAR-1998
                                                                                                                                                                              20-MAR-1998;
20-MAR-1998;
                                                                                                                                                                                                     20-MAR-1998
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                                                                                                                                                                                                                                                                                                      08-MAR-1999;
                                                                                                                                                                                                                                                                                                                            16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                           secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO944 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY41726 standard;
                                                                                                                                                                                                                                                           11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                 WO9946281-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                       11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (see AAZ06219 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wriysyag
                                                                                                                                                                                                                                                                                                                                                                                                       PRO; EST; expressed sequence tag; PCR primer; hybridisation; blood coagulation disorder; cancer; cellular adhesion disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
          98US-0080107.
98US-0080165.
98US-0080194.
98US-0080327.
                                                                           98US-0079689.
98US-0079728.
98US-0079786.
98US-0079920.
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98US-0078886.
                                                                                                                         98US-0079663
98US-0079664
                                                                                                                                                                              98US-0078910.
98US-0078936.
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98US-0077641.
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                                                                                                                                                         98US-0079294
                                                                                                                                                                      98US
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                                                                                                                                                                                                                                                                                                                                                                                            transmembrane protein.
                                                     3-0079923.
3-0080105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                -0079656
                                                                                                                                                                      0078939
                                                                                                                                                                                                                          0078004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.1%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
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13-MAY-1998
13-MAY-1998
13-MAY-1998
15-MAY-1998
15-MAY-1998
15-MAY-1998
15-MAY-1998
15-MAY-1998
15-MAY-1998
15-MAY-1998
22-MAY-1998
22-MAY-1998
22-MAY-1998
22-MAY-1998
22-MAY-1998
                                                                                                                                                                                                                                                               22-APR-1998
22-APR-1998
23-APR-1998
23-APR-1998
23-APR-1998
29-APR-1998
30-APR-1998
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21-APR-1998;
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01-APR-1998;
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15-APR-1998
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                                                                     (GETH )
                                                                      GENERTECH INC.
                                                                                                                                                                                                                                                                                                                                                                         98US-0081555

98US-0082569

98US-0082700

98US-0082700

98US-0082767

98US-0082767

98US-0083796

98US-0083322

98US-0083322

98US-0083395

98US-0083499

98US-0083499

98US-0083499

98US-0083499

98US-0083495

98US-0083495
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98US-0083559

98US-0084742

98US-0084441

98US-0084441

98US-0084441

98US-0084460

98US-0084600

98US-0084637

98US-0084637

98US-0084637

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98US-0085373

98US-0085573

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98US-0085573
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98US-0080334.
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WPI; 199 N-PSDB; Wood

1999-551358/46. DB; AAZ34118.

Goddard A,

Gurney ۶

Yuan 'n

Baker ΚP,

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adhesion

disorders

New secreted and transmembrane polypeptides and their polynucleotides useful for treating blood coagulation disorders, cancers and cellular adhesion disorders.

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    RESULT 19
AAY04143
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Best Local
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The present sequence represents human Tango-73. Tango polypeptides are useful for identifying compounds which bind the polypeptide via direct binding, competition binding assays or Tango-71, -73, -74, 76 or -83-mediated signal transduction. Tango polypeptides are also useful for identifying modulating compounds by determining effect on Tango activity. Tango polypeptides and nucleic acids are useful for diagnosing diseases related to aberrant expression of Tango, and Tango polypeptides are useful for raising antibodies which can be used in diagnostic assays for detection of Tango, and also for generating anti-idiotype antibodies for
                                                                                                                                                   Claim 8; Fig 2; 84pp; English.
                                                                                                                                                                               New TANGO polypeptides and nucleic acids encoding them - diagnostic agents and for treating disorders caused by all expression of TANGO \,
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                                                                                                                                                                                                                                                                                                                                                   05-SEP-1997;
06-AUG-1997;
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5; Conserv
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97US-0054966.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tango-73; Tango-74; Tango-76; Tango-83; diagnosis;
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62.5%;
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Pred. No.
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AAW99653
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Best Local :
                                                                                                                                   therapy for treating cancer, particularly where antisense oligonucleotides are useful for blocking normal or mutant p23 expression in cancer cells or other proliferating cells. Transgenic cells are also useful for producing the p23 polypeptide in large quantities. The antibodies are useful for raising antiserum against p23, and for identifying senescent cells in culture and tissue biopsies. The p23 polynucleotides are useful for modulating or altering p23 activity in a cell, and for identifying and isolating the whole gene encoding p23, and cell, and for identifying and isolating the whole gene encoding p23, and cell, and for identifying and isolating the whole gene encoding p23, and variants of p23. Assays based on p23 elements, which detect p23 levels and activity are useful as diagnostic markers for staging tumours, determining prognosis, and/or predicting therapeutic success. These elements also provide an assay for detecting chromosomal rearrangements in chromosome 3 in a human cell. The isolation of the p23 polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is human senescence factor p23. An expression vector for p23 is useful for inducing a senescent phenotype in a cell (preferably eukaryotic). This may help in regulating diseases, including cancer, persistent inflammation, and various proliferative and degenerative disorders. These transgenic cells are useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 35; 44pp; English.
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N-PSDB; AAX19461.
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     Sequence
                                                                                                    permits the manipulation of malignant growth in cancer.
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Query Match

86.1%;

Score 31;

DB 20;

Length 211;

Search completed: January 14, 2002, 07:36:01 Job time: 812 sec

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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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    protein search, using sw
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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    212252 segs, 22503292 residues
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/cgn2_6/ptodata/2/18a/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/18a/PCTUS_COMB.pep:*
    DB
US-07-876-280-4
US-07-675-772-4
US-08-053-170-4
US-08-053-170-4
US-08-158-232-4
US-08-316-301A-4
US-08-316-301A-4
US-08-316-301A-4
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US-08-761-890-15
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US-08-852-991-2
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| ; | 75.0 | 75.0 | 75.0 | 75.0 | 75.0 | 75.0 | 75.0 | 75.0 | 75.0 | 75.0 | 75.0 | 75.0 | 75.0 | 75.0 | 75.0 | | | 75.0 | | 75.0 | 75.0 | 75.0 | 75.0 |
| ! | 1385 | 1385 | 1385 | 1385 | 1385 | 1385 | 1385 | 1385 | 1385 | 1289 | 1289 | 1220 | 1220 | 1220 | 852 | 852 | 851 | 851 | 851 | 851 | 851 | 851 | 851 |
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| | US-09-076-137-2 | US-09-173-891-2 | US-08-611-928-2 | US-08-316-301A-2 | US-08-304-626-2 | US-08-158-232-2 | US-08-063-170-2 | US-07-675-772-2 | US-07-876-280-2 | 5426049-4 | 5281530-3 | US-09-173-891-43 | US-08-611-928-43 | US-08-158-232-43 | US-08-781-890-13 | US-08-276-099A-13 | PCT-US95-17025-2 | US-09-364-970-2 | US-09-087-465-4 | US-08-948-547-2 | US-09-012-710-2 | US-08-956-869-2 | US-08-956-652-2 |
| | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appl1 | Patent No. 5426049 | Patent No. 5281530 | Sequence 43, Appl | Sequence 43, Appl | Sequence 43, Appl | Sequence 13, Appl | Sequence 13, Appl | Sequence 2, Appli | Sequence 2, Appli | Sequence 4, Appli | Sequence 2, Appl1 | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli |

ALIGNMENTS

RESULT 1 US-07-876-280-4 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/876,280 FILING DATE: 19920430 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: Saliwanchik, David R. REGISTRATION UMBER: M/S 104 REFERENCE/DOCKET NUMBER: M/S 104 TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100 TELEPHONE: 904-375-88100 TELEPAX: 904-372-5800 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 1289 amino acids TYPE: AMINO ACID TYPE: AMINO ACID TYPE: AMINO SERVICEN SINGLE Patent No. Sequence GENERAL INFORMATION: APPLICANT: Payne, Jewel M. APPLICANT: Cannon, Raymond J.C. APPLICANT: Bagley, Angela L. TITLE OF INVENTION: No. 5262158el Bacillus thuringlensis Isolates for TITLE OF INVENTION: Controlling Acarides MOLECULE TYPE: | HYPOTHETICAL: YI ANTI-SENSE: NO ORIGINAL SOURCE: CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: COUNTRY: STREET: 2421 N.W. CITY: Gainesville STATE: FL TOPOLOGY: ADDRESSEE: 4, Application US/07876280 o. 5262158 32606 SOURCE: E: David R. Saliwanchik 2421 N.W. 41st Street, Suite A-1 USA ss: single linear YES

ORGANISM:

BACILLUS THURINGIENSIS

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                                                                                                            US-07-675-772-4
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US-07-675-772-4
                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                         INDIVIDUAL ISOLATE: PS17
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 ITTO-
CLONE: 17B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, VCURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/675,772 FILING DATE: 19910327 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                            TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                   ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 21,023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC 1628) NRRL B-18652
                                                                                                                                                                                                                   MOLECULE I
HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: SALIMANCHIK, ROMAN
                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1289 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: No. 5262399el Compositions and Methods
TITLE OF INVENTION: Flukes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                TYPE: AMINO ACID STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 32606
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1 wrxxsyxg 8
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Sick, August J.
Schwab, George E.
Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                              77.8%;
50.0%;
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                                              Score 28; DB 1;
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 1;
Pred. No. 3.5e+02;
                                Mismatches
                                                           Length 1289;
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US-08-158-232-4
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; Patent No. 5596071
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APPLICANT: Kim, Leo
APPLICANT: Schwab, G
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08063170 Patent No. 5350576
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,141
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,248
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: SALIMANCHIK, DAVID R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID STRANDEDNESS: sing TOPOLOGY: linear MOLECULE TYPE: prote
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                ORIGINAL
                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO ANTI-SENSE: NO
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LENGTH: 1289 amino aci
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                                                                                                                      382 WRAAQYGG
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                                                                                                                                                                                                                                                                                                              ORGANISM: Bacillus thuringiensis STRAIN: PS17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/063,170 FILING DATE: 19930517
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2421 N.W. 41st Street, Suite A-1
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Compositions and Methods for Inducing an Immune
Response for Protection Against Endoparasites and Exoparasi
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50.0%;
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                                                                                                                                                                                                         Score 28; DB 1;
Pred. No. 3.5e+02;
                                                                                                                                                                                         Mismatches
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RESULT 5
US-08-304-626-4
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                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645

FILING DATE: 25-NOV-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977

FILING DATE: 22-MAY-1991

ATTORNEY/AGENT INFORMATION:
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TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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REGISTRATION NUMBER: 31.794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: PS17b
IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC1628) NRRL B-18652
                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: PS17
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ANTI-SENSE: NO
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MOLECULE TYPE: pro
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                                                                   382 WRAAQYCG 389
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/887,980 FILING DATE: 22-MAY-1992
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2421 N.W. 41st Street, Suite A-1
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                                                                                                                                      Conservative
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Schnepf, H. Ernest
Schwab, George E.
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linear
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Randall, John Brooks
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                                                                                                                                                    77.8%;
50.0%;
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Pred. No. 3.5e+02;
0; Mismatches 4
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RESULT 6
US-08-316-301A-4
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Best Local Similarity
Thes 4; Conserv
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Sequence 4, Application US/08316301A Patent No. 5753492 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08304626 Patent No. 5616495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL: Y
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schnepf, Harry E.
APPLICANT: Schwab, George E.
TITLE OF INVENTION: No. 5616495el Bacillus thuringiensis Isolates
TITLE OF INVENTION: Active Against Hymenopteran Pests and Genes Encoding
TITLE OF INVENTION: Hymenopteran-Active Toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/07/887,980
FILING DATE:
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CITY: Gainesville
STATE: FL
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CLONE: E. coli
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LENGTH: 1289 amino acids
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                                                                                                                        382 WRAAQYGG
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OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: M/SCJ 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: David R. Sallwanchik STREET: 2421 N.W. 41st Street, Suite A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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STRANDEDNESS: si
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Foncerrada, Luis
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Randall, John Brooks
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                                                                                                                                                                                           Conservative
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linear
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                                                                                                                                                                                                                           Length 1289;
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US-08-316-301A-4
                                               Query Match
Best Local
                                Matches
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                                                                                                                                                                                       HYPOTHETICAL: Y
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                           IMMEDIATE SOURCE
CLONE: E. col:
                                                                                                                                                                                                                    MOLECULE TYPE: pro
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APPLICATION NUMBER: 07/565,544
FILING DATE: 10-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSITICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/871,510
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MATTELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 07/830,050
FILING DATE: 31-JAN-1992
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APPLICATION NUMBER: 07/693,018
FILING DATE: 03-MAY-1991
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                                                                                                                                                          ORGANISM: BACILLUS THURINGIENSIS INDIVIDUAL ISOLATE: PS17
                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/0 FILING DATE: 12-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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1 wrxxsyxg 8
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                              Similarity 4; Conserv
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VENTION: No. 5753492el Nematode-Active Toxins and Genes
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                                                                                                                        coli NM522(pMYC 1628) NRRL B-18652
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50.0%;
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                             Score 28; DB
Pred. No. 3.5e
0; Mismatches
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                                                                                                                                                                                                     TELEFAX: 904-3/2-5800
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/
FILING DATE: 25-NOV-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 22-MAY-1991
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1289 amino aci
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                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                       ANTI-SENSE:
                                                                                                       HYPOTHET ICAL:
                                                                                                                       MOLECULE TYPE:
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 CLONE: E. coli
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                            ORGANISM: BACILLUS THURINGIENSIS
STRAIN: PS17
INDIVIDUAL ISOLATE: PS17b
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STATE: FL
                                                                                                                                       TOPOLOGY:
                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: M/SCJ104.C1
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E. coli NM522(pMYC1628) NRRL B-18652
                                                                                                                                                                                  1289 amino acids
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2421 N.W. 41st Street, Suite A-1
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Schnepf, H. Ernest
Schwab, George E.
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Randall, John Brooks
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RESULT 8
US-09-173-891-4
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Patent No. 60779
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Matches 4; Conservative
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APPLICATION NUMBER: 1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/797,645
APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Sallwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
TELECHONE: 904-375-8100
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                                                                                                                INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1289 amino acids
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APPLICANT:
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APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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PRIOR APPLICATION DATA:
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STATE: FL
COUNTRY: USA
HYPOTHETICAL: Y
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                               TOPOLOGY: 11
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CITY: 0
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COEFFRANCE - CALLETTE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                TYPE: amino acid
STRANDEDNESS: sir
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                                                             uss: single
linear
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Schnepf, H. Ernest
Schwab, George E.
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Uick, Heidi Jane
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Randall, John Brooks
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Pred. No.
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3.5e+02;
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Query Match
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SEQ ID NO 4
LENGTH: 1289
                                                                                                                                                                                                                                                                          Sequence 4, Application PC/TUS9203624 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schnepf, Harry E. APPLICANT: Schwab, George E. APPLICANT: Payne, Jewel M. APPLICANT: Narva, Kenneth E. APPLICANT: Foncerrada, Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                        APPLICANT: Schnepf, Harry E.
APPLICANT: Schwab, George E.
APPLICANT: Payne, Jewel M.
APPLICANT: Narva, Kenneth E.
APPLICANT: Foncerrada, Luis
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                            TITLE OF INVENTION: Novel Nematode-Active Toxins and Genes TITLE OF INVENTION: Which Code Therefor NUMBER OF SEQUENCES: 40
                                                                                                             ADDRESSEE: David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 WRAAQYGG 389
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                                COUNTRY: UZIP: 32606
                                                                CITY: Gainesville
STATE: FL
                                                                                                STREET:
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2421 N.W. 41st Street, Suite A-1
                                                  USA
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Pred. No.
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Pred. No. 3
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3.5e+02;
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US-08-408-318-2
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; CLONE: E. coli NM522(pMYC 1628) NRRL B-18652
PCT-US92-03624-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08408318 Patent No. 5639858
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Matches 4; Conservative
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APPLICANT: Hoey, Timothy
TELEFAX: 415-494-8771
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
                              REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-494-8700
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach,
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 WRAAQYGG 389
                                                                                                                                                                                                                                                                                                                            STREET: 850 Hans
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                   APPLICATION NUMBER: US/08/408,318 FILING DATE:
                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: BACILLUS THURINGIENSIS INDIVIDUAL ISOLATE: PS17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
STRANDEDNESS: Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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50.0%;
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                                                                A-60845
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Pred. No. 3.5e+02;
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                                            Query Match
Best Local Similarity
Conserv
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US-08-369-796-10
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                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 748 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: FÜNCTIONALLY ACTITLE OF INVENTION: TRANSDUCER AND NUMBER OF SEQUENCES: 39
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APPLICANT: Zhong Zhong
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TELLEFAX: 133521
500 WQFSSYVG 507
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CITY: Hackensack
STATE: New Jerse
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                           1 wrxxsyxg 8
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                                                                                                                                                                       : 748 amino acids
amino acid
GY: linear
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411 Hackensack Avenue
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                                                           Conservative
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                                                                           75.0%;
50.0%;
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50.0%;
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                                                                                                                                                                                                                                                                                                                   600-1-116
                                                                           Score 27;
Pred. No.
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Pred. No. 3.4e+02;
1; Mismatches 3
                                                              Mismatches
                                                                           3.4e+02;
                                                                                        Length 748
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RESULT 13 US-08-839-164-2 0;

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-839-164-2
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                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08852091 Patent No. 5883228 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-494-8771
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                TITLE OF INVENTION: FÜNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-60845
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-8700
TELEPHONE: 415-494-8700
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                               APPLICANT: James E. Darnell, Jr. APPLICANT: Zilong Wen APPLICANT: Curt M. Horvath APPLICANT: Zhong Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/839,164 FILING DATE: 23-APR-1997 CLASSIFICATION: 536
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CITY: Palo Alto
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nes 4; Conserv
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ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                 COUNTRY: UZIP: 07603
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Pred. No. 3.4e+02;
1; Mismatches 3
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APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEEXA: 13521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LERGTH. 746 Emits 2014
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Best Local Similarity 50.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Patent No. 5
                               APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION UMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
OUR PROTECT NUMBER: PG 15/08/090 75/
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thong, Zhong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                     LIREET: 411 Hackensack Avenue CITY: Hackensack STATE: New To
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APPLICATION NUMBER: US 07/854,296 FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 07601
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50.0%;
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n Release #1.0, Version #1.25
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Pred. No. 3.4e+02;
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US-08-956-652-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Darnell Jr., J
APPLICANT: Schindler, Chr
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                 APPLICATION NUMBER: 19-MAR-
FILING DATE: 19-MAR-
PRIOR APPLICATION DATA:
*APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
              FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                 FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 11-MA
                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hackensack
STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                  07601
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11-MAR-1994
                                                                                     19-MAR-1992
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50.0%;
                                                                                                                                                      US 07/980,498
                                                   WO US93/02569
                                                                                                   US 07/854,296
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US 08/126,588
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Pred. No. 3
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US-08-956-869-10
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Best Local Similarity 50.0%;
                APPLICATION NUMBER: WO US93/02569
ETILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO US93/02569
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/956,869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEINTILE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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TOPOLOGY: linear
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
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                  600-1-073 CIP

    Mismatches

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Pred. No. 3.4e+02;
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Best Local Similarity 50.u
""rches 4; Conservative
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
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APPLICATION NUMBER: V
FILING DATE: 19-MAR-1
PRIOR APPLICATION DATA:
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                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 24-SEP-1993 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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CITY: Hackensack
STATE: New Jersey
                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
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                            TELEPHONE: 201 487-58
TELEFAX: 201 343-1684
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5, 6124118
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                                                                                                                                                               NUMBER: US 08/126,588
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50.0%;
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Pred. No.
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APPLICANT: Vinkemeler, Uwe
APPLICANT: Chen, Xiaomin
APPLICANT: Chen, Xiaomin
APPLICANT: Chen, Xiaomin
APPLICANT: MITTON: A CRYSTAL OF THE CORE POF
TITLE OF INVENTION: USE
FILE REFERENCE: 600-1-229
CURRENT APPLICATION NUMBER: US/09/087,465A
CURRENT FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-09-087-465-8
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PCT-US95-17025-10
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Best Local Similarity 50.0
Matches 4; Conservative
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SEQ ID NO 8
LENGTH: 748
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                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Applicat GENERAL INFORMATION:
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Best Local Similarity
Matches 4; Conserv
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TYPE: amino acid
TOPOLOGY: line
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LENGTH: 748 amino acid
              COMPUTER READABLE FORM:
MEDIUM TYPE: F1Dpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                    APPLICANT: Zilong Wen APPLICANT: Curt M. Hor' APPLICANT: Zhong Zhong
                                                                                                                                                                                                                                TITLE OF INVENTION: FÜNCTIONALLY ACTIVE REGIONS OF SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                            APPLICANT:
CURRENT APPLICATION DATA:
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CITY: Hackensack
STATE: New Jersey
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ZIP: 07601
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                                                                                                                          USA
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Curt M. Horvath
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Pred. No. 3.
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3.4e+02;
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APPLICATION NUMBER: PCT/US95/17025

FILING MATE: 22-DEC-1995

CASABETCATION BOTC:

APPLICATION NUMBER: 00/369,796

FILING DATE: 06-JAN-1995

CLASSIFICATION NUMBER: 600-1-116

FELEX: APPLICATION NUMBER: 600-1-116

TELECOMMEN: 20-148-1881

REFERENCE/OCKET NUMBER: 600-1-116

TELECOMMUNICATION HYPORATION:

TELEPHONE: 20143-1864

TELEX: 133521

INFORMATION FOR ESQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGIH: 718 anino acids

TYPE: maino acids

TYPE:
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Result
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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36
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Copyright (c) 1993 - 2000 Com
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| 238 | 224 | 216 | 211 | 198 | 189 | 188 | 179 | 160 | 154 | 148 | 133 | 100 | 90 | 1289 | 886 | 538 | 531 | 370 | 362 | 330 |
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| T51072 | G75087 | T49795 | в71058 | G85506 | D71006 | D75125 | A33164 | E64158 | н83160 | T31141 | CCQFCT | F84231 | в81035 | T18212 | H71338 | F83354 | T49058 | в83191 | 869698 | T34972 |
| hypothetical prote | transcription regu | related to 3-oxoac | hypothetical prote | hypothetical prote | probable GMP synth | gmp synthase, nter | hypothetical prote | hypothetical prote | hypothetical prote | transcription regu | cytochrome c' - Rh | hypothetical prote | hypothetical prote | parasporal crystal | conserved hypothet | probable sulfatase | hypothetical prote | alcohol dehydrogen | ERD1 protein - yea | probable membrane |

ALIGNMENTS

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A;AcCession. A;AcCession. A;AcCession. A;AcCession. A;AcCession. A;Rolecule type: protein
A;Residues: 128-170 <MATS>
C;Superfamily: subtilisin; subtilisin homology
C;Superfamily: subtilisin; subtilisin homology
C;Keywords: extracellular protein; hydrolase; serine proteinase
F;1-14/Domain: signal sequence #status predicted <SIG>
F;15-127/Domain: propeptide #status predicted <PRO>
F;128-408/Product: aqualysin I #status experimental <MAT>
F;157-364/Domain: subtilisin homology <SBT>
F;255-257,281-283/Region: S1 specificity crevice #status predicted
F;409-513/Domain: carboxyl-terminal propeptide #status predicted <Crief (197.349/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 75-442 < KMO>
A; Residues: 75-442 < KMO>
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A; Residues: 75-442 < KMO>
A; Cross-references: EMBL: X07734; NID: 948069; PIDN: CAA30559.1; PID: 9602091
A; Cross-references: EMBL: X07734; NID: 948069; PIDN: CAA30559.1; PID: 9602091
A; Note: part of this sequence, including the amino and carboxyl ends of the mature pr
R; Matsuzawa, H.; Tokugawa, K.; Hamaoki, M.; Mizoguchi, M.; Taguchi, H.; Terada, I.; K
Eur. J. Biochem. 171, 441-447, 1988
A; Title: Purification and characterization of aqualysin I (a thermophilic alkaline se
A; Reference number: S00324; MUID: 88151937
A; Accession: S00324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Cross-references: GB:J90108; GB:D90108; GB:J05414; NID:g217171; PII A:Note: the authors translated the codon CTG for residue 470 as Val, R:Kwon, S.T.; Terada, I.; Matsuzawa, H.; Ohta, T. Biochem. 173. 491-497, 1988
A:Title: Nucleotide sequence of the gene for aqualysin I (a thermophia.) Reference number: S00620; MUID:88225062
A:Accession: S00620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Unique precursor structure of an extracellular protease, A;Reference number: A35742; MUID:90216674
A;Accession: A35742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Thermus aquaticus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A35742; S00620; S00324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-513 <TER>
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J. Biol. Chem. 265, 6576-6581, 1990
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Matches
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Best Local
   Similarity
5; Conserv
      Conservative
                               86.1%;
   Score 31; DB Pred. No. 17; 0; Mismatches
      0;
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WRKMAYFG

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A;Cross-references: GB:U32724; GB:L42023; NID:g1573378; PII
C;Superfamily: conserved hypothetical protein HI0360
C;Keywords: transmembrane protein; transport protein
F;4-20/Domain: transmembrane #status predicted <TM1>
F;38-54/Domain: transmembrane #status predicted <TM2>
F;88-74/Domain: transmembrane #status predicted <TM4>
F;88-14/Domain: transmembrane #status predicted <TM4>
F;127-143/Domain: transmembrane #status predicted <TM5>
F;127-143/Domain: transmembrane #status predicted <TM6>
F;168-184/Domain: transmembrane #status predicted <TM6>
F;186-202/Domain: transmembrane #status predicted <TM6>
F;186-202/Domain: transmembrane #status predicted <TM8>
F;218-234/Domain: transmembrane #status predicted <TM8>
F;218-234/Domain: transmembrane #status predicted <TM8>
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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane protein HI0407 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-261 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I k.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic
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A;Experimental source: serogroup
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A; Residues: 1-260 <HEI>
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                                                     Matches
                                                                             Query Match
Best Local
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5; Conser
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Pred. No. 15;
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I.; Sellers,
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A;Cross-references: EMBL:AC004238; NID:g3033373; PID:g3033393

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T00479; B84763
R; Rounsley, S.D.; Lin, X.; Ketchum,
submitted to the EMBL Data Library,
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                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487 A;Accession: B84763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Description: Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence A;Reference number: Z14160 A;Accession: T00479
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                                                                                                                   A; Map position:
                                                                                                                                              A; Gene: At2g34980;
                                                                                                                                                                                                      A; Cross-references:
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A; Residues: 1-303 < ROU>
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A; Residues: 1-262 <STO>
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                                                                                                                                                                                                                              1-303 <STO>
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                                                                                                                                                                                                      GB:AE002093;
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bata Library, April 1998
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62.5%;
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Pred. No. 15;
0; Mismatches
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18;
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Conservative

0,

83.3%; 62.5%;

Score 30; Pred. No.

2;

Length 303; Indels

0;

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C:Species: phage lambda
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 23-Jul-1999
C:Accession: H43009; G43013; A04355
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submitted to the Nucleic Acid Sequence Database, systematic and the Nucleic Acid Sequence Database, systematic and Sequence Database, systematic and Sequence Database, as A;Accession: H43009
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                                                                                                                                                    A;Genc: ZU9/s
C;Superfamily: phage lambda tail assembly protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable tail component of prophage CP-933K Z0978 [imported] - Escherichia coli
C;Species: Escherichia coli
C;Dato: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
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C; Superfamily: phage lambda
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A;Title: Nucleotide sequence of bacteriophage lambda DNA. A;Reference number: A92891; MUID:83189071
A;Accession: G43013
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A; Residues: 1-199 <DAN>
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                      A:Status: preliminary A:Molecule type: DNA
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A; Residues: 1-199 <SAN>
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WRASAFTG 212
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    Matches
                    Query Match
Best Local
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RyFinch, P.W.; Storey, A.; Chapman, K.E.; Brown, K.; Hickson, I.D.; Emmerson, Nucleic Acids Res. 14, 8573-8582, 1986

A;Title: Complete nucleotide sequence of the Escherichia coli recB gene. A;Reference number: A2532; MUID:87066729

A;Reference number: A2532; MUID:87066729

A;Accession: A2532

A;Rolecule type: DNA
A;Residues: 1-1180 <FIN>
A;Residues: 1-1180 <FIN>
A;Residues: 1-180 <FIN>
A;Ross. references: GB:X04581; NID:942680; PIDN:CAA28250.1; PID:942682

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Ril
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Reference number: A64720; MUID:97426617
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R;Cole, S.T.; Brosch, R.; Parkhill, J.;.Garnier, T.; Churcher, C.; Harris, D.; Gordon R;Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987
A;Accession: H70947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exodeoxyribonuclease V (EC 3.1.11.5) 135K chain - Escherichia coli
N;Alternate names: exonuclease 135K polypeptide; recBC DNase 135K polypeptide
C;Species: Escherichia coli
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 19-Jan-2001
C;Accession: A25532; E65064
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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A;Experimental source: strain H37Rv
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A; Residues: 1-448 <COL>
                                                                                                                                                                A;Map position: 61 min
C;Superfamily: exodeoxyribonuclease V 135K chain
C;Keywords: ATP: DNA repair; hydrolase; nucleotide binding; P-loop
F;23-30/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000365; GB:U00096; NID:g2367163; PIDN:AAC75859.1; PID:g17891 A;Experimental source: strain K-12, substrain MG1655 C:Comment: This enzyme is required for efficient DNA repair; it catalyzes the unwindil of these activities require concomitant hydrolysis of ATP.
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A; Residues: 1-1180 <BLAT>
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Conservative

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RESULT 12
E72167 t
   A32L protein - variola minor virus (strain Garcia-1966) C; Species: variola minor virus C; Date: 24-NQv-1999 #sequence_revision 24-Nov-1999 #tex
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A; Molecule type: DNA
A; Residues: 1-1208 <HEI>
A; Cross references: GB: AE004303; GB: AE003852; NID: 99656890; PIDN: AAF95464.1; GSPDB: GNO01
A: Fyperimental source: serogroup O1; strain N16961; biotype E1 Tor
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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A; Molecule type: DNA
A; Residues: 1-1180 <STO>
A; Cross-references: GB:AE005174; NID:g12517302; PIDN:AAG57931.1; GSPDB:GN00145; UWGP:Z41
A; Cross-reference: strain O157:H7, substrain EDL933
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A;Map position: 1
C;Superfamily: exodeoxyribonuclease V 135K chain
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C;Superfamily: exodeoxyribonuclease V 135K chain
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Nature 409, 529-533, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 4; Conser
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tbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta,
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 1.1e
1; Mismatches
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Pred. No.
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24-Nov-1999 #text_change 20-Jun-2000
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Lanta, E.;
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H.; Dragoi, I.; Sellers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.D.; Rose, Potamousis,
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K.; Aj
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Apodaca,
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A31L protein - variola virus
N;Alternate names: A28L protein
C;Species: variola virus
C;Species: variola virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C;Accession: S46858; E36851
C;Accession: S46858; E36851
R;Kolykhalov, A.A.; Blinov, V.M.; Frolov, I.V.; Totmenin, A.V.; Shchelkunov submitted to the EMBL Data Library, April 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z20488; MUID:94088747 A; Accession: T28573 A:Stratus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain Harver R; Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, Nature 366, 748-751, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60883.1; PID:g623596
A;Experimental source: strain Bangladesh 1975
C;Superfamily: sheep pox virus HM3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-146 <MAS>
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A; Residues: 1-146 < AGU>
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A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI-E gen
                                                                                                                                                                                   S46858
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J. Gen. Virol. 73, 2887-2902, 1992
A;Title: Nucleotide sequence of 21.8 kbp of
A;Reference number: JQ1832; MUID:93057361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3L protein - variola major virus
C;Species: variola major virus
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change
C;Accession: JQ1834; T28573
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C;Superfamily: sheep pox virus HM3 protein
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A; Residues: 1-146 <SHC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JQ1834
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Best Local
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62.5%;
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62.5%;
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R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137
A;Recession: H71119
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Recoule type: DNA
A;Residues: 1-278 <KAW>
                                                                                          R; Domler, S.A.; de Zocten, G.A.

J. Gen. Virol. 72, 1819-1834, 1991

A; Title: The nucleotide sequence and luteovirus-like
A; Reference number: JQ1382; MUID:91341468

A; Accession: JQ1386
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A; Residues: 1-146 <BLI>
A; Residues: 1-146 <BLI>
A; Cross references: GB:X69198; NID:9456758; PIDN:CAA49076.1; PID:9457026
A; Experimental source: strain India-1967, ssp. major, isolate Ind3
C; Superfamily: sheep pox virus HM3 protein
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A;Molecule type: DNA
A;Residues: 1-146 <KOL>
A;Cross-references: GB:L04573; NID:g294105; PIDN:AAA72298.1; PID:g294107 A;Experimental source: strain WSG A;Note: this reading frame extends between two stop codons and does not
                                                                                                                                                                                                                hypothetical 33K protein - pea enation mosaic virus C;Species: pea enation mosaic virus, PEMV C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change C;Accession: J01386
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A; Accession: E36851
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                                                                 A; Molecule type: genomic RNA
A; Residues: 1-303 <DEM>
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A; Note: this accession replaces an interim accession
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C:Accession: H71119
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A;Experimental source: strain India-1967, isolate Ind3
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A;Experimental source: strain OT3
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    does not begin with
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                                                                                                                                                                                                                                           08-Oct-1999
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hypothetical protein K04E7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Jate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Ac@ession: T16557
R;Nhan, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
T16557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: 65-Asp was also C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΥ
                                                                                                                              A; Map position: 4
A; Introns: 44/3; 76/3; 128/3; 174/3; 194/1;
A; Note: F7J7.120
                                                                                                                                                                          A; Experimental source: cultivar Columbia; BAC clone C; Genetics:
                                                                                                                                                                                                                      A; Reference number: Z15391
A; Accession: T04949
A; Molecule type: DNA
A; Residues: 1-648 <BEV>
                                                                                                                                                                                                                                                                                                            hypothetical protein F7J7.120 - Arabidopsis thallana C;Species: Arabidopsis thallana (mouse-ear cress) C;Decies: Arabidopsis thallana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999 C;Accession: T04949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, October 1995 A; Description: The sequence of C. elegans cosmid
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                         δÃ
                                                                                                                                                                                                                                                                                R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: CESP:K04E7.3
A;Introns: 43/3; 81/3; 112/3; 153/1; 191/2;
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A; Residues: 1-551 <NHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: The sequence A; Reference number: 218535
                                                                                                                                                                                                        A; Cross-references: EMBL: ALO21960
                                                                                                                                                                                                                                                                                                                                                                          T04949
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Pred. No.
                                                                       Score 28;
Pred. No.
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probable tRNA/rRNA methyltransferase NMA2218 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: E81795 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MUID:20222556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphoketolase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Abe: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C;Accession: F86812
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. in press, 2001
A;Title: The complete genome sequence of the lactic acid bacterium.
A;Reference number: A86625
A;Accession: F86812
A;Accession: F86812
                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-154 <PAR>
A;Cross-references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85429.1; PID:g738083
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
Search completed: January 14, 2002, 07:37:30 Job time: 900 sec
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A;Residues: I-822 <STO>
A;Cross-references: GB:AE005176; NID:g12724499; PIDN:AAK05600.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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Best Local Similarity
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Best Local Similarity 50.0
Matches 4; Conservative
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Pred. No. 1.3e+02;
0; Mismatches 4; Indels
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Title:
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Maximum Match 100%
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AOFH_MYCTU
EX5B_ECOLI
VA2B_YARV
CLD1_HUMAN
CLDX_BRARE
XYPD_LACLA
HIRA_CHICK
VAT_CAMVP
QOX2_SULAC
CLD4_CERAE
CLD4_CERAE
CLD4_HUMAN
CLD2_BRARE
CLD4_HUMAN
CLD3_HOUSE
CLD3_HUMAN
CLDB_HOUSE
CLD3_HUMAN
CLD1_HUMAN
CLD1_HUMAN
CLD1_HOUSE
CSAB_BACUB
CYCP_RHOTE
YIBK_HAEIN
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7.778 Million cell updates/sec
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ALIGNMENTS

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| ANDARD; PRT; 513 AA. 08, Created) 15, Last sequence update) 32, Last annotation update) 32, Last annotation update) RSOR (EC 3.4.21). /Deinococcus group: Thermus group; Thermus. /Deinococcus group: Thermus group; Thermus. -T., Miyata Y., Matsuzawa H., Ohta T.; structure of an extracellular protease, accoon-terminal pro-sequences and its process. -T., Matsuzawa H., Ohta T.; a I., Matsuzawa H., Ohta T.; crease) of Thermus aquaticus YT-1 and the enduced primary structure of the enzylored protease) of Thermus aquaticus YT-1 and the enduced primary structure of the enzylored protease) produced by Thermus aquaticus YT-1171.441-447(1988). -T., Ohta T.; charcterization of aqualysin I (a thermoprotease) produced by Thermus aquaticus YT-1171.441-447(1988). -T., STAGE: SECRETED. -C. STAGE: SECRETED FROM THE EARLY STATIONARY EMPLEMENTAL PRO-SEQUENCES ARE REMOVED THIS OF SEQUENCE IS REQUIRED FOR TRANSLOCATION ON OS THE OUTER MEMBRANE. LETDE BONDS ARE PRESENT. ELDORGS TO PEPTIDASE FAMILY S8: ALSO KNOWN J | SEQUENCE OF MEDLINE-8811 MATSUZAWA H TERADA I., I TERADA I., I TERADA I., I TERADA I., I TERADA I., I TERADA I., I TERADA I., I TERADA I., I BIOO I., I BI | J. Biol. Che [2] SEQUENCE OF SEQUENCE OF STRAIN=YT1; MEDLINE=882; KWON ST., "Nucleotide alkaline sei characterise Eur. J. Bioo [3] | Thermus aqua Bacteria; TI NCBI_TaxID= [1] SEQUENCE FRO STRAIN=Y11; MEDLINE=902; Terada I., F "Unique prec I, with NH2; Escherichia | TT 1 _THEAQ _AQL1_THEAQ _P08594; 01-AUG-1988 01-AUG-1990 01-NOV-1995 AQUALYSIN I |
| ce update) tion update) tion update) tion update) -). OF 15-23. Matsuzawa H., Ohta T.; extracellular protease, ac o-sequences and its process)). H., Ohta T.; for aqualysin I (a thermop) mus aquaticus YT-1 and imary structure of the enz)). ETG GROW. TO GROW. THE EARLY STATIONARY THE TO GROW. TO SEQUENCES ARE REMOVED THI NESSNT. PRESENT. PRESENT. PRESENT. | 1128-170 11937; PubMed=1 1937; PubMed=2 1937; PubMe | 265:6576-65 265:6576-65 275-442 FROM N. 25062; PubMed=: Terada I., Mat Sequence of the sequence of the ine protease) ics of the dec them. 173:491-4 | ermus/Deinococ 271; M N.A., AND SE 16674; PubMed=2 Woon ST., Mij pursor structur - and CoOH-term | ANDARD; 08, Cre 15, Las 32, Las RSOR (EC |
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074164;
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                                                                            "Increased carotenoid production by the food yeast Candida utilis through metabolic engineering of the isoprenoid pathway.";
Appl. Environ. Microbiol. 64:2676-2680(1998)
-!- FUNCTION: INVOLVED IN THE CONTROL OF CHOLESTEROL BIOSYNTHESIS.
-IS THE RATE-LIMITING ENZYME OF THE STEROL BIOSYNTHESIS.
-!- CATALYTIC ACTIVITY: (R)-MEVALONATE + COA + 2 NADP(+) = (S)-3-
- HYDROXY-3-METHYLGLUTARYL-COA + 2 NADPH.
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                                                                                                                                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE
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PIR; A35742; A35742.
HSSP; P06873; 3PRK.
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                   MEDLINE=98320604; PubMed=9647847; Shimada H., Kondo K., Fraser P.D.
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Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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REPLINE=95350630; PubMed=7542800;

RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Kelley J.M.,

RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

RA Weidman J.F., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

RA Fine L.D., Fritchman J.L., Small K.V., Fraser C.M., Smith H.O.,
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pfam; PF00368; HMG-COA_red; 1.

PRINTS: PR00071; HMGCOARDTASE_1; 1.

PROSITE; PS00066; HMG_COA_REDUCTASE_1; 1.

PROSITE; PS001318; HMG_COA_REDUCTASE_2; 1.

PROSITE; PS01192; HMG_COA_REDUCTASE_4; 1.

PROSITE; PS01055; HMG_COA_REDUCTASE_4; 1.

PROSITE; PS01055; MG_COA_REDUCTASE_4; 1.
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P44691;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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N-LINKED (GLCNAC...) (POTENTIAL).

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P03729;
21-JUL-1986
21-JUL-1986
01-APR-1993
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MEDLINE-B3189701; Pubmed:6221115;

Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;

"Nucleotide sequence of bacteriophage lambda DNA.";

"Nucleotide sequence of bacteriophage lambda DNA.";

J. Mol. Biol. 162:729-773(1982).

-I- FUNCTION: GENE K PROTEIN IS INVOLVED IN THE ASSEMBLY OF THE INITIATOR COMPLEX FOR TAIL POLYMERIZATION. IT HAS NOT BEEN IN THE MATURE PHAGE.
                         use by non-profit institutions as lon modified and this statement is not removentiles requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-I- FUNCTION: INVOLVED IN THE HIGH-AFFINITY ZINC UPTAKE TRANSPORT SYSTEM (BY SIMILARITY).
                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDN
Lambda phage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lambda phage group.
NCBI_TaxID-10710;
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                                                                                                                                                                                                                         -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-11 IS THE INITIATOR
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SIMILARITY: BELONGS TO THE ABC-3
PROTEINS. STRONG, TO E.COLI ZNUB.
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5 (Rel. 01, Last sequ
3 (Rel. 25, Last anno
BLY PROTEIN K.
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                                                               moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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Matches 4
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                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-98311639; PubMed-9647647;
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InterPro; IPRO00064; NLPC_P60.
Pfam; PF00877; NLPC_P60; 1.
SEQUENCE 199 AA; 23011 MW;
                                                                                                                                                                                                        MGD; MGI:1276110;
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PROSITE; PS01346; CLAUDIN; 1.
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MEM 8
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AA; 23011 MW; CEEB88F01E31ABAE CRC64;
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137 F
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Rodentia;
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Pred No. 10;
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Pred. No. 12;
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RESULT 6
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ID EX5B_ECOLI
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole genome comparison of Mycobacterium tuberculosis clinical laboratory strains.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: FAD (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AOFH_MYCTU STANDARD; PRT; 454 AA. 053320; 053320; 05-20-20-20 (Rel. 37, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) PUTATIVE FLAVIN-CONTAINING MONOAMINE OXIDASE RV3170 OR MT3259 OR MTV014.14.
                                                                                                                                                                                                                                                                                     InterPro; IPR002937; Amino_oxidase
InterPro; IPR000205; NAD_binding.
Pfam; PF01593; Amino_oxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delchar A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                          TIGR;
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NCBI_TaxID=1773;
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AE007139; AAK47598.
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J. Biol.
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                                                                                                                                                                                                                     encoding protease III.";
Nucleic Acids Res. 14:7695-7703(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perr Riley M., Collado-vides J., Glasner J.D., Rode (Gregor J., Davis N.W., Kirkpatrick H.A., Goeden Mau B., Shao Y.;
                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Arnold D.A., Kowalczykowski S.C.;
"Facilitated loading of RecA prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update
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MEDLINE-87040734; PUBMed-3534791;
Finch P.W., Wilson R.E., Brown K., Hickson I.D.,
"Complete nucleotide sequence of the Escherichia
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J. Biol. Chem.
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                                                                                                                  European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
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SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD SUBULARITY: BELONGS TO THE UVRD SUBFAMILY OF HELICASES.
; X04581; CAA28250.1; -., AFT9304; AAD56369.1; -., U29581; AAB40467.1; -., AEG00365; AAC75859.1; -., X06227; CAA29577.1; -.
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01-FEB-1994
15-DEC-1998
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STRAIN-INDIA-1967
MEDLINE-92209372;
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InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase;
                                                     STRAIN BANGLADESH-1975;
MEDLINE.94088747; PubMed-9264798;
Massung R.F., Esposito J.J., Liu L., Qi J., L
Knight J.C., Aubin L., Yuran T.E., Parsons J.
Sclivanov N.A., Cavallaro K.F., Kerlavage A.F
                                                                                                                                    MEDLINE 93057361; PubMed 1331292; Aguado B., Selmes I.P., Smith G.L.; Aguado B., Sequence of 231th of variola and comparison with vaccinia virus."; J. Gen. Virol. 73:2887-2902(1992).
                                                                                                                                                                                                                                                                  MEDLINE-93202281;
Shchelkunov S.N.,
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NCBI_TaxID-10255;
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Nature
[5]
          smallpox virus genome.";
Nature 366:748-751(1993)
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                                                                                                                                                                                                                                            "Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms.";
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EMBL; X67115; CAA47802.1; -
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EMBL; X76266; CAA53857.1; -
PIR; E36851; E36851.
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SEQUENCE 146 AA; 16244 M
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095832;
"Assignment(1) of claudin-1 (CLDN1) to human chromosome with somatic cell hybrids."; Cytogenet. Cell Genet. 88:217-217(2000).
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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CLDN1 OR CLD1 OR SEMP1.
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MEDLINE=99132301; Publ
Swisshelm K.L., Machl
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                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-20290992;
                                                                                                                                                                                                                                                           Mitic L.M., Anderson J.M.;
"Human claudin-1 isolated from Caco-2
Submitted (DEC-1998) to the EMBL/GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                "SEMP1, a senescen epithelial cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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the European Bioinformatics Institute.
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Adamson P.;
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                                                                                                                                                                                                                                                                                                                                                                                                               superfamily."
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er P., Greenwood
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achl A., Planitzer
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62.5%;
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                                                                                                                               MEDLINE-20525589; PubMed-11071763;
Chin A.J., Tsang M., Weinberg E.S.;
"Heart and gut chiralities are controlled independently from initial heart position in the developing zebrafish.";
Dev. Biol. 227:403-421(2000).
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-i- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                            Q9YH92;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
CLAUDIN-LIKE PROTEIN ZF4A22 (CLAUSIN 7).
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
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                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
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InterPro; IPR000729; pmp22_Claudin
Pfam; PF00822; PMP22_Claudin; 1.
                                                                                                                                                                                                                                                                                     Keen T.J., Inglehearn C.F.; Submitted (OCT-1998) to the
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Keen T.J., Inglehe
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               an email to license@isb-sib.ch).
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Interpro; IPRO01832; Claudin.
Interpro; IPRO0180729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
PROSTIE; PS01346; CLAUDIN.
PROSTIE; PS01346; CLAUDIN: 1.
Tight junction; Transmembrane.
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HSSP; P00740; 11XA.
WormPep; K04E7.3; CE02798.
InterPro; IPR001506; Astacin.
InterPro; IPR000859; CUB.
InterPro; IPR000859; CUB.
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                         Pfam; PF01400; Astacin; 1. Pfam; PF00431; CUB; 1. SMART; SM00042; CUB; 1. SMART; SM000209; TSP1; 1. SMART; SM00235; ZnMC; 1.
PROSITE; PS01180; CUB; FALSE_NEG. PROSITE; PS00102; EGF_1; 1. PS01186; EGF_2; FALSE_NEG PROSITE; PS50092; TSP1; 1.
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Rhabditidae; Peloderinae;
                                                                                                InterPro;
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IPR000130; Zh_MTpeptdse.
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Pred. No. 19;
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RESULT 12
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SEQUENCE
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       Lyase; F
SEQUENCE
                               PROSITE;
                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                 MEDLINE-21235186; PubMed-11337471; Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403."; Genome Res. 11:731-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-IL1403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE XYLULOSE-5-PHOSPHATE/FRUCTOSE-6-PHOSPHATE PHOSPHOKETOLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last seg
20-AUG-2001 (Rel. 40, Last ann
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Hypothetical protein; Hydrolase; Metalloprotease; Zinc;
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XFP OR PTK.
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                                                                                                                                                                            COPACTOR: THIAMINE PYROPHOTE (POTENTIAL).
                                                                                                                                                         SIMILARITY: BELONGS TO THE XFP FAMILY.
AE006381; AAK05600.1; -.
TE; PS00187; TPP_ENZYMES; FALSE_NEG.
; Flavoprotein; Thiamine pyrophosphate; Complete proteome.
NCE 822 AA; 93363 MW; C686D569D3E8E22F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-like
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Pred. No. 46;
1; Mismatches
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EGF-LIKE.
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ZINC (CATALYTIC) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL);
7CFC9A16B56C887E CRC64;
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BY SIMILARITY.
ZINC (CATALYTIC) (BY
ZINC (CATALYTIC) (BY
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TSP TYPE-1
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46;
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P79987;
15-JUL-1998
                                                                                  DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and developmental expression analysis of chick Hira (Chira),
"cloning and developmental expression analysis of chick Hira (Chira),
a candidate gene for DiGeorge syndrome.";
Hum. Mol. Genet. 6:237-245(1997).
-i- FUNCTION: COULD PLAY A PART IN MECHANISMS OF TRANSCRIPTIONAL
-i- REGULATION SIMILAR TO THAT PLAYED BY YEAST HIR1 AND HIR2 TOGETHER
-i- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-i- SIMILARITY: CONTAINS 4 WD REPEATS (TRR-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97217783; PubMed=9063744; Roberts C., Daw S.C., Halford S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998
15-JUL-1999
                                                                                                                                                                                                                    PROSITE; PS00678; WD_REPEATS_1; 1.
PROSITE; PS50082; WD_REPEATS_2; 3.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                     Pfam; PF00400; WD40; 7. PRINTS; PR00320; GPROTEINBRPT.
                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                DOMAIN
                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                           SMART; SM00320; WD40;
                                                                                                                                                                                                                                                                                                          EMBL; X99375; CAA67754.1;
                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                         REPEAT
                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                 REPEAT
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                                                                                                                                                                                                                                                                                               InterPro; IPR001680;
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128
172
266
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407
                         Conservative
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(Rel. 36, Last sequence update)
(Rel. 38, Last annotation update)
(TUP1 LIKE ENHANCER OF SPLIT PROTEIN 1) (CHIRA).
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50.0%;
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Pred. No.
                                    Score 28;
Pred. No.
                                                                                                                                                           WD 1.
WD 2.
WD 3.
                                                                                     POLY-LYS.
W; 58CBC710A8FA7BF1 CRC64;
                                                                                                                                  NUCLEAR LOCALIZATION NUCLEAR LOCALIZATION
                                                                                                            POLY-SER.
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                          Mismatches
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68;
                                    DВ
83;
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RESULT 14
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Best Local
              Luebben M., Kolmerer B., Saraste M.;

"An archaebacterial terminal oxidase combines core structures of two mitochondrial respiratory complexes.";

EMBO J. 11:805-812(1992).

-I. FUNCTION: THE TERMINAL OXIDASE IS THE COMPONENT OF THE RESPIRATOR CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX.

-I. FUNCTION: SUBUNIT 2 TRANSFERS THE ELECTRONS FROM CALDARIELLA QUINOL TO THE BIMETALLIC CENTER OF THE CATALYTIC SUBUNIT 1 THAT I FORMED BY HEME A3 AND CU(B).
                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
QUINOL OXIDASE POLYPEPTIDE II (EC 1.9.3.-) (CYTOCHROME AA3 SUBUNIT (OXIDASE AA(3) SUBUNIT 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAT_CAMVP
P19818;
                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 33909 / NCIB 11770 / DSM
MEDLINE-92192013; PubMed=1372250;
                                                                                                                                                                                                                                                                                                                                                                                     QOX2_SULAC P39479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cauliflower mosaic virus (strain PV147) (CaMV). Viruses; Retroid viruses; Caulimovirus. NCBI_TaxID=10647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
APHID TRANSMISSION PROTEIN (PROTEIN 2).
   <del>.</del>
                                                                                                                                                                                                                                                         Sulfolobus acidocaldarius.
Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                      SULAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M37581; AAA96697.1; -. SEQUENCE 159 AA; 17843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cauliflower mosaic virus strains."; FEBS Lett. 181:223-228(1985).
                                                                                                                                                                                                                                                                                            SOXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modjtahedi N., Volovitch M., Mazzolini L., Yot P.; "Comparison of the predicted secondary structure of aphid
                                                                                                                                                                                                                                          NCBI_TaxID=2285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: THIS PROTEIN IS INVOLVED IN VIRUS TRANSMISSION -!- SIMILARITY: BELONGS TO THE CAULIMOVIRUSES ORF II FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmission factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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|| :| |
 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
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Pred. No.
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TRANSMEM
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                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                            Clostridium perfringens enterotoxin.";
J. Cell Biol. 136:1239-1247(1997).
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                         PRINTS; PR01077; CLAUDIN. PROSITE; PS01346; CLAUDIN
                                                                                                                   InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
                                                                                                                                                                                   use by non-profit institutions as long amodified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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CLDN4 OR CPETR1 OR CPER.
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 SEQUENCE
                                                                                                                                                               EMBL; D88492; BAA22781.1;
                                                                                                                                                                                                                                                                                                                                                                                   Katahira J., Inoue N., Horiguchi Y., Matsuda M., Su
"Molecular cloning and functional characterization
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97242441; PubMed=9087440;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae; Cercopithecus.
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                           junction; 10 mem 10 mem 82 mem 118
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se; Transmembrane; Respiratory chain;
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 AA;
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474DB3099F95289E CRC64;
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RESULT 18
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CLD4_HUMAN
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CLAUDIN-4 (CLOSTRIDIUM PERFRINGENS ENTEROTOXIN RECEPTOR) (CPE-RECEPTOR) (CPE-R).
CLDN4 OR CPETR1 OR CPER.
                                                                                                                                                                                                                    Pfam; PF00822; PMP22_Claudin; PRINTS; PR01077; CLAUDIN. PROSITE; PS01346; CLAUDIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Katahira J., Sugiyama Sugimoto N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Fetal brain;
MEDLINE=97476271; PubMed=9334247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo supiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro: IPR000729; PMP22_Cl
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Pred. No.
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
CLAUDIN-LIKE PROTEIN 2F-A9.
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035054;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CLAUDIN-4 (CLOSTRIDIUM PERFRINGENS ENTEROTOXII
RECEPTOR) (CPE-R).
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SEQUENCE
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                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00822; PMP22_Claudin; 1. PRINTS; PR01077; CLAUDIN. PROSITE; PS01346; CLAUDIN; 1.
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NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Zebra danio).
                                                                                       SEQUENCE FROM N.A. MEDLINE=97476271;
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                        "Ciostridium perfringens enterotoxin utilizes two structurally related membrane proteins as functional receptors in vivo.";
J. Biol. Chem. 272:26652-26658(1997).
                                                               Sugimoto N.;
                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                CLDN4 OR CPETR1 OR CPER.
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                                                                          Katahira J., Sugiyama
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yama H., Inoue N
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179 F
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C413143811853D58
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                                                                           Horiguchi Y., Matsuda
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Q920G9;

Q0-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

30-MAY-2000 (Rel. 39, Last annotation update)

CLAUDIN-3 (CLOSTRIDIUM PERFRINGENS ENTEROTOXIN RECEPTOR 2) (CPE-
           Morita K., Furuse M., Fujimoto K., Tsukita S.; "Claudin multigene family encoding four-transmembrane components of tight junction strands."; Page. Natl. Acad. Sci. U.S.A. 96:511-516(1999).

-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-99097345; PubMed=9878248;

MEDLINE-99097345, PubMed=9878248;

Paperna T., Peoples R., Wang Y.K., Kaplan P., Francke U.;

"Genes for the CPE receptor (CPETRI) and the human homolog of RVP1

(CPETR2) are localized within the Williams-Beuren syndrome deletion.";

Genomics 54:453-459(1998).
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TRANSMEM
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"Claudin multigene family encoding four-transmembrane domain protein components of tight junction strands.";
Proc. Natl. Acad. Sci. U.S.A. 96:511-516(199).
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-i- SURCELJULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SURCELJULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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CLDN3 OR CPETR2.
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PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
                                                                                                              MEDLINE=99110921; PubMed=9892664;
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BELONGS TO THE CLAUDIN FAMILY
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Pfam; PF00822; PMP22_Claudin; 1.
PRINTS; PR01077; CLAUDIN; 1.
PROSITE; PS01346; CLAUDIN; 1.
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Pred. No.
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POTENTIAL.
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sp_unclassified:*
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sp_virus:*
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10.366 Million cell updates/sec
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Q9a956 caulobacter
Q9a96 sugarcane y
Q9jh75 sugarcane y
Q9jh75 sugarcane y
Q9brr6 homo sapien
Q9kqb7 vibrio chol
Q9cp25 pasteurella
Q9ht72 pseudomonas
Q64761 arabidopsis
Q9f131 streptomyce
Q91de7 oryza sativ
Q9xe23 oryza sativ
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Q9rd18 streptomyce
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ALIGNMENTS

RESULT Q9A956 A CONTRACTOR OF THE CONTRACTOR Query Match Best Local S Matches 5 SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=21173608; PubMed=11259647; Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Pisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001). EMBL; AE005792; AAK23122.1; -. TIGR; CC1138; -. Q9A956; Q9A956; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) TONB-DEPENDENT RECEPTOR, PUTATIVE. Receptor; Complete proteome. SEQUENCE 613 AA; 64411 MW; NCBI_TaxID=69394; Caulobacter Bacteria; Proteobacteria; Caulobacter crescentus. Similarity 5; Conserv PRELIMINARY; 91.7%; 62.5%; alpha subdivision; Caulobacter group; Score 33; DB Pred. No. 27; PRT; ED65208A3D82B97D CRC64; Ą Length 613;

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Best Local
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Q9JH75;
01-OCT-2000
                      MEDLINE=20318675; PubMed=10859394;
Smith G.R., Borg Z., Lockhart B.E.L., Braithwaite K.S., Gibbs M.J
"Sugarcane yellow leaf virus: a novel member of the Luteoviridae
probably arose by inter-species recombination.";
J. Gen. Virol. 81:1865-1869(2000).
EMBL; AJ249447; CAB75437.1;
InterPro; IPR000893; Luteo_ORF6.
InterPro; IPR000893; Luteo_ORF5.
InterPro; IPR002929; PLRV_ORF5.
InterPro; IPR002929; PLRV_ORF5.
    PRINTS; PR00910; LVIRUSORF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE APHID TRANSMISSION FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polerovirus, Luteovirus, and Enamovirus properties.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF157029; AAD45687.1; -
InterPro; IPR000893; Luteo_ORF6.
InterPro; IPR002929; PLRV_ORF5.
InterPro; IPR002929; PLRV_ORF5.
InterPro; IPR002929; PLRV_ORF5.
Pfam; PF01690; PLRV_ORF5; 1.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=CV. CP65-357;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=CV. CP65-357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unassigned Luteoviridae.
NCBI_TaxID=94290;
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                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sugarcane yellow leaf virus.
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"Sugarcane yellow leaf virus
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01-MAY-2000
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Q9KGB7;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
ZINC ABC TRANSPORTER, PERMEASE PROTEIN.
                                                                    SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE O1;

MEDLINE-2040683; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam Dodson R.J., Nelson K.E., Read T.D., Tettelin H., Richardson Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., W Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BCC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9BRR6 PRELIMINARY; PRT; 497 AA.
Q9BRR6;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 2610017G09 GENE.
                     Nature 406:477-483(2000).
EMBL; AE004282; AAF95229.1;
                                                                  Salzberg S.L
Fraser C.M.;
                                                                                                                                                                                             Bacteria; Proteobacteria;
NCBI_TaxID=666;
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          EMBL; AE004282; TIGR; VC2083; -
                                                                                                                                                                                                                      Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-KIDNEY ADENOCARCINOMA;
                                             cholerae.";
                                                       "DNA sequence of both
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Mammalia; Eutheria;
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 InterPro;
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VCE 497 AA; 54088 MW;
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5; Conserv
IPR001626; ABC-3.
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                                                        chromosomes
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37;
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35;
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Sellers P.,
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Matches 5
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Best Local S
Matches 5
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01-MAR-2001
01-JUN-2001
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01-JUN-2001
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Complete proteome.
SEQUENCE 260 AA; 2:
MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21145866; PubMed-11248100; May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001). EMBL; AE006058; AAK02325.1; -. InterPro; IPR001626; ABC-3. 1. Pfam; PF00950; ABC-3; 1. Pfam; PF00950; ABC-3; 1. Pfam; PF00950; ABC-3; 1. Complete proteome.
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                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                            ZNUB OR PASSO1.
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(Tremblrel 16, Last sequence (Tremblrel 17, Last annotate ABC ZINC TRANSPORTER ZNU
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62.5%;
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Pred. No. 52;
0; Mismatches
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25309B50B38A7223 CRC64;
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: annotation
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SEQUENCE FROM IA.;

STRAIN=CV. COLUMBIA;

STRAIN=CV. COLUMBIA;

STRAIN=CV. COLUMBIA;

ROUNSley S.D., Lin X., Ketchum K.A., Crosw;

ROUNSley S.D., Lin X., Ketchum K.A., Crosw;

S.D., Kanl S., Mason T.M., Kerlavage A.R., Adams ...

Sykes S.M., Kanl S., Mason T.M., Kerlavage A.R., Adams ...

Sykes S.M., Kanl S., Wenter J.C.;

Somerville C.R., Venter J.C
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Nature 406:959-964 (2000).
EMBL; AE004962; AAG008886.1;
InterPro; IPR001626; ABC-3.
Pfam; PF00950; ABC-3; 1.
Complete proteome.
SEQUENCE 262 AA; 27343 MW;
                                                                                                                                                                                                                                                                                                                                                                         Q9RD13; PRELIMINARY; Q9RD13; Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 13, Q1-MAY-2000 (TrEMBLrel. 14, Q1-MAY-2000 (TrEMBLrel. 14, Q1-MAY-2000 (TrEMBLrel. 14, Q1-MAY-2000 (TrEMBLrel. 14, Q
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Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                 SEQUENCE FROM N.A. STRAIN=A3(2);
                                                                                                                                                                                                                                  Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Streptomycineae; Str
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
                                                           Submitted
                                                                                 Saunders D.
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SEQUENCE FROM N.A
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                                                           EMBL/GenBank/DDBJ
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Best Local
Q9XE23;
Q9XE23;
01-NOV-1,999
                                                                                                                                                                                                                                                                                                                                               Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chr
clone:P0469E09."
Submitted (MAR-2000) to the EMBL/GenRank/DDBJ
EMBL; AP002817; BAB03449.1; -
EMBL; AP001366; BAA92402.1; -
InterPro: IPR001878; Znf_CCHC.
SMART; SM00343; ZnF_CC2HC; 1.
SEQUENCE 938 AA; 108048 MW; B7689BD9E483C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza.
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"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).

EMBL; AL133422; CAB62689.1;
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"Oryza sativa nipponbare(GA3) genomic
clone:P0699D11.";
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EST_C28952(C62945) CORRESPONDS TO A REGION OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2000) to
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NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIPPONBARE;
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  (TrEMBLrel. 12,
                                                                                                                                                                                                                                            Conservative
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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62.5%;
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e EMBL/GenBank/DDBJ databases.
Created)
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                                                                                                                                                                                                                                                              Score
Pred.
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Pred. No.
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                                             955
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ches 3;
                                                                                                                                                                                                                                                              DB 10;
1.9e+02;
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                                             AA
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                                                                                                                                                                                                                                                                                  Length 938;
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RESULT
Q9LDA3
ID Q9I
AC Q9I
DT 01-
DT 01-
DT 01-
DT ES1-
OS Ory
OC Spe
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Q9FRA2
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Best Local
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Best Local
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Q9LDA3 PRELIMINARY; PRT; 1281 AA.
Q9LDA3;
Q1DA3;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
C1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
C28992(C62945) CORRESPONDS TO A REGION OF THE PREDICTED GENE.
C172a Sativa (Rice).
C172a Sativa (Rice).
C172a Sativa (Rice).
C172a Sativa (Rice).
C172a Sativa (Rice).
C172b Spermatophyta; Magnoliophyta; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9FRA2
Q9FRA2;
Q9FRA2;
Q9FRA2;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Q1-MAR-2001 (TrEMBLRel. 16, Last annotation update)
SIMILAR TO ORYZA SATIVA MUTATOR-LIKE TRANSPOSASE (AC068924).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; Liliopsida; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

NCBL_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                         Chow T. Y., Hsing Y.-I.C., Chen H.-H., Liu S.-M., Hsiao Y.-Y., Huang J.-J., Lu Shaw J.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 109.6 KDA PROTEIN.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta
                                                                                                                                                                                                                                                                                                                                              "Oryza sativa PAC P0001A07 genomics sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ d
EMBL; AC084218; AA648840.1; -
SEQUENCE 1011 AA; 113856 MW; EEE9AE49910C52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Oryza sativa Nipponbare(GA3) genomic DNA, chromosome 2. clone: p0437H03 (contig b)."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AP000367; BAA62378.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                      Local Similarity
les 5; Conserv
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                                                                                                                                                                                                         WRVHAYKG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 5; Conserv
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Pred.
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Pred. No.
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No.
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ches 3;
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a; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                   DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                         P.-F.,
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Su C.-L., Chen C.-S
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RESULT
Q9LDW9
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Best Local 9
                                                                                                           Query Match
Best Local
                                                                                         Matches
                                                                                                                                                                                             Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DN
clone:P0511C01.";
Submitted (WAY-2000) to the EMBL/GenBank
EMBL; AP002480; BAA96559.1; -.
EMBL; AP002070; BAA96559.1; -.
Interpro; IPR001878; Znf_CCHC.
SMART; SM00343; Znf_CCHC.
SMART; SM00343; Znf_CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:P0469E09.",
Submitted (MAR-2000) to the EMBL/GenBa
EMBL; AP002817; BA803445.1;
EMBL; AP00201366; BAA92398 1;
SEQUENCE 1281 AA; 148721 MW; D6BE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:P0699D11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9LDW9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN CV. NIPPONBARE; Sasaki T., Matsumoto T., Yamamoto K.; Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, clone:P0469E05.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EST C28952(C62945) CORRESPONDS TO A REGION OF THE PREDICTED GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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266
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                                       wrxxayxg
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  WRVHAYKG
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5; Conserv
                                                                                    Similarity
5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JUN-2000)
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                                                                                         Conservative
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62.5%;
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Pred. No. 2.7e
0; Mismatches
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2.7e+02;
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RESULT 15
Q9FW81
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AC Q9FW81
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DT 01-JUN
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OC ENARTA
OC EVARTA
OC EVARTA
OC EVARTA
OC EVARTA
OC SPERMA
OC EVARTA
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RN [1]
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RC STRALN
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Q9FW81;
Q1-MAR-2001
01-MAR-2001
01-JUN-2001
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MTPATOR-LIKE TRANSPOSASE.
Oryza sativa (Rice).
ELKaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
ELKaryota; Viridiplantae; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

See L.H., Spiegel L.A., Nascimento L.U., de la Bastide M., Preston R.R., Huange E.N., Rodriguez M.A., Vil M.D., Baker Bahret A., Shah R.S., Miller B., Kirchoff K.A., King L., TO'Shaughnessy A., Dedhia N.N., McCombie W.R.;

"Genomic Sequence For Oryza sativa, Nipponbare Strain, Chr Clone OSJMBa0094109, complete sequence.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. NIPPONBARE;
STRAIN-CV. NIPPONBARE;
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBA0026L12 genomic sequence.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC068924; AAG13514.1; -.
Interpro; IPR001878; Znf-CCHC.
SMART; SM00343; Znf-C2HC; 1.
SMART; SM00343; Znf-C2HC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
NCBI_TaxID=4530;
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Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9AYG3;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
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Bal H.P., See L.H., Spiegel L.A., Nascimento L.U., de la Preston R.R., Huange E.N., Rodriguez M.A., Vil M.D., Bak. Bahret A., Shah R.S., Miller B., Kirohoff K.A., King L., O'Shaughnessy A., Dedhia N.N., McComble W.R.;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. McCombie W.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUTATOR-LIKE TRANSPOSASE.
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                            Submitted
                                                                                                                                                                                       McCombie
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Last annotation updat
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Pred.
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No. 3.4e+02;
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a; Poales; Poaceae;
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J.L., Toth K.,
                                                      Baker
                                                      la Bastide M.,
Baker J.P.,
                                Toth
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RESULT Q9RDL8
ID Q9RDL8
AC Q9
AC Q9
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D7 0:
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DB H
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Q9DDQ2;
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MYPOTHETICAL 6.9 KDA PROTEIN.
Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacterida
Macteria; Streptomycineae; Streptomycetaceae;
                                                                                  Q9RDI8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation updat
HYPOTHETICAL 7.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=97000351; PubMed=8843436;
MEDIINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A.,
Kinashi H., Hopwood D.A.;
"A set of crdered cosmids and a detailed genetic and
"A set of crdered cosmids and a detailed genetic and
                                             Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
  Actinomycetales; NCBI_TaxID=1902;
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Seeger K.J., Harris I
Submitted (DEC-1999)
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EMBL; AL136519; CAB66278.1; -.
                                               Hypothetical SEQUENCE 65
                                                                                                                                                                        STRAIN=A3(2);
Thomson N.R.,
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Seeger K.J.,
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Bacteria; Firmicutes; Actinobacteria;
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EMBL; AL136519; CAB66277.1;
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RC STRAIN-EL TOR N16961 / SEROTYPE 01;

RX MEDLINE-20406833; PubMed-10952301;

RX MEDLINE-20406833; PubMed-10952301;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

RA Codson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Righardson D.,

RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

RA McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

RA McDonald L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

RT TORA sequence of both chromosomes of the cholera pathogen Vibrio

RT TORA (1972)

RI Nature 406:477-483(2000).

RL Nature 406:477-483(2000).

RE MBL; AE004302; AAF95464.1; -.

DR TIGR; VC2320; -.

DR TIGR; VC2320; -.

RT TORA (2000) (1970-helicase.)

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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EXODEOXYRIBONUCLEASE V, 135 KDA SUBUNIT.
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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Copyright (c) 1993 - 2000 Comp
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| and is derived by analysis of the total score distribution. | score greater than or equal to the score of the result being printed, | Pred. No. 19 the number of results predicted by chance |
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SUMMARIES

| Result | Score | % Query Match | % Query Match Length DB | в | ID | Description |
|--------|---------------|---------------------|-------------------------------|----|----------|--------------------|
| 1 | 32 | 88.9 | 496 | 22 | AAG81335 | Human AFP protein |
| N | 32 | 88.9 | 496 | 22 | AAB88466 | Human membrane or |
| w | 32 | 88.9 | 497 | 21 | AAB12138 | Hydrophobic domain |
| 4 | <u>د</u> 1 | 86.1 | 513 | 11 | AAR04585 | Aquaricine I. The |
| U | ω L | 86.1 | 513 | 12 | AAR13181 | T.aquaticus Aquari |
| 6 | 31 | 86.1 | 513 | 16 | AAR67653 | Aqualysin I. Ther |
| 7 | 31 | 86.1 | 934 | 19 | AAW82254 | JP10248575 Seq ID |
| 8 | 29 | 80.6 | 8 | 21 | AAB06521 | Claudin-2 cell adh |
| 9 | 29 | 80.6 | 8 | 21 | AAB06574 | Claudin-2 cyclic c |
| 10 | 29 | 80.6 | 10 | 21 | AAB06530 | Claudin-2 cyclic c |
| 11 | 29 | 80.6 | 10 | 21 | AAB06539 | Claudin-2 cyclic c |
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| AAW88629 AAB40533 AAB52100 | AAB06672 AAB06681 AAB06680 | AAB06654 AAB066663 | AAB06619 AAB06628 | AAB06601 AAB06610 | AAB06598 AAB06592 | AAB06645 | AABU6583 AABU6636 | AAG90433 | AAY76130 | AAY38430 | AAB44282 AAV68679 | AAW99653 | AAY04143 | AAY41726 | AAK 38421 | AAB06503 | AAB06497 | AAB06491 | AAB06485 | AAB06427 | AAB06512 | AAB06426 | AAB52467 | AAY51676 | AAB06566 | 0655 | AAB06548 |
| protein FX ORF297 | laudin-4 laudin-4 | 4 cyclic | | | ω.a | 4 cell ad | Claudin-3 cert adn Claudin-3 cyclic c | icum pi | secreted | uman secreted pr | Human PRO944 (UNQ4 A human molecule a | senesc | | PRO944 PI | Human secreted pro | 1 cyclic | 5 | 1 cyclic | 1 cyc | | 1 646 | Claudin-1 cell adh | terium tu | Murine clodin 2 pr | N | -2 cýclic | Claudin-2 cyclic c |

ALIGNMENTS

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                                                                                               Conklin
                                                                                                                                                                      (ZYMO ) ZYMOGENETICS INC.
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    WPI; 2001-300340/31
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This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAF98317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA
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11-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAH52186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 wrxxayxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                   therapy
                                                                                                                                                                                                                                                                                                                                          2001-093989/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wrgsayag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ated polypeptide for directing secretion of proteins of interest a host cell including, e.g. bacteria, includes contiguous amino residues of polypeptide with specified amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Page 337-338; 617pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secretory protein; membrane protein; vaccine; gene therapy;
toid arthritis; diabetes.
                                                                                                                                                                                                                                acids encoding secretory proteins/membrane erapy or as candidate target molecules in dr
                                                                                                                                                                                                                                                                                                                  AAF93893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                          Isogai T,
                                                                                                                                                                                      SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496
                                                                                                                                                                                      ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000JP-0118775
2000JP-0183766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0194179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA,
                                                                                                                                                                                   300;
                                                                                                                                                                                                                                                                                                                                                                                                                                            TRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secretory protein clone PSEC0260
                                                                                                                                                                                                                                                                                                                                                                                             Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 496
                                                                                                                                                                                 609pp + CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32;
Pred. No.
                                                                                                                                                                                   ROM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Kawai Y,
                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
55;
                                                                                                                                                                                                                                                                                                                                                                                       Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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••
                                                                                                                                                                                                                                   drug
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                                                                                                                                                                                                                                                              proteins,
                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                      development
                                                                                                                                                                                                                                                                                                                                                                                       Hayashi
                                                                                                                                                                                                                                        useful
roment -
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AAB12138
ID AAB1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and control disposis of diseases associated with inappropriate secretory control protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and cutivity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                  22-DEC-1998;
16-MAR-1999;
27-APR-1999;
                                                           N-PSDB; AAA62021,
                                                                                                         Kato
                                                                                                                                      (SAGA)
                                                                                                                                                                                       19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrophobic
                                                                                                                                                                                                                                               17-NOV-1998;
                                                                                                                                                                                                                                                                                17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                          WO200029448-A2
                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressant; haematopoiesis regulator; chemotactic; chemok
haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
autoimmune disease; Alzheimer's disease; Parkinson's disease; ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB12138 standard; Protein; 497 AA.
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB12138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arthritis
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les 5; Conserv
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                                                                        2000-387753/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wrgsayag 11
                                                                                                                                      SAGAMI CHE PROTEGENE
                                                                                                         Kimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     æ
                                                                                                                                                                                  98JP-0326255.
98JP-0364315.
99JP-0069811.
99JP-0119299.
99JP-0138169.
                                                                                                                                                      CHEM RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                99WO-JP06412
                                                                                                         T;
                                                           AAA62031.
                                                                                                                                        INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein isolated from HT-1080 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.9%;
62.5%;
                                                                                                                                                      CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                     chemokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic,

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AAR04585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is a human protein which has at least one hydrophobic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, hacmatopolesis activity, tissue growth activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity, anti-inflammatory activity and tumour inhibition activity. The present protein could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aquaricine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR04585 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hemơstatic,
                         Disclosure; ; p; Japanese
                                                    Gene to code precursor of Aquaricine I-and Colibacillus contg. vector, for proteolytic enzyme prodn. for detergent additive
                                                                                                 N-PSDB;
                                                                                                                                                                                                   30-JUL-1988;
                                                                                                                                                                                                                               03-APR-1990
                                                                                                                                                                                                                                                           JP02092288-A
                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aquaricine I; Colibacillus; detergents;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR04585;
                                                                                                                                          (NISB ) JAPAN TOBACCO AND SALT
                                                                                                                                                                      30-JUL-1988;
                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 wrgsayag 11
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                                                                                                                1990-144901/19
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5; Conserv
                                                                                                 AAQ04339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 286-288; 410pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       497 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                        88JP-0243981
                                                                                                                                                                                                   88JP-0243981
                                                                                                                                                                                                                                                                                                   /label⇔mature Aquaricine
409..513
                                                                                                                                                                                                                                                                                                                                                              /labelosignal peptide
23..127
                                                                                                                                                                                                                                                                                                                                 ∕label∺pro-Aquaricine I region
128..408
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                       /label⇔tail region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%;
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Pred. No.
                                                                                                                                           PUB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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                                                                   expression
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The Aquaricine I precursor is

expressed in a Collibacillus host.

The

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495 wriyaysg 502

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AAR13181
ID AAR:
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Š
                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mature protein is recovered following processing.
Aquaricine I is a heat resistant proteolytic enzyme, used eg as an additive in detergents and as a catalyst for peptide synthesis.
                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                 T.aquaticus Aquaricin 1.
                                                                                             The sequence encoding this protein was derived from T.aquaticus YT-1. Aquaricin 1 is secreted from T.thermophilus HB27 transformed
                                                                                                                                        Expression vector contains aquaricin I coding gene thermophilic gram negative bacteria
                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                        08-NOV-1989;
                                                                                                                                                                                                                                                                             JP03151880-A
                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                            Thermus aquaticus YT-1.
                                                                                                                                                                                                                                                                                                                                                                                                               thermophilic bacteria; Thermus thermophilus HB27; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR13181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR13181 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                Sequence
                                                                                   with a vector (pNK006) containing the
                                                                                                                        Disclosure; Fig 1; 10pp; Japanese.
                                                                                                                                                                                 WPI; 1991-234066/32
                                                                                                                                                                                                 (NISB ) JAPAN TOBACCO
                                                                                                                                                                                                                      08-NOV-1989;
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                                                                                                                                                                                                                                                                                                                                                                Peptide
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1 wrxxayxg 8
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                   Similarity 5; Conserv
                                                                                                                                                                       AAQ12838
                                                                 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                       89JP-0288813
                                                                                                                                                                                                                                         89JP-0288813
                                                                                                                                                                                                                                                                                                                                              /label= signal_peptide 23..127
                                                                                                                                                                                                                                                                                                                            128..408
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                /label= tail region
                                                                                                                                                                                                                                                                                                                 /label Aquaricin 1
                                                                                                                                                                                                                                                                                                                                    /label- pro_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.1%;
62.5%;
                            86.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB Pred. No. 92; 0; Mismatches
                    0;
                           Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĄΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
92;
                           DB 12;
92;
                                                                                    coding
                                                                                    sequence.
                                     Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                    Indels
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RESULT
AAR67653
ID AAR6
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XX AQUA
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                                                                                                                                                                             JP10248575-A.
                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                 JP10248575 Seq ID 4.
                                                                                                                                                                                                                                                                                                                              HMG-CoA; 3-hydroxy-3-methylglutaryl coenzyme A reductase; carotenoid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW82254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production of aqualysin I in yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ75858 is the yeast glucomylase (AAR67652) DNA, into which the aqualysin I (AAR67653) DNA (AAQ75859) minus its C-terminal prosequence can be inserted. Resulting in the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Pages 8-10; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant DNA having sequence deleted from the aqua-lysin I precursor gene - for expression of mature aqua-lysin I in yeast
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                                                                                                                                                                                                   Claim 46; Page 97; 121pp; English.
                                                                                                                                                                                                                                                                                     Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-365610/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Blaschuck OW, Symonds JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claudin-2 cell adhesion recognition sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel method for the preparation of carotenoids using genes and proteins isolated from Candida utilis. This sequence represents a protein which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-NOV-1998;
30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAR sequence; autoimmune disease; inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claudin-2 modulating agent; cell adhesion recognition sequence;
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N-PSDB; AAV73463.
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                                                                                                                                                                                                                  cyclic cell adhesion recognition sequence
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99US-0282029.
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Pred. No. 5
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                                                                                                                                                                                                                       SEQ ID NO: 128
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RESULT :
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Best Local Similarity
"hes 4; Conserv
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                               03-NOV-1998;
30<sup>1</sup>-MAR-1999;
                                                                                                                                                        graft
                                                                03-NOV-1999;
                                                                                                             WO200026360-A1
                                                                                                                                                                            Claudin-2 modulating agent; cell adhesion recognition sequence;
                                                                                                                                                                                                   Claudin-2
         (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                                                                                   Mammalia
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                                                                                                                                                                                                                                                                   AAB06548 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  conformation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the {\tt skin} -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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30-MAR-1999;
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                                                                                                                                                                                                                                                                                                                         wrtssyvg
                                                                                                                                                       equence; autoimmune disease; inflammatory disease; rejection; cyclic.
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                                                                                                                                                                                                 cyclic cell adhesion recognition sequence SEQ ID NO: 137
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99US-0282029.
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Best Local Similarity
Matches 4; Conserv
                                                                                       Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin -
                                                              Claim 49;
                                                                                                                                                                  Blaschuck
                                                                                                                                                                                                                     03-NOV-1998;
30-MAR-1999;
                                                                                                                                                                                                                                                         03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                          CAR sequence; autoimmune disease; inflammatory disease; graft rejection; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                            Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell adhesion modulators. The claudin-2 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and ald wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                                                                         WPI; 2000-365610/31.
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                                                                                                                                                                                                                                                                                                                                    Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                   Claudin-2 modulating agent; cell adhesion recognition sequence;
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                                                                                                                                                                                          (ADHE-) ADHEREX TECHNOLOGIES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 49; Page 98; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conformation.
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                                                           Page 98; 121pp; English.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the use of peptides as claudin-mediated
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situations, cell adhesion occurs at abnormal

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these peptides

The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-2 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claudin-2 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer;
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                                                                                                                                                                                                                                                     Claim 49; Page 98; 121pp; English.
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30-MAR-1999;
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                          Local Similarity
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99US-0282029.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-285512/25.
N-PSDB; AAZ89137.
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                                                                                                         Claim 39; Page 96; 121pp; English
                                                                                                                                                                                                  Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Symonds
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99US-0282029
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99US-0132503.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gour BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Pred. No. 2.1e+02;
0; Mismatches 4;
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The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-1 group of proteins are cadherins,

Query Match
Best Local Similarity
...+ches 4; Conserv

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Score 28; DB 21; Pred. No. 4.3e+05; 1; Mismatches 3

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Best Local :
                                                                                                           The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-1 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous systand across the skin -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 43; Page 97; 121pp; English.
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30-MAR-1999;
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                                                                                 conformation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO:
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nes 4; Conserv
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AA;
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Pred. No. 4.30
1; Mismatches
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                              Claudin-1 cyclic cell adhesion recognition sequence SEQ ID NO:
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30-MAR-1999;
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Copyright (c) 1993 - 2000 Compugen
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US-08-477-459-6
US-08-479-859-6
US-08-486-414-6
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US-07-876-280-4
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US-08-304-626-4
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US-08-316-301A-4
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| 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 24 | 25 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 |
| 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | • | • | • | • | 72.2 | ٠ | • | • | • | • |
| 748 | 748 | 748 | 748 | 748 | 748 | 748 | 748 | 376 | 376 | 376 | 376 | 164 | 164 | 432 | 1620 | 1620 | 1385 | 1385 | 1385 | 1385 | 1385 | 1385 |
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| US-08-948-547-10 | US-08-956-869-10 | US-08-956-652-10 | US-08-820-754-10 | US-08-852-091-10 | US-08-839-164-2 | US-08-369-796-10 | US-08-408-318-2 | US-09-192-983-2 | US-08-919-953-2 | US-08-922-182-2 | US-08-608-241-2 | US-09-352-619-1 | US-08-911-319A-1 | US-08-677-049-8 | US-09-100-089-2 | US-08-542-363-2 | 5426049-1 | 5281530-1 | PCT-US92-03624-2 | US-09-076-137-2 | US-09-173-891-2 | US-08-611-928-2 |
| Sequence 10, Appl | Sequence 10, Appl | Sequence 10, Appl | Sequence 10, Appl | Sequence 10, Appl | ~ | Sequence 10, Appl | | | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 8, Appli | Sequence 2, Appli | Sequence 2, Appli | Patent No. 5426049 | Patent No. 5281530 | Sequence 2, Appli | Sequence 2, Appli | ` | • |

ALIGNMENTS

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RESULT 1
US-08-484-575A-6
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                                                                                                                                             ; MOLECULE TYPE:
US-08-484-575A-6
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White Esq. John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0450
TELEFAX: (212)391-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                             Query Match
Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mark D. TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/484,575A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
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CITY: New York
STATE: New York
                                                             Local Similarity
nes 4; Conserv
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WRTEIYSG 12
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                                                                                                                                                             protein
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                                                                            75.0%;
                                                                           Score 27;
Pred. No.
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Version
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2e+02;
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US-08-477-459-6

Sequence 6, Application US/08477459
Patent No. 6001369

GENERAL INFORMATION:

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RESULT 3
US-08-479-869-6
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                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08479869 Patent No. 6123949 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 6:
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
PPERATING SYSTEM: PC-DOS/MS-DOS
            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         APPLICANT: Cochran TITLE OF INVENTION: TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                  CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 422 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
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30 Rockefeller Plaza
                                                                                                                                    USA
                                                                                                                                                                                                                                                                    COChran Ph.D, Mark D
NVENTION: Recombinant Fowlpox Virus S-FPV-043 and
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US/08/479,869
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RESULT
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                                                                                                                                                                               Sequence 6, Application PC/TUS9401826A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 422
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Best Local S
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CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES AND USES THEREOF
FILE REFERENCE: 42771D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 422523
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 08/024,15
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                APPLICANT: Syntro Corporation, et al. TITLE OF INVENTION: Recombinant Fowlp NUMBER OF SEQUENCES: 20
                                                                                                                CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
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                                           ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
                           COUNTRY:
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Local Similarity 50.0%;
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CLASSIFICATION:
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                                 USA
                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                Recombinant Fowlpox Virus S-FPV-043 and Uses
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50.0%;
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Pred. No.
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Pred. No. 2e+02;
0; Mismatches
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                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US94-02252A-6
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TELEX: 422523
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
A cid
                                                                                                                                      ATTORNEY/AGENT INFORMATION:

NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 umino acids
TYPE: amino acids
TYPE: amino acids
Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity 50.0%;
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01826A
FILING DATE: 28-FEB-1994
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02252A
FILING DATE: 28-FEB-1994
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NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEPAX: (212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Syntro Corporation, et al.
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 30 Rocke
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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75.0%;
ilarity 50.0%;
Conservative
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Score 27; DB 5;
Pred. No. 2e+02;
0; Mismatches
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                                    Length 422;
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US-07-675-772-4
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                                                    Sequence 4, Application US/07675772 Patent No. 5262399
                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
GENERAL INFORMATION:
APPLICANT: Hickle
APPLICANT: Sick,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                     ORGANISM: BACILLUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS17
IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC 1628) NRRL B-18652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/8: FILING DATE: 19920430 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: Sallwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Payne, Jewel M.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for
TITLE OF INVENTION: Controlling Acarides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1289 amino acids
TYPE: AMINO ACID
STRANDEDNESS: Single
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                              382 WRAAQYGG 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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2421 N.W. 41st Street, Suite A-1
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Hickle, Leslie A.
Sick, August J.
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50.0%;
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Pred. No. 5.6e+02;
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                                                                                                                                                                                                                                                                    Length 1289;
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US-08-063-170-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1289 amino acids
                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: BACLILUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS17
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 LIBL
CLONE: 17B
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPAX: 004-375-600
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             APPLICANT: Kim, Leo
APPLICANT: Schwab, George E.
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Response for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                          382 WRAAQYGG 389
                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity hes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID STRANDEDNESS: Sit TOPOLOGY: linear
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                               COUNTRY:
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                                                                 Gainesville
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                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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50.0%;
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Pred. No. 5.6e+02;
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                                                                                                                                                  and Methods for Inducing an Immune Protection Against Endoparasites as
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1289;
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08158232 Patent No. 5596071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
COUNTRY: USA
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/768,141
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,248
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Payne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: Y
NATT-SENSE: NO
                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                               APPLICANT: Fu, Jenny
APPLICANT: Fu, Jenny
TITLE OF INVENTION: No. 5596071el Bacillus thuringiensis Toxins Active
TITLE OF INVENTION: Against Hymenopteran Pests
NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compattble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                          NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: M/TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382 WRAAQYGG 389
                                                                                                            STREET: 2421
CTTY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bacillus thuringiensis STRAIN: PS17
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STRANDEDNESS: Sir
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                                                                                                                                           E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
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Foncerrada, Luis
Schnepf, H. Ernest
Schwab, George E.
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50.0%;
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Pred. No. 5.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1289;
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CURRENT APPLICATION DATA:

OPERATING SYSTEM:

SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25

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US-08-304-626-4
                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08304626 Patent No. 5616495
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1289 amino acids
                                                                                                                                             APPLICANT: Schnepf, APPLICANT: Schwab, GTITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPAY: 001-27-7-7-8100
                                                                                                                                                                                                                                                                                                         APPLICANT:
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FILING DATE: 22-MAY-1991
ATTORNEY/ACENT INFORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 25-NOV-1991 PRIOR APPLICATION DATA:
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                                                                                        NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 WRAAQYGG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/887,980 FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                   STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/158,232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
COUNTRY: USA
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: PS17b
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                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS17
                                                                                                                                           Uick, Heldi Jane
Foncorrada, Luis
Schnepf, Harry E.
Schnepf, Harry E.
Schwab, George E.
VENTION: No. 5616495el Bacillus thuringlensis Isolates
IVENTION: Active Against Hymenopteran Pests and Genes Encoding
VENTION: Hymenopteran-Active Toxins
                                                                                                                                                                                                                                                                                    Kennedy, M. Keith
Randall, John Brooks
                                                                                                                                                                                                                                                                       Meier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                           Payne, Jewel M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACILLUS THURINGIENSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                         Henry
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Pred. No. 5.6e+02;
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US-08-316-301A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Schnep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE: CLIONE: E. coli NM522(pMYC1628) NRRL B-18652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                      STREET: 2421
CITY: Gainesville
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
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              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                         TITLE OF INVENTION: NO. 5753492el Nematode-Active Toxins and Genes TITLE OF INVENTION: Which Code Therefor NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                            APPLICANT: Narva, Kenn
APPLICANT: Foncerrada,
                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1289 amin
TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 WRAAQYGG 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                       ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: PS17b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: BACILLUS THURINGIENSIS STRAIN: PS17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/304,626
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                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 wrxxayxg 8
                                                                                                                      32606
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                                                                                                                                                                                                                                                                                                        Schnepf, Harry E.
Schwab, George E.
Payne, Jewel M.
Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1289 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/07/887,980
US/08/316,301A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31,794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27; DB 1;
Pred. No. 5.6e+02;
                                                                                                                                                                                           A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

30-SEP-1994

PRIOR APPLICATION DATA:

CLASSIFICATION:

23-APR-1992

07/871,510

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В
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                                                                                                                                                                                                                                                  US-08-611-928-4
                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Payne, J
APPLICANT: Kennedy,
APPLICANT: Randall,
                                                                                                                                                                                                                  Sequence 4, Application US/08611928 Patent No. 5824792
                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 904-J. 1.
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1289 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MA20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNGANISM: BACILLUS THURINGIENSIS INDIVIDUAL ISOLATE: PS17
IMMEDIATE SOURCE:
            APPLICANT: Fu, Jenny
TMIL OF INVENTION: 40. 5824792el Bacillus thuringiensis Toxins Active
TITLE OF INVENTION: Against Hymenopteran Pests
NUMBER OF SEQUENCES: 51
                                                                                                                      APPLICANT:
CORRESPONDENCE ADDRESS:
                                                                            APPLICANT:
                                                                                          APPLICANT:
                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
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ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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APPLICATION NUMBER: 07/830,050
FILING DATE: 31-JAN-1992
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
07/565,544
                                                                                                                                                                                                                                                                                                              382 WRAAQYGG 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS: sir TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/0 FILING DATE: 12-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 10-AUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/69
FILING DATE: 03-MAY-1991
                                                                                                                                                                                                                                                                                                                                            1 wrxxayxg 8
                                                                       Foncerrada, Luis
Schnepf, H. Ernest
Schwab, George E.
                                                                                                                  Meier, Henry
Uick, Heidi Jane
                                                                                                                                                   Kennedy, M. Keith
Randall, John Brooks
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                     Payne, Jewel
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linear
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RESULT 14
US-09-173-891-4
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                                                                                             Sequence 4, Application US/09173891 Patent No. 6077937
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                   Best Local Similarity Matches 4; Conserv
                                                                                                                                                                                                                                                                                  Query Match
                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                 APPLICANT:
                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 22-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Saliwanchik, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                        382 WRAAQYGG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24 NO.
APPLICATION NUMBER: US 07
APPLICATION 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                  CLONE:
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 06-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: PS17b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                               PS17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1289 amino acids
                                                                                                                                                                                                                                                      Conservative
Kennedy, M. Keith
Randall, John Brooks
Meier, Henry
Uick, Heidi Jane
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                                                            Payne, Jewel
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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YES
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24-NOV-1993
UMBER: US 07/887,980
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50.0%;
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Pred. No. 5.6e+02;
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RESULT 15
US-09-076-137-4
; Sequence 4, Application US/09076137B
; Patent No. 6166195
; GENERAL INFORMATION:
                                                                                                                           В
                                                                                                                                                                                                                                                                                     ; CLONE: US-09-173-891-4
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/887,980
ETILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
ETILING DATE: 25-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sullwanchik, David R. REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M.*
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: No. 6077937el Bacillus thuringiensis Toxins Active TITLE OF INVENTION: Against Hymenopteran Pests NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE: COLI NM522(pMYC1628) NRRL B-18652
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                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
                                                                                                                           382 WRAAQYGG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: signopology: linear
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                                                                                                                                                                                               Local Similarity
hes 4; Conserv
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Schnepf, H. Ernest
Schwab, George E.
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50.0%;
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Pred. No. 5.6e+02;
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                                                                                                                                                                                                                                  Length 1289;
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; TYPE: PRT ; ORGANISM: Bacillus thuringlensis US-09-076-137-4
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PCT-US92-03624-4
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Best Local Similarity
When A; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 42 SOFTWARE: PatentIn Ver.
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                                                                             TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03624
FILING DATE: 19920501
CLASSIFICATION: 435
CLASSIFICATION: 435
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                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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 MOLECULE TYPE:
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                                                                                                                                                             REFERENCE/DOCKET NUMBER: MA
                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                               STRANDEDNESS:
                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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                 TOPOLOGY:
                                                             LENGTH:
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                                             AMINO ACID
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                                                                 1289 amino acids
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2421 N.W. 41st Street, Suite A-1
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Narva, Kenneth E.
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                 linear
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protein
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50.0%;
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Pred. No. 5.6e+02;
Nismatches 4;
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Best Local Similarity
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                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
APPLICATION TORNAL OF THE PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                      TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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IMMEDIATE SOURCE:
CLONP: "
                                                                                                                                     REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: No. 5596071el Bacillus thuringiensis Toxins Active TITLE OF INVENTION: Against Hymenopteran Pests NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                   SEQUENCE CHARACTERISTICS:
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CTTY: Gainesville
                                                                                      TELEPHONE: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                  STRANDEDNESS:
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                                 amino acid
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2421 N.W. 41st Street, Suite A-1
                                                 1220 amino acids
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Schwab, George E.
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Schnepf, H. Ernest
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Randall, John Brooks
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linear
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Pred. No. 5.6e+02;
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; IMMEDIATE SOURCE:
; LIBRARY: Lambdagem (TM) - 11 library of Luis
; LIBRARY: Foncerrada
; CLONE: 86Q3c
US-08-158-232-43
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US-08-611-928-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                             FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                               ATTORNEY/AGENT INFORMATION: NAME: Saliwanchik, David
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 32606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fu, Jenny
TITLE OF INVENTION: No. 5824792el Bacillus thu:
TITLE OF INVENTION: Against Hymenopteran Pests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                  CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 WRAGQYGG 389
                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 22-MAY-1991
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/611,928 FILING DATE: 06-MAR-1996 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bacillus thuringiensis INDIVIDUAL ISOLATE: 86Q3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 wrxxayxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                             32606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ε
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Foncerrada, Luis
Schnepf, H. Ernest
Schwab, George E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uick, Heidi Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kennedy, M. Keith
Randall, John Brooks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Payne, Jewel
                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 5824792el Bacillus thuringiensis Toxins Active
                                                                                                                                                                                                                                                                     US 08/158,232
                                                                                                  US 07/703,977
M/SCJ104.C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No. 8.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1220;
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TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100

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US-08-611-928-43
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US-09-173-891-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43, Application US/09173891 Patent No. 6077937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6077937
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.0 Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus thuringiensis INDIVIDUAL ISOLATE: 86Q3 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fu, Jenny
TITLE OF INVENTION: No. 6077937el Bacillus thuringiensis Toxins Active
TITLE OF INVENTION: Against Hymenopteran Pests
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US 07/887,980 FILING DATE: 22-MAY-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/797,645 FILING DATE: 25-NOV-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: pro
                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 WRAGQYGG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: Lambdagem (TM) - 11 library of Luis
LIBRARY: Foncerrada
CLONE: 8603c
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
                                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                 APPLICATION NUMBER: US/09/173,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meier, Henry
Uick, Heidi Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Foncerrada, Luis
Schnepf, H. Ernest
Schwab, George E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kennedy, M. Keith
Randall, John Brooks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Payne, Jewel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.28;
50.08;
                                                                                                                   08/158,232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26; I
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5e+02;
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INDIVIDUAL ISOLATE: 86Q3
IMMEDIATE SOURCE:
LIBRARY: Lambdagem (TM) - 11 library of Luis
LIBRARY: Foncerrada
CLONE: 86Q3c
US-09-173-891-43
 DЬ
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                                                                                                                     ; LENGTH: 1289
5281530-3
                                                                                                                                                                                                                                                                                                                                 Patent No. 5281530
APPLICANT: SICK,
                                                                                                                                                                                                                                                                                                                                                            RESULT 20
5281530-3
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                                                                                                                                                                                                                                                                                           CLONED FROM BACILLUS
                                                                                                                                                                                                                                                                                                                     JEWEL M.
                                                                                                                                                  SEQ ID NO:3:
                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                            APPLICATION NUMBER: US/07/557,246
FILING DATE: 24-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 535,810
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 84,653
FILING DATE: 12-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 22-MAY-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENES ENCODING NEMATODE-ACTIVE TOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                    382 WRAGQYGG 389
382 WRAGQYGG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1220 amin
TYPE: amino acid
STRANDEDNESS: si
                         1 wrxxayxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 wrxxayxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1220 amino acids
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                  AUGUST J.; SCHWAB, GEORGE E.; PAYNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                    72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26; DB
Pred. No. 8.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,;
                                                      0,
                                                                   Score 26; DB 6;
Pred. No. 8.9e+02;
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.5e+02;
                                                                                Length 1289;
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                                                      Indels
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Search completed: January 14, 2002, 07:23:44
Job time: 75 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 50 summaries
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                                                          Database :
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Maximum DB
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PIR_68:*
1: pir1:*
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3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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35
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Copyright (c) 1993 - 2000 Compugen Ltd
            pir1:*
pir2:*
pir3:*
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                                                                                                                                                                                                                                                                                                                                                                  Search time 63.57 Seconds (without alignments)
9.586 Million cell updates/sec
                                                                                                                                                                                                   219241
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | T50853 | N | 231 | 74.3 | 26 | 29 |
|--------------------|--------|------|--------|----------------|-------|---------------|
| hypothetical prote | G85506 | N | 198 | | 26 | 28 |
| ~ | E70971 | ພ | 154 | | 26 | 27 |
| hypothetical prote | E72594 | N | 141 | | 26 | 26 |
| | F82861 | N | 122 | | 26 | 25 |
| hypothetical prote | G70659 | ผ | 85 | 74.3 | 26 | 24 |
| | G83022 | ຎ | 866 | 77.1 | 27 | 23 |
| hypothetical prote | T16557 | N | 551 | 7. | 27 | 22 |
| O. | в83191 | N | 370 | | 27 | 21 |
| hypothetical prote | T34153 | N | 344 | 77.1 | 27 | 20 |
| П | T34972 | N | 330 | 77.1 | 27 | 19 |
| hypothetical prote | A84529 | N | 329 | 77.1 | 27 | 18 |
| 5 | A39484 | N | 280 | 77.1 | 27 | 17 |
| | н71119 | N | 278 | 77.1 | 27 | 16 |
| hypothetical prote | S72873 | N | 212 | 77.1 | 27 | 15 |
| gene 36 protein - | S41178 | N | 159 | 7. | 27 | 14 |
| exodeoxyribonuclea | в82091 | N | 1208 | 0 | 28 | 13 |
| hypothetical prote | G85933 | N | 1180 | 0 | 28 | 12 |
| exodeoxyribonuclea | NCECX5 | Н | 1180 | 0 | 28 | 11 |
| phosphoglycerate d | T45418 | N | 528 | 80.0 | 28 | 10 |
| probable serA prot | G70854 | N | 528 | 0 | 28 | 9 |
| | S22923 | N | 308 | 0 | 28 | 8 |
| n | H64449 | N | 70 | 0 | 28 | 7 |
| hypothetical prote | G84429 | N | 1715 | Ņ | 29 | 6 |
| transposase-like p | T00208 | N | 777 | .~ | 29 | Ų |
| probable tail comp | B85584 | N | 224 | | 29 | 4 |
| tail assembly prot | TJBPKL | _ | 199 | | 29 | w |
| regulator protein | S54293 | ผ | 1083 | 85.7 | 30 | ผ |
| probable 3-demethy | н75258 | N | 206 | | 31 | 1 |
| Description | ID | DB . | Length | Query Match | Score | Result No. |

| 50 | 49 | 48 | 47 | 46 | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | သ | 32 | 31 | 30 |
|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-----------------|--------------------|-------------------|--------------------|--------------------|
| 25 | 25 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 |
| 71.4 | 71.4 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 | 74.3 |
| 54 | 54 | 2347 | 2154 | 2082 | 937 | 888 | 604 | 483 | 458 | 409 | 404 | 392 | 379 | 371 | 362 | 346 | 261 | 261 | 259 | 239 |
| N | N | ب | N | N | ν | N | N | N | N | ب | Ν | N | N | N | N | N | N | N | N | N |
| G72040 | F86583 | TVHURS | A84669 | T37056 | S78561 | A71720 | S60182 | G84113 | T16123 | S32905 | G83322 | D70475 | D70786 | A71359 | JU0353 | A82971 | E85798 | C64948 | T48851 | 565825 |
| hypothetical prote | hypothetical prote | kinase-related pro | hypothetical prote | probable multi-don | CS3 pilin synthes | hypothetical prote | ATP-binding transp | hypothetical prote | hypothetical prote | serine proteinase | hypothetical prote | conserved hypothe | probable gcvT pro | conserved hypothe | hypothetical 39.7 | low specificity | hypothetical prote | probable membrane | response regulator | hypothetical prote |

ALIGNMENTS

```
C;Genetics:
A;Gene: DR2562
A;Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable 3-demethylubiquinone-9 3-methyltransferase - Deinococcus radiodurans (strain c;Species: Deinococcus radiodurans c;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000 C;Accession: H75258 R;White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-206 CHI)
A;Residues: 1-206 CHI)
               regulator protein p122-RhoGAP - rat
C; Species: Rattus norvegious (Norway rat)
C; Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 01-Sep-1995
C; Accession: S54293
R; Homma, Y.; Emori, Y.
EMBO J. 14, 286-291, 1995
A; Title: A dual functional signal mediator showing RhoGAP and phospholipase C-delta
A; Reference number: S54293; MUID:95137008
A; Accession: S54293
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-1083 < HOMP
A; Residues: 1-1083 < HOMP
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H75258
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S54293
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A; Cross-references:
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Best Local S
Matches 5
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nes 5; Conserv
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EMBL: D31962
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62.5%;
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0; Mismatches
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6.6;
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RESULT 3
TJBPKL
tail assembly |
                                                                                        A;Gene: Z0978
C;Superfamily:
                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-224 <STO>
A;Residues: 1-224 <STO>
A;Cross-references: GB:AE005174; NID:g12513746; PIDN:AAG55134.1; GSPDB:GN00145; UWGP:Z09
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                      A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: B85584
                                                                                                                                                                                                                                                                                           R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                C; Genetics:
                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
C;Accession: B85584
                                                                                                                                                                                                                                                                                                                                                                                        probable tail component of prophage CP-933K Z0978 [imported] - Escherichia coli
C; Species: Escherichia coli
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C; Superfamily: phage lambda tail assembly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: phage lambda
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983
C;Accession: H43009; G43013; A04355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the Nucleic Acid
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Best Local Similarity
5; Conserv
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A; Residues: 1-199 <SAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: H43009
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                    Query Match
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                                                                                          phage lambda tail assembly protein
   Conservative
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50.0%;
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62.5%;
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Score 29; DB
Pred. No. 21;
1; Mismatches
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Pred. No. 18;
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Pred. No.
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                                   Length 224;
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K.; A
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C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: H64449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein At2g01840 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: G84429
    R; Bult,
                                                      ribosomal protein L24E - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
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A: Map position: 2
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A; Residues: 1-1715 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
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A;Mobile element: Ac-type transposon Tfol
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A;Molecule type: DNA
A;Residues: 1-777 <OKU>
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C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C:Accession: T00208
R:Okuda, M.; Ikeda, K.; Namiki, F.; Nishi, K.; Tsuge, T.
Mol. Gen. Genet. 258, 599-607, 1998
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O.; Olsen, G.J.;
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50.0%;
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62.5%;
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1; Mismatches
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Zhou, L.; Fleischmann, R.D.; Sutton, G.G.;
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rson, J.D.; Sadow, P.W.; Han
Sclence 273, 1058-1073, 1996
probable serA protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 2
C:Accession: G70854
                                                                                                   RESULT
G70854
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Proc. R. Soc. Lond. B Biol. Sci. 243, 99-107, 1991
A;Title: Mitochondrial resolution of a deep branch in the A;Reference number: S22919; MUID:91288587
A;Accession: S22923
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C:Superfamily: Haloarcula ribosomal protein HL21
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                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                   F;146-168/Domain: transmembrane #status predicted <TM4>
F;189-307/Domain: plastoquinol--plastocyanin reductase 17K protein homology <17K>
F;189-307/Domain: transmembrane #status predicted <TM5>
F;197-213/Domain: transmembrane #status predicted <TM5>
F;256-272/Domain: transmembrane #status predicted <TM65
F;656-164/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted
F;150/Binding site: heme iron (His) (axial ligand) (low potential) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Genome: mitochondrion
A;Genome: molochondrion
A;Genotic code: SGC1
C;Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion;
F;1-307/Domain: cytochrome b homology (fragment) <CBH>
F;1-77/Domain: cytochrome b6 homology (fragment) <CB6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Andean flicker C; Species: mitochondrion Colaptes rupicola (Andean flicker) C; Datc: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 04-Mar-2000
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A; Residues: 1-70 <BUL>
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F;49-67/Domain: transmembrane #status predicted <TM2>
F;85-101/Domain: transmembrane #status predicted <TM3>
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A;Residues: 1-308 <EDW>
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hk Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Tille: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
A;Accession: G70854
A;Residues: 1-1180 <FIN>
A;Residues: 1-1180 <FIN>
A;Cross-references: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42682
A;Cross-references: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42682
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A;Cross-references: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42682
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A;Cross-references: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42682
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A;Cross-references: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42682
A;Cross-references: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42682
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A;Cross-references: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42682
A;Cross-references: GB:X04581; NID:g42680; PIDN:CAA28250.1; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g42680; PID:g4268
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A; Molecule type: DNA
A; Mesidues: 1-528 <PAR>
A; Cross-references: EMBL: Z99263; PIDN: CAB16440.
A; Cross-references: cosmid B637
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                                                                                                                                                                                                                                                                                                    R:Finch, P.W.: Storey, A.: Chapman, K.E.;
Nucleic Acids Res. 14, 8573-8582, 1986
A:Title: Complete nucleotide sequence of a:Reference number: A25532; MUID:87066729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Escherichia coli
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 19-Jan-2001
C;Accession: A25532; E65064
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C; Superfamily:
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A;Experimental source: strain H37Rv
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A;Title: DNA Sequence of both chromosomes A;Reference number: A82035; MUID:20406833 A;Accession: B82091 A;Status: preliminary
                                                                                           C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Date: 18-Discreption: B2091 C;Accession: B2091 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; I chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene:
C;Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
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C;Superfamily: exodeoxyribonuclease V 135K chain
C;Keywords: ATP; DNA repair; hydrolase; nucleotide binding; P-loop
F;23-30/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1180 <BLAT>
A;Residues: 1-1180 <BLAT>
A;Residues: 1-1180 <BLAT>
A;Cross-references: GB:AE000365; GB:U00096; NID:g2367163; PIDN:AAC75859.1; PID:g1789183;
A;Experimental source: strain K-12, substrain MG1655
C;Comment: This enzyme is required for efficient DNA repair; it catalyzes the unwinding 1 of these activities require concomitant hydrolysis of ATP.
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A;Status: Profile genome sequence of Escherichia coli K-12.
A;Status: Profile genome sequence of Escherichia coli K-12.
A;Status: Profile genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                             exodeoxyribonuclease V, 135 kDa chain VC2320 [imported] - Vibrio cholerae (strain
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R; Perna, N.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein recB [imported] - Escherichia coli (strain 0157:H7) C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001) Accession: G85933
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A; Residues: 1-1180 <STO>
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A; Accession: G85933
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Best Local S
Matches 4
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50.0%;
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1; Mismatches
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Pred. No.
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1.7e+02;
3;
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1.7e+02;
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I.; Sellers,
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C; Genetics:
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hypothetical protein B2126_F2_70 - Mycobacterium leprae C;Species: Mycobacterium Leprae C;Species: Mycobacterium Leprae C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001 C;Accession: S72873
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C;Species: phage SPP1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 11-May-2000
C;Accession: $43804; T42337; $41178
R;Pedre, X.; Weise, F.; Chai, S.; Lueder, G.; Alonso, J.C.
J. Mol. Biol. 236, 1324-1340, 1994
A;Title: Analysis of cis and trans acting elements required for the initiati A;Reference number: $43798; MUID:94172631
A;Accession: $43804
                                                                                      A; Description: Mycobacterium A; Reference number: $72585 A; Accession: $72873
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S72873
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C;Superfamily: single-stranded DNA-binding protein;
F;17-93/Domain: single-stranded DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X67865; NID:g472886; PIDN:CAA48055.1; PID:g439635 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A. Gene 204, 201-212, 1997
                                                                                                                                                                                    R; Smith, D.R.; Robison,
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A; Accession: T42337
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A;Residues: 1-1208 <HEI>
A;Cross-references: GB:AE004303; GB:AE003852; NID:g9656890; PIDN:AAF95464.1; GSPDB:GN
A;Experimental source: serogroup O1; strain NI6961; biotype El Tor
C:Genetics:
A;Cross-references: EMBL:U00017; NID:g466994; PIDN:AAA17213.1;
                   A; Molecule type: DNA
A; Residues: 1-212 <SMI>
                                                                A; Status: preliminary
                                                                                                                                                              submitted to the EMBL Data Library,
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A; Residues: 1-159 <ALO>
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A; Residues: 1-159 < PE2>
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C;Superfamily: exodeoxyribonuclease
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Pred. No. 1.8e
1; Mismatches
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Pred. No. 42;
                                                                                                                                    November 1993 cosmid B2126.
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1.8e+02;
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PID: 9467028
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A; Title: Isolation and characterization of transcripts A; Reference number: A39484; MUID:92130987 A; Accession: A39484 A; Molecule ****
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A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137
A;Accession: H71119
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H71119
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RESULT
A84529
                                                                                                                                                                                        C:Genetics:
A:Gene: RVP.1
A:Superfamily: rat androgen-withdrawal apoptosis protein RVP1
                                                                                                                                                                                                                                                                                                                                                                                      androgen-withdrawal apoptosis protein RVP1, prostatic -C;Speciles: Rattus norvegicus (Norway rat) C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text C;Accession: A39484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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A; Gene: PH0727
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A;Residues: 1-278 <KAM>
A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29818.1; PID:d1030761; PID:g3257
A;Experimental source: strain OT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999 C;Accession: H71119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein PH0727 Pyrococcus horikoshii
C; Species: Pyrococcus horikoshii
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                                                                В
                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-280 <BRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                          A;Cross-references: GB:M74067; NID:g205857; PIDN:AAA41760.1; PID:g205858
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Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487

A;Accession: A84529
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M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein At2g15440 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-330 <SAU>
A; Cross references: EMBL: AL109663; PIDN: CAB52011.1;
A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T34972
R;Saunders, D.C.; Harris, D.; James
submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
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A; Map position: 2
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A; Residues: 1-329 <STO>
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                                                                                                                                  submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid A; Reference number: 221482
                                                                                                                                                                                                  C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T34153 R;Bradshaw, H.; Stellyes, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: 221563
A; Accession: T34972
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                                            A; Molecule type: DNA
A; Residues: 1-344 <BRA>
                                                                                                           A; Reference number: A; Accession: T34153
                                                                                                                                                                                                                                                                 hypothetical protein C33H5.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
A;Cross-references: EMBL:U41007; PIDN:AAA82262.1; CESP:C33H5.1
A;Experimental source: strain Bristol N2
                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBC
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Aidnicos: 59/3; 133/3; 171/1; 293/3

Cuery Match
Best Local Similarity 50.0%; Fred. No. 99;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 wrxsis 9

Db 125 WRRWFWG 112

Search completed: January 14, 2002, 07:37:32

Job time: 902 sec
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Minimum
Maximum
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R24E_METJA
CLD2_MOUSE
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| P24467 agrobacteri | P29954 rhizobium m | Q52977 rhizobium m | 074540 schizosacch | 074685 pichia past | P81600 gadus morhu | P56412 macaca neme | 097663 macaca mula | P49685 homo sapien | 018982 cercopithec | P75328 mycoplasma | P47562 mycoplasma | P57739 homo sapien | P98087 rattus norv | Q45689 brucella su | Q45326 brucella ne | Q45321 brucella me |

ALIGNMENTS

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RESULT
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15-JUL-1999 (Rel. 38, Last senence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SELENIDE, WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE (SELENIUM DONOR PROTEIN 2).
                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 93:15086-15091(1996).
-i- FUNCTION: SYNTHESIZES SELENOPHOSPHATE FROM SELENIDE AND ATP.
-I- CATALYTIC ACTIVITY: ATP + SELENIDE + H(2)0 = AMP + SELENOPHO
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97140286; PubMed=8986768; Guimaraes M.J., Peterson D., Vicari A., Co Gilbert D.J., Jenkins N.A., Ferrick D.A., Zlotnik A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHIMER PROM N.A.
SEQUENCE FROM N.A.
MEDLINE-96017645; PubMed-7588067;
GHIMERAES M.J., Bazan J.F., Zlotnik A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPS2_MOUSE
P97364;
                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                 ENCODED BY THE OPAL CODON, UGA.
-!- SIMILARITY: BELONGS TO THE SELENOPHOSPHATE SYNTHETASE 1 FAMILY.
CLASS I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A new approach to the study of haematopoietic development in yolk sac and embryoid bodies."; Development 121:3335-3346(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guimaraes M.J., Baza
Lee F., McClanahan T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
              EMBL; U43285; AAC53024.1; MGD; MGI:108388; Sps2.
                                                                                                                                                                                                                                     -!- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE ENCODED BY THE OPAL CODON, UGA.
                                                                                                                                                                                                                                                                                                                                                       and archaea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                metabolism?";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                       from eukaryotes, bacteria, mechanism in selenocysteir
                                                                                                                                                                                                                                                                                                                                                                                                       Cocks B.G., Copeland N.G., ., Kastelein R., Bazan J.F.,
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for
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IPR000728;

AIRS_related

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RESULT 3
R24E_METJA
ID R24E_M
AC P54064
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VTAK_LAMBD
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R24E_METJA
P54064; •
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of bacteriophage lambda DNA.";

"Nucleotide sequence of bacteriophage lambda DNA.";

J. Mol. Biol. 162:729-773(1982).

-i- FUNCTION: GENE K PROTEIN IS INVOLVED IN THE ASSEMBLY OF THE INITIATOR COMPLEX FOR TAIL POLYMERIZATION. IT HAS NOT BEEN I
                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viru
Lambda phage group.
NCBI_TaxID=10710;
                                                                                                                                                                    SEQUENCE
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01-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=83189071; PubMed=6221115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage lambda.
Viruses, dsDNA viruses,
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P03729;
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AA; 23011 MW;
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Best Local Similarity
Matches 5; Conserv
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi.";
                                                                                                                                                                                                                                 30-MAY-2000
30-MAY-2000
30-MAY-2000
               Furuse M., Fujita K., Hiiragi T., Fujimoto K., "Claudin-1 and -2: novel integral membrane prottight junctions with no sequence similarity to J. Cell Biol. 141:1539-1550(1998).
                                                                                SEQUENCE FROM N.A. MEDLINE=98311639;
                                                                                                                              Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  CLAUDIN-2
                                                                                                                                                                                                                                                                                 088552;
                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosomal protein; SEQUENCE 70 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
20-AUG-2001 (Rel. 40,
50S RIBOSOMAL PROTEIN
 -!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS
                                                                                                                                                                                                                                                                                                  CLD2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01246; Ribosomal_L24e; 1.
PROSITE; PS01073; RIBOSOMAL_L24E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67562; AAB99205.1; -. TIGR; MJ1201; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 273:1058-1073(1996).
-I- SIMILARITY: BELONGS TO THE L24E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                    4
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(Rel.
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                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                  PubMed=9647647;
                                                                                                                                                                                                                              39, Created)39, Last sequence up39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
8249 MW; 3EB6DE18F26E6FCF CRC64;
                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28; D
Pred. No. 8;
                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                  230 AA.
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                                                 proteins
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                                                                    Tsukita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Crea
01-APR-1993 (Rel. 25, Last)
30-MAY-2000 (Rel. 39, Last)
CYTOCHROME B (FRACMENT).
MTCYB OR COB OR CYTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF072128; AAC27079.1; -. MGD; MGI:1276110; Cldn2. InterPro; IPR001832; Claudin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an cmail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pfam; pF00822; pMp22_Claudin;
pRINTS; pR01077; CLAUDIN;
PROSITE; pS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-91288587; PubMed-1676522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Piciformes; Picidae; Colaptes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colaptes rupicola (Andean flicker).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYB_COLRU
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Employment of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edwards S.V., Arctander P., Wilson A.C.; "Mitochondrial resolution of a deep bran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for perching birds.";
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                                                                                                                                                                                                        COUPLED TO ATP SYNTHESIS.

COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.

SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.

SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                     C. R. SOC. LOND., B, Biol. Sci. 243:99-107(1991).
FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHEME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an email to license@isb-sib.ch).
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117
163
230
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25, Last sequ
39, Last anno
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102 P
137 P
183 P
24483 MW;
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50.0%;
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EMBL;

Z99263; CAB16440.1; -. AL583923; CAC30645.1;

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RESULT 6
SERA_MYCLE
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Matches
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NON_TER
SEQUENCE
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                                                                                                                                                                        "MASSIVE gene decay in the leprosy bacillus.";

Nature 409:1007-1011(2001).

- CATALYTIC ACTIVITY: 3-PHOSPHOGLYCERATE + NAD(+) =

3-PHOSPHOHYDROXYPYRUVATE + NADH.

- PATHWAY: FIRST COMMITTED STEP IN THE "PHOSPHORYLATED" PATHWAY

OF L-SERINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                      MEDLINE-21/2002;
MEDLINE-21/2002;
MEDLINE-21/2004
MEDLINE-21/2007
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Ouail M.A., Rajandream M.-A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.
SERA OR ML1692 OR MLCB637.25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000179; Cyt_b_b6.
Pfam; PF00032; cytochrome_b_C;
Pfam; PF00033; cytochrome_b_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR;
                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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                                                                                                                                                                                                                                                              Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-TN;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium leprae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1769;
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                                                                                                                                                 SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; x60949; CAA43284.1;
$22923; $22923.
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5; Conserv
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R InterPro; IPR002162; D.2_hydroxyacid_DH.

R InterPro; IPR002162; D.2_hydroxyacid_DH.

R Pfam; PF00389; 2-Hacid_DH; 1.

R Pfam; PF001842; ACT; 1.

R PROSITE; PS0065; D.2_HYDROXYACID_DH_1; 1.

R PROSITE; PS00671; D.2_HYDROXYACID_DH_3; 1.

R PROSITE; PS00671; D.2_HYDROXYACID_DH_3; 1.

R PROSITE; PS00671; D.2_HYDROXYACID_DH_3; 1.

R ACT_SITE; PS00671; D.2_HYDROXYACID_DH_3; 1.

R ACT_SITE 232 SUBSTRATE-BINDING (BY SIM SCT_SITE 232 SUBSTRATE-BINDING (BY SIM ACT_SITE 261 261 BY SIMILARITY.

PROSITE; PS00671; D.2_HYDROXYACID_DH_3; 1.

R SEQUENCE 528 AA; 54469 MW; 1A6DC60F9FB71222 CRC64.
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Nature 393:537-544(1998).
                                                  "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-i-CATALYTIC ACTIVITY: 3-PHOSPHOGLYCERATE + NAD(+) = 3-PHOSPHOHYDROXYPYRUVATE + NADH.
-i-PATHWAY: FIRST COMMITTED STEP IN THE "PHOSPHORYLATED" PATHWAY OF L-SERINE BIOSYNTHESIS.
-i-SIMILARITY: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PGDH).
SERA OR RV2996C OR MT3074 OR MTV012.10.
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NCBI_TaxID=1773;
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   Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
"The complete genome sequence of Escheric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-87066729; PubMed=3537960; MEDLINE-87066729; A., Chapman K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P08394;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
EXODEOXYRIBONUCLEASE V BETA CHAIN (EC 3.1.1
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                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                           Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado Vides J., Glasner J.D., R
                                                                                                                                                                                                                                                                                                                                  RecBCD enzyme."
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                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20229837; PubMed=10766864; Arnold D.A., Kowalczykowski S.C.;
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yhew G.F.
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PIR; A25532; NCECX5.
HSSP; P56255; 1PJR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finch P.W., Storey A., Brown K., Hickson I.D., Emmerson P.T.;

"Complete nucleotide sequence of recb, the structural gene for the alpha subunit of Exonuclease V of Escherichia coll.";

Nucleic Acids Res. 14:8583-8594(1986).

1- FUNCTION: REQUIRED FOR EFFICIENT DNA REPAIR: IT CATALYZES THE UNWINDING OF DOUBLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE-STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION.

ALL OF THESE ACTIVITY: EXONUCLEOLYTIC CLEAVAGE (IN THE PRESENCE OF ATP. 1-1-CATALYTIC ACTIVITY: EXONUCLEOLYTIC CLEAVAGE (IN THE PRESENCE OF ATP) IN EITHER 5'. TO 3'-OR 3'-TO 5'-DIRECTION TO YIELD 5'-
                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
CLAUDIN-4 (CLOSTRIDIUM PERFRINGENS ENTEROTOXIN RECEPTOR) (CPE-
RECEPTOR) (CPE-R).
CLDN4 OR CPETR1 OR CPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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[4]
Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalla; Butherila; Primales; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EcoGene; EG10824; recB.
InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE::87066730; PubMed::3537961;
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SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD SIMILARITY: BELONGS TO THE UVRD SUBFAMILY OF HELICASES.
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RESULT 10
CLD4_HUMAN
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Best Local
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-!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-97242441; PubMed-9087440;
                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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InterPro; IPR000729; PMP22_Claudin.
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[1]
 between the
the European
                                               -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PR
-!- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                       Sugimoto N.;
                                                                                                                                 Katahira J., Sugiyama
                                                                                                                                                                        SEQUENCE FROM N.A
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8MEM 82

8MEM 118

8MEM 118
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RESULT 11
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TRANSMEM 8 28 POT
TRANSMEM 102 POT
TRANSMEM 118 138 POT
TRANSMEM 161 181 POT
SEQUENCE 209 AA; 22077 MW; (
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
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CLAUDIN-LIKE PROTEIN ZF-A9.
  TRANSMEM SEQUENCE
                                           TRANSMEM TRANSMEM
                                                                 PRINTS; PRO1077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
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                                                                                                                                                                                                                                                                                             Keen T.J., Inglehearn C.F.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
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InterPro; IPRO01729; pMp22_Claudin.
Pfam; pF00822; pmp22_Claudin; 1.
PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
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InterPro; IPR000729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygii; Neopterygii; Teleostei; Eutel
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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MIM; 602909;
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Euteleostei; Ostariophysi;
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Query Match

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CLD4_MOUSE
ID CLD4_MOUSE
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                                                                                              Query Match
Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB000713; BAA22985.1; -.
EMBL; AF087822; AAD09757.1; -.
MGD; MGI:1313314; Cldn4.
InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claud
Pfam; PF00822; PMP22_Claudin; 1.
                                                                                                                                                                                                                    TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MORITA K., Furuse M., Fujimoto K., Tsukita S.;

"Claudin multigene family encoding four-transmembrane
"Claudin multigene family encoding four-transmembrane
components of tight junction strands";

Proc. Natl. Acad. Sci. U.S.A. 96:511-516(1999).

-!- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANI
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SUBCELLULAR LOCATION: THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97476271; PubMed=9334247;
MEDLINE=97476271; PubMed=9334247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foe entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99110921; PubMed=9892664;
Morita K., Furuse M., Fujimoto K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             035054;

30-MAY 2000 (Rel. 39, Created)

30-MAY 2000 (Rel. 39, Last sequence update)

30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1077; CLAUDIN. PROSITE; PS01346; CLAUDIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Clostridium perfringens enterotoxin utilizes two structurally related membrane proteins as functional receptors in vivo."; J. Biol. Chem. 272:26652-26658(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugimoto N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLDN4 OR CPETR1 OR CPER.
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                                                                                                                                                                                                                                                                                                                                                 right
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30
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WRVTAFIG
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161
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37
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102
137
181
22338 .
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                                                                                                                   77.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%;
                                                                                                                                                                                                                         WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             _Claudin.
                                                                                              Score 27; DB Pred. No. 36; 1; Mismatches
                                                                                                                                                                                                                                                                    POTENTIAL.
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1; Mismatches
                                                                                                                                                                                                                 POTENTIAL.
3B6D571EC71D6564 CRC64;
                                                                                                                                                                                                                                                                                                                       POTENTIAL
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••
                                                                                                                                            Length 210;
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CLD1_HUMAN
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                                          Query Match
Best Local 9
                                                                                                  Tight junction:
TRANSMEM 8
TRANSMEM 116
TRANSMEM 116
TRANSMEM 164
CONFLICT 135
SEQUENCE 211 A
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cutities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with somatic cell hybrids.";
Cytogenet. Cell Genet. 88:217-217(2000).
-I- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE: 20290992; Pubmed=10828592;
Halford S., Spencer P., Greenwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitic L.M., Anderson J.M.;
"Human claudin-1 isolated from Caco-2 mRNA.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epithelial cells, is a member of an epithelial membrane superfamily."; Gene 226:285-295(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-99132301; PubMed-9931503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CLAUDIN-1 (SENESCENCE-ASSOCIATED EPITHELIAL MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          095832;
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                                                                                                                                                                                                                  InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
                                                                                                                                                                                                                                                                                                        EMBL; AF101051; AAD16433.1; -. EMBL; AF115546; AAD22962.1; -. EMBL; AF134160; AAF61393.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Swisshelm K.L., Machl A., Planitzer S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLDN1 OR CLD1 OR SEMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adamson P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - I - SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Assignment(1) of claudin-1 (CLDN1) to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a senescence-associated cDNA isolated from human mammary
                                                                                                                                               82
116
164
                               Conservative
                                                                                                     AA;
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                                                                                                                                                                                                        Transmembrane
                                                                                                                                 28
102
136
184
62
                                                                                                  135 V
22744 MW;
                                          77.1%;
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                            1;
                                          Score 27; DB 1; Length 211, Pred. No. 37;
                                                                                                    I -> V (IN REF. 2).
V -> A (IN REF. 2).
; 07269000E6C214F0
                                                                                                                                               POTENTIAL.
                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                           POTENTIAL.
                               Mismatches
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                                                                                                       CRC64;
                               Indels
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                              0;
                              Gaps
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CLD3_RAT
ID CLD3
AC Q634
DT 30-M
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                                                   RESULT
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                                                                                                                                    Matches
                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLD3_MOUSE STANDARD; PRT; 219 AA. 092069; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) CLAUDIN-3 (CLOSTRIDIUM PERFRINGENS ENTEROTOXIN RECEPTOR 2) (CPE-
CLD3_RAT STANDARD;
Q63400;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paperna T., Peoples R., Wang Y.K., Kaplan P., Francke U.; "Genes for the CPE receptor (CPETR1) and the human homolog (CPETR2) are localized within the Williams-Beuren syndrome Genomics 54:453-459(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                           Tight junction;
                                                                                                                                                                                                                                                        PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
                                                                                                                                                                                                                                                                                                                                        EMBL; AF095905; AAD14608.1; -. EMBL; AF087821; AAD09756.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR 2) (CPE-R 2).
CLDN3 OR CPETR2.
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                     InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claudin.
                                                                                                                                                                                                                                                                                                                              MGD; MGI:1329044; Cldn3
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                                                                                                                                   Similarity 50.(
4; Conservative
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116
160
219 /
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                                                                                                                                                                                               AA;
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                                                                                                                                                                                                                     136
                                                                                                                                                                                              23284 MW;
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                                                                                                                                                77.1%;
50.0%;
                                                                                                                                   ; Score 27; Pred. No. 1; Mismatc
                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                             62F67810D9B9BD37 CRC64;
                                                                                                                                      Mismatches
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four-transmembrane domain protein
                            219
                                                                                                                                            DB 38;
                                                                                                                                                            ۲.
                                                                                                                                                          Length 219;
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CLD3.
ID
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Best Local
                                     CLD3_HUMAN STANDARD; PRT; 220 AA.

O15551;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CLAUDIN-3 (CLOSTRIDIUM PERFRINGENS ENTEROTOXIN RECEPTOR 2)
RECEPTOR 2) (CEE-R 2) (VENTRAL PROSTATE.1 PROTEIN HOMOLOG)
CLDN3 OR CPETR2.
                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keen T.J., Inglehearn C.F.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
-I- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-I- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00822; PMP22_Claudin; PRINTS; PR01077; CLAUDIN. PROSITE; PS01346; CLAUDIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (Some or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
            Eukaryota; Metazoa;
                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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InterPro; IPR000729; PMP22_Claudin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                           Similarity
Eutheria; Primates;
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            Chordata;
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50.0%;
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; 820CC6BFC20D122D CRC64;
                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.

G -> S (IN REF. 1).

MISSING (IN REF. 1).

DYV -> TISERPGARTPHHHHYQPSMYPTRPACSLASETT

PPSRRLQTPRSLLARLEEDRQPGVPFSPVAT (IN REF.
            Craniata;
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
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            Vertebrata;
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Hominidae; Homo
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            Euteleostomi;
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CLDH_HUMAN
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SEQUENCE
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                                                                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa; (
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J. Biol. Chem. 272:36652-26658(1997).
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ)
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PRO-
-i- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
SEQUENCE FROM N.A. MEDLINE=20289799; PubMed=10830953;
                                                                   Keen T.J., Inglehearn C. Submitted (NOV-1999) to
                                                                                                                                                                                                                                                                   CLDN17
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                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                           Mammalia; Eutheria;
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Pro; IPR000729; PMP22_Claudin
PF00822; PMP22_Claudin; 1.
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yama H., Inoue N., Horiguchi Y.,
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                                                                                                                                                                                             Primates;
                                                                                                                                                                                                                 Chordata;
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RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
Rammeer J., Beck A., Klages S., Hennig S., Riesschmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
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RA Wehrmeyer S., Borzym G., Gardiner K., Mizetic D., Francis E.,
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Best Local
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"A new approach to the study of yolk sac and embryoid bodies.";
Development 121:3335-3346(1995).
                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SELENIDE WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE
(SELENIUM DONOR PROTEIN 2).
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SEQUENCE
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                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=96017645; PubMed: 7588067;
Guimaraes M.J., Bazan J.F., Zlotnik A.,
                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9606;
                                                                                                                                                                                                                     SELUCION (SELUCION SAPIENS (Human).
Homo sapiens (Human).
Charta; Metazoa; Chordata;
Charta; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00822; PMP22_ClaudIn; 1.
PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claudin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ250712; CAB60616.1; -. AP001707; BAA95566.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
125
165
224 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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50.0%;
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Pred. No.
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1833ED3178B7F63A CRC64;
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                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                            haematopoietic development in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448
                                                                                                                        Wiles M.V., Grimaldi J.C.
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                                                                                                                                                                                                                                                                                                                                                                 SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Best Local :
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SE_CYS
SITE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NADPH:ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR
(EC 1.18.1.2) (ADRENODOXIN REDUCTASE) (AR) (FERREDOXIN-NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE ENCODED BY THE OPAL CODON, UGA.
-i- SIMILARITY: BELONGS TO THE SELENOPHOSPHATE SYNTHETASE 1 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guimaraes M.J., Peterson D., Vicari A., Cogilbert D.J., Jenkins N.A., Ferrick D.A., Zlotnik A.;
                                                                                                                                      SEQUENCE FROM N.A., FUNCTION, AND STRAIN=WIll8; TISSUE=Testis, and H MEDLINE=99429818; PubMed=10498693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9V3T9;
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of a novel selD homolog and archaea: is there an autoregulatory
                                           "The dare gene: steroid hormone production, olfactory behavior, neural degeneration in Drosophila.";
Development 126:4591-4602(1999).
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; H
Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                     REDUCTASE).
DARE OR CG12390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metabolism?";
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SEQUENCE FROM N.A
                        Development
[2]
                                                                                                                                                                                                                                                         Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADRO_DROME
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                                                                                                             Freeman M.R., Dobritsa A., Gaines P.,
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47258
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50.08;
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POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
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Pred. No.
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ATP (POTENTIAL)
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                                                                                                                                                                                       AND TISSUE
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                                                                                                                                                              Head;
                                                                                                                  Segraves W.A., Carlson J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DВ
73;
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mechanism in selenocysteine
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., Kastelein
                                                                                                                                                                                       SPECIFICITY
                                                                                                                                                                                                                                                                                   Hexapoda; Ins
a; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 448
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R., Bazan J.F.
                                                                                                                                                                                                                                                                                                         Insecta
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galler R.F. RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galler R.F. RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D., Ra Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C.R., Miklos G.L.G., Ra Hardell J., Bayraktaroglu L., Beasley E.M., Ra Ballew R.M., Beasu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Belson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C.D., Daven D.T. B., Davies P., Bardell J.H., Gu Z., Gaun P., Barris M., Chasser K., Ra der Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M., Ra der Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M., Ra der Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M., Ra der P., Barris M., Glasser K., Garg N.S., Gelbart W.M., Glasser K., Ra Jelai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum W., Talai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum W., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalai M., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., Ra Ainmel B.E., Kodira G.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., Resee M.G., Palai M., Wang X., Wang X., Palai M., Wang X., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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                                                                              Elèctron transport; Oxidoreductase; Flavoprotein; NADP; FAD; Mitochondrion; Transit peptide.
                                                                                                                                                                 PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00469; PNDRDTASEII.
                                                                                                                                                                                                                                               InterPro; IPR000759; Adrndx_redctse.
InterPro; IPR000103; Pyridine_redox_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                    TRANSIT
                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0015582; dare.
                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P08165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN PROTHORACIC GLAND OF THE LARVAL RING GLAND AND NURSE CELLS OF THE ADULT OVARY. LOW EXPRESSION IS ALL ADULT TISSUES EXAMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY:
ADRENODOXIN + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM. SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COFACTOR: FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUPARIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                              AF168685; AAD50819.1; AE003826; AAF58678.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REDUCED ADRENODOXIN + NADP(+) = OXIDIZED
NADPH: ADRENODOXIN OXIDOREDUCTASE
                                       MITOCHONDRION (POTENTIAL)
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YVD3_CA
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P55114;
01-OCT-1996
01-OCT-1996
20-AUG-2001
                       DOMAIN
DOMAIN
METAL
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DOMAIN
                                                                                                                                                                                                                                                    PROSITE; PS01180; CUB; FALSE_NEG.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01400; Astacin; 1.
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00235; ZnMC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAEEL
                                                                                                                                                                CHAIN
                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                           Hypothetical protein; Hydrolase; Metalloprotease; Zinc; Signal; EGF-like domain; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormPep; K04E7.3; CE02798
InterPro; IPR001506; Astac
InterPro; IPR000859; CUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U39666; AAA80412.1; HSSP; P00740; 1IXA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000884; TSP1.
IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000561;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34, Last sequence update)
40, Last annotation update)
METALLOPROTEINASE K04E7.3 PRECURSOR (EC 3.4.24.-).
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358
484
535
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EGF-like.
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Pred. No.
CUB.
TSP TYPE-1.
ZINC (CATALTTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                   POLY-PRO
                                                                                                                                        HYPOTHETICAL K04E7.3.
                                                                                             EGF-LIKE.
                                                                                                                                                                                        POTENTIAL
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75;
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FT METAL 223 223 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 551 AA; 61673 MW; 7CFC9A16B56C887E CRC64;

Query Match 77.1%; Score 27; DB 1; Length 551;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 wrxsfxg 8
Db 376 WRNISYSG 383

Search completed: January 14, 2002, 07:40:40

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Perfect score:
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     SPTREMBL_17:*

SP_archea:*

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sp_manme;

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10:
sp_f;

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sp_f;

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SPTREMBL_17:*

sp_archea:*

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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
3-DEMETHYLUBIQUINONE-9 3-METHYLTRANSFERASE, PUTATIVE.
                                                                                                                      InterPro; IPR001601; Meth-transf.
InterPro; IPR000051; SAM_bind.
Transferase; Methyltransferase; Ubiquinone; Complete proteome.
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Science 286:1571-1577(1999).
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Oss2v4 streptomyce
Ol8417 caenorhabdi
OshyOl pseudomonas
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Osacl6 caulobacter
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EMBO J. 14:286-291(1995).
ÈMBL; D31962; BAA21675:1; -.
HSSP; Q07960; 1RGP.
InterPro; IPR001005; Myb_DNA_bind.
InterPro; IPR001018; RhoGAP.
InterPro; IPR001660; SAM.
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01-JAN-1998
01-JUN-2001
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Q63744;
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InterPro; IPR001019; RhoGAP.
InterPro; IPR001018; START.
InterPro; IPR002913; START.
Pfam; PF00620; RhoGAP; 1.
Pfam; PF01852; START; 1.
SMART; SM00324; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
SMART; SM000234; START; 1.
PROSITE; PS000037; MYB.1; UNKNOWN_1.
PROSITE; PS000037; MYB.1; UNKNOWN_1.
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014868;
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Homma Y., Emori Y.
                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                01-NOV-1996 (TREMBLrel. 01, 01-NOV-1996 (TREMBLrel. 01, 01-JUN-2001 (TREMBLREL. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wei M.-H., Pack S., Ivanov Submitted (SEP-1997) to the EMBL; aF026219; AAB81637.1; HSSP; Q07960; 1RGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                       TISSUE-BRAIN;
                                                                                   "A dual functional signal mediator showing RhoGAP and phospholipase
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                         RHOGAP PROTEIN.
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Pred. No. 1.9e+02;
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                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
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DELETED IN LIVER CANCER 1.
ARHGAP7 OR DLC-1.
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Pfam; PF00620; RhoGAP; 1.
Pfam; PF01852; START; 1.
SMART; SM00324; RhoGAP; 1.
SMART; SM00454; SAM; 1.
SMART; SM00234; START; 1.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Pfam; PF01852; START; 1.
SMART; SM00324; RhoGAP; 1.
SMART; SM00454; SAM; 1.
SMART; SM00234; START; 1.
SMART; SM00234; START; 1.
UNKNOWN_1.
SPOON37; MYB 1; UNKNOWN_1.
SEQUENCE 1091 AA; 122816 MW; 5171ZDE7ECD0F52A CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
DELETED IN LIVER CANCER-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF035119; AAB87700.1; -. HSSP; Q07960; 1RGP. HSSP; Q07960; 1RGP. TITEPPTO; IPRO01005; Myb_DNA_bind.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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InterPro; IPR002913; START.
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Pred. No. 1.9e+02;
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Pred. No. 1.9e+02;
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RESULT
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Q9NMI3;
Q9NMI3;
01-OCT-2000
01-OCT-2000
01-OCT-2000
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Pfam; PF01852; START; 1.

Pfam; PF01852; START; 1.

SMART; SM00324; RhoGAP; 1.

SMART; SM00454; SAM; 1.

SMART; SM000234; START; 1.

PROSITE; PS00037; MYB_1; UNKNOWN_1.

PROSITE; PS00037; MYB_1; UNKNOWN_1.
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InterPro: IPR001660; SAM.
InterPro: IPR001660; SAM.
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                                                                                                                                                                                            "Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which c for large proteins in vitro.";

DNA Res. 7:347-355(2000).
                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-21082932;
                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TREMBLREL. 17, KIAAI723 PROTEIN (FRAGMENT))
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Yuan B.Z., Yang Y., Keck C.L.,
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074636;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-JUN-2001 (TrEMBLrel. 17,
TRANSPOSASE-LIKE PROTEIN.
                                                                                                                                                                                    Q9SIS9 PRELIM
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01-MAY-2000 (TrEMB
01-MAY-2000 (TREMB
01-JUN-2001 (TREMB
PUTATIVE NON-LTR R
AT2G01840
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core everosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
[1]
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STRAIN-MAFF305118; TRANSPOSON-AC-TYPE
MEDLINE-98334103; PubMed-9671028;
Okuda M., IKeda K., Namiki F., Nishi K
"Tfol: an Ac-like transposon from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusarium oxysporum.
Eukaryota; Fungi; Ascomycota; mitosporic
NCBI_TaxID=5507;
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Murphy L., Quall M., Harris
Submitted (JUL-2000) to the
EMBL; ALI60493; CAB97727.1;
NON_TER 149 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Gen. Genet. 258:599-607(1998).
EMBL; AB008746; BAA32244.1; -.
InterPro; IPR003556; BED_finger.
SEQUENCE 777 AA; 88602 MW; 5A067280645B836E
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                                                                                                                                                                                                                    (TTEMBLrel. 13, Created)
(TTEMBLrel. 13, Last sequence update)
(TTEMBLrel. 17, Last annotation update)
N-LTR RETROELEMENT REVERSE TRANSCRIPTASE
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Pred. No. 2.26
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STRAIN=CV.

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RESULT Q98D022 ID 298D022 ID 298D022 ID 299 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 DT 011 
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
Copenhaver G.P., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome II of Arabidopsis thaliana.";
"Sequence and analysis of chromosome II of Arabidopsis thaliana.";
"Nature 402:761-768(1999).
                           the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996). EMBL; AL133423; CAB62714.1; -. Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000477; RVTse.
InterPro; IPR000130; Zn_mTpeptdse.
Pfam; PF00078; rvt; 1.
PROSITE; PS00081; PROTEIN_SPLICING; UNKNOWN_1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                             MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapa Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a d
                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2);
Cerdeno A.M.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2001 (TrEMBLrel. 13, Last annotation update)
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EMBL; AC007069; AAD21778.1;
InterPro; IPR002203; Intein.
InterPro; IPR000504; RRM.
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     F283FA15A0650DCE CRC64;
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Pred. No. 4.9e+02;
1; Mismatches 3;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 7.0 KDA PROTEIN.
                                                                                                                  Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Streptomycineae; Streptomycetaceae; Streptomyces.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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Seeger K.J., Harris I
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                                           STRAIN-A3(2);
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EMBL; AL136519; CAB66277.1; -.
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"Cloning and characterization of a novel precerebellin-related Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF218380; AAF32315.1; -.
EMBL: AF218379; AAF32314.1; -.
MGD; MGI:1889286; Cbln3.
InterPro; IPR001073; Clq.
Pfam; PF00386; Clq; 1.
PRINTS; PR000007; COMPLEMNTC1Q.
SMART; SM00110; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
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EMBL; AL136519; CAB66278.1; -
Hypothetical protein.
SEQUENCE 65 AA; 7127 MW; 4C9A4476C44B727A CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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Thomson N.R., Parkhill J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the 8 Mb Streptomyces coelicolor Mol. Microbiol. 21:77-96(1996). EMBL; ALS89707; CAC33901.1; -. Hypothetical protein. SEQUENCE 243 AA; 27350 MW; 81
                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Adephaga; Car
Carabidae Conjunctae; Blackburnia.
NCBI_TaxID=155379;
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a
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Cerdeno A.M.,
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Saunders D.C.
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                                                                                                                                       (Coleoptera: Carabidae) evidence.";
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NCBI_TaxID=1902;
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                                                                                                         Mitochondrion.
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                    Conservative
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R-2001) to the
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                    Score 28; DB Pred. No. 1.2e 0; Mismatches
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endemic Hawaiian Platynini
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1.2e+02
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01-MAR-2001
01-JUN-2001
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21173698; PubMed=11259647;
Mterman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.
Mterman W.C., Feldblyum T.V., Laub M.T., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., E
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry
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"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).

EMBL; AL512667; CAC21620.1; -
InterPro; IPR001753; Enoyl_CoA_hydrtse.

Pfam; PF00378; ECH; 1.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Streptomyces.
                                                                                                                                                                                                                                                 Caulobacter crescentus. Bacteria; Proteobacteria;
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Cerdeno A.M., Parkhill J.,
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Seeger K.J.,
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Q1-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 183.5 KDA PROTEIN.
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Q9KPP6;
01-OCT-2000
01-OCT-2000
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STRAIN-EL TOR N1691 / SERCTYPE 01;

MEDLINE-20406833, PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.

Fraser C.M., Fleishmann R.D., Mekalanos J.J., Venter J.C.
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                                                                                                                                                                                             Q9NE65
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Eukaryota;
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Pfam; PF00580; UvrD-helicase; 2.
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Pred. No.
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Best Local Similarity 62:
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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09BUQ2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SELENOPHOSPHATE SYNTHETASE 2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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EMBL; AL352980; CAB68218.1; -.
Hypothetical protein.
SEQUENCE 1778 AA; 183516 MW; A4CEC69BDFF6B30D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-BHABDOMYOSARCOMA;
Strausberg R;
Strausberg R:
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0023B1; AAH023B1.1; -.
SEQUENCE 59 AA; 5897 MW; BDFC9070558436D5 CRC64;
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MEDLINE-98146435; PubMed-9477341;
IVens A.C., Lewis S.M., Bagherzadeh A.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-FRIEDLIN; Gabel C., Mueller-Auer S., Schaefer M., Rieger M., Fuchs M., Gabel C., Mueller-Auer S., Schaefer M., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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Pred. NO. 8.3e+02;
0; Mismatches 3;
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                                                                                         Popescu NC,
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                                                                                              Thorgeirsson SS,
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Best Local
                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 13 human colon cancer associated polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers (especially colon cancer), Parkinson's disease and diabetic retinopathy
Sequence
                                                        expression
                                                                                                             proteins. These proteins and the nucleic acid encoding them may used in the prevention, diagnosis and treatment of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is encoded by the DLC-1 gene. The gene is a putative tumor suppressor gene which is frequently deleted in liver cancer cells. Detecting deletion of this gene, or absence of the expressed protein, indicates increased susceptibility to cancer, or presence of cancer
                                                                                   associated with inappropriate
                                                                                                                                                                         The present invention relates to 13 human colon cancer-associated
                                                                                                                                                                                                                              Claim 11; Page 320-321; 326pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; I
Pred. No. 2.
                                                                                      colon
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                                                                                cancer-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20; 1
2.4e+02;
hes 3;
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RESULT
AAB53841
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Best Local Similarity
Thehes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                              neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders,
                                                gastrointestinal disorders, wounds, repnal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the accomplishment.
                                                                                                                                                                                                                                                                                                                                                              Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
Sequence
                                                                                                                                                                                                                                                          human colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                                                                                                                                                                                       AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The
                                                                                                                                                                                                                                                                                                                            Claim 11; Page 1952; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-587534/55
N-PSDB; AAC98598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunomodulatory; muscular; gynaecological; gastrointestinal;
nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2000; 2000WO-US05883.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB53841 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB53841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dentification; cytostatic;
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 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardioactive; neuroprotective; vulnerary;
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Pred. No.
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18;
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                                                 the present
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Query Match Best Local

Similarity 5; Conserv

Conservative

82.9%;

Score 29; DB pred. No. 48; 0; Mismatches

DB 48;

Length 120;

Indels

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                                              Query Match
Best Local Similarity
                                 Matches
                                                                                                                                                  The specification describes a DNA sequence which partially encodes a functional portion of polypeptide component required for synthesizing the polyketide antibiotic Tel-aviv, postmodification of antibiotic Tel-aviv, or regulation of biosynthesis of antibiotic Tel-aviv. The antibiotic Tel-aviv is a macrocyclic polyketide synthesised through the incorporation of acetate, methionine, and glycine. It inhibits cell wall synthesis by interfering with the polymerisation of the lipid-disaccharide-pentapeptide. Antibiotic Tel-aviv genes are useful in combinatorial genetics, and for encoding protein components for the synthesis, modification and regulation of antibiotic antibiotic Tel-aviv. Antibiotic Tel-aviv is useful in a wide range of clinical applications such as treating gingivitis. Antibiotic Tel-aviv is also useful for generating new biological agents from its secondary metabolites. The present sequence represents a protein involved in synthesis of antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                               Novel DNA sequence involved in polyketide antibiotic Tel-Aviv production useful for inhibiting cell wall synthesis and in wide range of clinical applications such as treating gingivitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nisc-difference 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB07679 standard; Protein; 417 AA.
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 10; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polyketide; antibiotic Tel-Aviv; cell wall synthesis; lipid-disaccharide-pentapeptide; gingivitis.
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1 wrxxsfxg 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of TaK, a 3-oxoacyl (ACP) synthase
                                                                                                          417 AA;
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ron E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0240537
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                                               82.9%;
50.0%;
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                               Score 29; DB 21;
Pred. No. 1.6e+02;
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                                 Mismatches
                                                          Length 417
                               Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claudin-2 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer;
Claudin-2 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer;
                                  Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 46; Page 97; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Blaschuck OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-NOV-1998;
30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-2000 (first entry)
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                                                                                                                                                                                                                                                                             Sequence
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                                                          28-SEP-2000
                                                                                   AAB06574;
                                                                                                         AAB06574 standard; peptide; 8
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                                                                                                                                                                                                                   Conservative
                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0185908
99US-0282029
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                                                                                                                                                                                                                             80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gour BJ
                                                                                                                                                                                                                               Score 28; DB 21;
Pred. No. 4.3e+05;
                                                                                                                                                                                                                    Mismatches
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the nervous syst
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Best Local
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                      03-NOV-1998;
30-MAR-1999;
(ADHE-) ADHEREX TECHNOLOGIES INC
                                                          03-NOV-1999;
                                                                                                                                                      graft rejection; cyclic.
                                                                                                                                                                              Claudin-2 modulating agent;
                                                                                                                                                                                                    Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO:
                                                                                                                                                                                                                               28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 49; Page 98; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-NOV-1998;
30-MAR-1999;
                                                                                  11-MAY-2000
                                                                                                        WO200026360-A1
                                                                                                                                 Mammalia
                                                                                                                                                                                                                                                     AAB06530;
                                                                                                                                                                                                                                                                          AAB06530 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conformation.
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nes 4; Conserv
                                                                                                                                                                 udin-2 modulating agent; cell adhesion recognition sequence;
sequence; autoimmune disease; inflammatory disease; cancer;
                                                                                                                                                                                                                                                                                                                                                 wrxxsfxg 8
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                                                                                                                                                                                                                             (first entry)
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                      98US-0185908
99US-0282029
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                                                          99WO-CA01029
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99US-0282029
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50.0%;
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Pred. No. 4.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 8;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-2 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                         Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous sysand across the skin - \frac{1}{2}
                                                                                                                               WPI; 2000-365610/31
                                                                                                                                                                                                         03-NOV-1998;
30-MAR-1999;
                                                                                                                                                                                                                                               03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                   graft rejection; cyclic.
                                                                                                                                                                                                                                                                                                                                                                Claudin-2 modulating agent; cell adhesion recognition such sequence; autoimmune disease; inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                      Claudin-2 cyclic cell adhesion recognition sequence SEQ ID NO: 128
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                                                                                                                                                                                (ADHE-) ADHEREX TECHNOLOGIES INC
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Pred. No.
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The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-2 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some

Claim 49;

Page

98;

121pp;

English.

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                                                                                                           The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-2 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                                                                                                                                                                                            Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin - \,
                                                                                                                                                                                                                                   Claim 49; Page 98; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-1998;
30-MAR-1999;
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sease; inflammatory disease; cancer;
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Claudin-2 cyclic cell adhesion recognition sequence SEQ
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 \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac
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01-APR-1996;
                                                                                                            06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW20137 standard; Protein; 59 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          duodenal ulcer disease; chronic gastritis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H. pylori cytoplasmic
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30-MAR-1999;
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     96US-0630405
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99US-0282029.
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Pred. No. 7.6;
1; Mismatches
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7.6;
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01-SEP-1998;
01-SEP-1998;
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09-SEP-1998;
09-SEP-1998;
09-SEP-1998;
09-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence shows a Helicobacter pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide
                                                                                                                       01-SEP-1998,
                                                                                                                                                   01-SEP-1999;
                                                                                                                                                                              09-MAR-2000
                                                                                                                                                                                                       WO200012708-A2
                                                                                                                                                                                                                                                           Human; PRO polypeptide; membrane bound protein; transmembrane; secretion; immunoadhesion; pharm
                                                                                                                                                                                                                                                                                                 Human PRO1486 (UNQ755) amino acid sequence SEQ ID NO:287
                                                                                                                                                                                                                                                                                                                            08-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                Homo sapiens
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DB; AAT67380.
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98US-0098716
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98US-0098803
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50.0%;
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40;
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30-OC
                                                                                                                                                                                        AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                   New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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N-PSDB; AAA37102.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 12;
                                                                                                                                                              Sequence
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98US-0106586

98US-0106586

98US-0106596

98US-0106902

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98US-0105882.
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                                                                     Score 28; DB
Pred. No. 1.3e
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                                                                                      DB 21;
1.3e+02;
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                                                                                                           21;
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                                                                                                       Length 205;
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98US-0099542 98US-0099741 98US-0099763 98US-0099815 98US-0099815 98US-0099816 98US-0100386 98US-0100386 98US-0100662 98US-0100662 98US-0100662 98US-0100664 98US-0100664 98US-0100684 98US-0100684 98US-010071 98US-0100684 98US-010071 98US-010071 98US-010174 98US-010174 98US-010174 98US-010177 98

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RESULT 1
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ID AAB66169
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   RESULT 15
AAW88747
ID AAW887
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AC AAW887
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Best Local S
Matches 4
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20-JUL-1999
26-JUL-1999
20-SEP-1999
29-CCT-1999
30-NOV-1999
10-DEC-1999
16-DEC-1999
05-JAN-2000;
                                                                                                                                                                                                                                                                                                The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
   AAW88747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                     AAW88747 standard; Protein; 206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 162; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene
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Gao W, Goddard A, Godowsk
Pan J, Paoni NF, Roy MA,
Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                     Sequence
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2000WO-US00219.
2000WO-US00376.
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99US-0145698
99US-016250111
99US-0162506
99WO-US28313
99WO-US28551
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owski PJ, Grimaldi CJ, Gu
MA, Smith V, Stewart TA,
PM, Wood WI;
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                                                                                                                                                                                    Score 28; DB 22;
Pred. No. 1.3e+02;
1; Mismatches 3;
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Gurney AL,
FA, Tumas D;
                                                                                                                                                                                                                   Length 205;
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Hillan KJ;
                                                                                                                                                                                  Gaps
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   06-JUN-1997
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97US-0048899. 97US-0048915. 97US-0048949. 97US-0048964. 97US-0048972.

98WO-US11422

97US-0049020 97US-0049375 97US-0057628 97US-0057644 97US-0057661 97US-0057761 97US-00577761 97US-0057776 97US-0057776 97US-0048878 97US-0048878 97US-0048894 97US-0048994 97US-0048996 97US-0048996 97US-0048974 97US-0048974 97US-0048974 97US-0048974 97US-0048974 97US-0049775 97US-0049775 97US-0057645 97US-0057648 97US-0057668 97US-0057765 97US-0057765 97US-0057765 97US-0057765 97US-0057765 97US-0057765 97US-0057765 97US-0057765 97US-0057765 97US-0057765 97US-0057765 97US-0057765

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Or-MAR-1999 (first entry)

XX

DE Secreted protein encoded by gene 45 clone HCESF40.

XX

Human; secreted protein; fusion protein; gene therapy; protein therapy;

XX

Human; secreted protein; fusion protein; gene therapy; protein therapy;

XX

KW

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

KW

developmental abnormality; foetal deficiency; blood; allergy; renal;

KW

immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;

inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;

KW

cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

KW

osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

KW

endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX

OS

Homo sapiens.
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97US-0048883. 97US-0048892.

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The invention relates to nucleic acid sequences (AAV84411 to AAV8463)
CC encoding human secreted proteins (AAW88534 to AAW88756). The secreted compositing phase sequences are deposited with the ATCC under deposit numbers are composited with the ATCC under deposit numbers compositing recombinant vectors containing the nucleic acid could comprising recombinant vectors containing the nucleic acid couseful for the recombinant production of the secreted couseful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also composed by determining the amount of the new polypeptides in a sample cor by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, neurodegenerative consistences, hepatic and renal disease, lymphomas, inflammation, allergies, cushemic shock, Alzheimer's and cognitive disorders, schizophrenia, coused are also useful for identifying their binding partners. The present sequence represents human secreted protein (see descriptor counters).
 Query Match
Best Local Similarity
Matches 4; Conserv
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05-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA
Fan P, Feng P, Ferrite AM, Fischer CL, Florence C;
Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW;
Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM;
Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 589-590; 772pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV84624.
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                                                                              Sequence
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                                                                             206 AA;
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970S-0057654.
970S-005766.
970S-0057760.
970S-0057763.
970S-0057769.
970S-0057774.
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97US-0048917.
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97US-0048971.
97US-0049019.
97US-0049374.
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97US-0057634.
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              80.0%;
50.0%;
Score 28; DB 20;
Pred. No. 1.3e+02;
1; Mismatches 3
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Gaps

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RESULT I
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel murine nucleic acid sequences encoding to clodin family of tight junction (TJ)-constituting membrane protein can be used in medical field. This sequence represents the clodin 2 protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tight junction-constituting membrane protein clodin family - useful in the medical field % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left
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N-PSDB; AAZ89137.
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Best Local
Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system
                                                                                                             WPI; 2000-365610/31
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30-MAR-1999;
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nes 4; Conserv
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                                                                                                                                                                              MĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell adhesion recognition sequence;
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Pred. No. 4.3e+05;
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                                   The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-3 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-1 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                                                                                                                   Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous sysand across the skin -
                                                                                                                                                                                                                                                                                                                                03-NOV-1998;
30-MAR-1999;
                                                                                                                                                      Claim 52; Page 99; 121pp; English.
                                                                                                                                                                                                                                             WPI; 2000-365610/31
                                                                                                                                                                                                                                                                         Blaschuck OW,
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50.0%;
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1; Mismatches
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e; cancer;
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Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the use of peptides as claudin-mediated ceil adhesion modulators. The claudin-3 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-NOV-1998;
30-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                   conformation.
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                                                                                                                        Conservative
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Search completed: January 14, 2002, 07:36:01 Job time: 812 sec

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| 68.6 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 74.3 | • | | | | | | 74.3 | |
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| | Sequence 9, | Sequence 10, | Sequence 12, | Sequence 2, | Sequence 2, | Sequence 12, | Sequence 10, | Sequence 8, | Sequence 7, | Sequence 36, | Sequence 36, | Sequence 36, | Sequence 38, | Sequence 29, | Sequence 29, | Sequence 31, | Sequence 31, | Sequence 25, | Sequence 25, | Sequence 27, | Sequence 27, | Sequence 33, |
| Appli | Appli | • | | | Appli | - | | Appli | Þ | - | - | , Appl | • | - | • | • | • | • | - | - | • | • |

ALIGNMENTS

; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-222-817-2 RESULT 2 US-09-222-786-2 дb 8 RESULT 1 US-09-222-817-2 TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION FILE REFERENCE: OP813 CURRENT APPLICATION NUMBER: US/09/222,817 CURRENT FILING DATE: 1998-12-30 EARLIER APPLICATION NUMBER: JP 10-3751 EARLIER FILING DATE: 1998-01-12 EARLIER APPLICATION NUMBER: JP 10-353521 EARLIER APPLICATION NUMBER: JP 10-353521 EARLIER APPLICATION NUMBER: JP 10-353521 EARLIER FILING DATE: 1998-12-11 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 Sequence 2, Application US/09222786A Patent No. 6258573 GENERAL INFORMATION: Sequence 2, Application US/09222817 Patent No. 6037154 Matches Query Match Best Local Similarity APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO TITLE OF INVENTION: METHOD OF PRODUCING L: FILE REFERENCE: OP812 CURRENT APPLICATION NUMBER: US/09/222,786A CURRENT FILING DATE: 1998-12-30 EARLIER FILING DATE: 1998-01-12 EARLIER FILING DATE: 1998-01-12 EARLIER APPLICATION NUMBER: JP 10-353513 LENGTH: 132 WKRSSFNG 139 1 wrxxsfxg 8 345 Conservative 77.1%; 50.0%; Masakazu SUGIMOTO, Tsuyoshi OSUMI, DD OF PRODUCING L-SERINE BY FERMENT Score 27; I Pred. No. 1 Mismatches DB 3; 1 1.2e+02; Length 345; BY FERMENTATION Indels Tsuyoshi NAKAMATSU TSuyoshi NAKAMATSU, 0; 0

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; ORGANISM: Brevibacterium flavum
US-09-222-817-14
                                                                                                                                                                                                                                                                                                                                                                  US-09-222-817-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT ; ORGANISM: Brevibacterium flavum US-09-222-817-12
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US-09-222-817-12
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TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-222-786-2
                                                                           SEQ ID NO 14
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09222817 Patent No. 6037154
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                                                                                         CURRENT APPLICATION NUMBER: US/09/222,817
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER FILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: JP 10-353521
EARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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Best Local
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CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: UP 10-3751
EARLIER FILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: UP 10-353521
                                                                                                                                                                                                                                                 APPLICANT: Mikiko SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU, TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION FILE REFERENCE: OP813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
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FILE REFERENCE: 00813
CURRENT ADDITION.
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TYPE: PRT
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50.0%;
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Pred. No. 1.2e+02;
Pred. No. 3;
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TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION
FILE REFERENCE: OP812
CURRENT APPLICATION NUMBER: US/09/222,786A
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER FILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: JP 10-353513
EARLIER APPLICATION NUMBER: JP 10-353513
EARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 530
Type: nom
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SEQ ID NO 14
LENGTH: 530
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                                                                       Matches
                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              APPLICANT: Mikiko SUGA, MASAKAZU SUGIMOTO, TSUYOShi OSUMI, TSUYOShi NAKAMATSU, TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION
FILE REFERENCE: OP812
CURRENT APPLICATION NUMBER: US/09/222,786A
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-12-11
NUMBER: JP 10-353513
EARLIER FILING DATE: 1998-12-11
NUMBER: OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09222786A Patent No. 6258573
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Best Local :
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Best Local Similarity
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132 WKRSSFNG 139
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| 132 WKRSSFNG 139
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                               1 wrxxsfxg 8
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                                                                     Conservative
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                                                                                    77.1%;
50.0%;
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50.0%;
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50.0%;
                                                                 Score 27; DB Pred. No. 1.8e 1; Mismatches
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Pred. No.
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Pred. No. 1.8e+02;
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1.8e+02;
                                                                                        .8e+02;
                                                                                                     Length 530;
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; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-6
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В
                                                                                                                                                                                LENGTH: 462
TYPE: PRT
CORGANISM: Exophiala spinifera
US-09-352-159-8
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09352159A Patent No. 6211434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
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Best Local Similarity
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                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Amino Polyol Amine Oxidase TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use FILE REFERENCE: 1134
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310 WREQGFSG 317
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hilarity 50.0%;
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                                                                            Score 26; DB
Pred. No. 2.6e
0; Mismatches
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Pred. No. 2.6e+02;
                                                                                                   6e+02;
                                                                                                                  Length 462
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RESULT 9 US-09-352-168-6

RESULT 11
US-09-352-159-11
Sequence 11, Application US/09352159A
Patent No. 6211434

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; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-168-8
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US-09-352-168-8
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Best Local Similarity
Conserva
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
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                                                                             Matches
                                                                                            Query Match 74.3%;
Best Local Similarity 50.0%;
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Folkerts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
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APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
APPLICANT: Maddox, Joyce R.
APPLICANT: Maddox, Joyce R.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides (
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT APPLICATION NUMBER: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER ETLING DATE: 1998-07-25
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SOFTWARE: FastSEQ for Windows Version 3.0
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310 WREQGFSG 317
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                                   1 wrxxsfxg 8
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o. 6211435
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                                                                             Conservative
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Pred. No.
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Pred. No. 2.6e+02;
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2.6e+02;
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RESULT 13
US-09-352-159-21
; Sequence 21, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-11
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                 Query Match
Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 33 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related
FILE REFERENCE: 0875
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CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
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APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods
FILE REFERENCE: 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Duvick, Jonathan P.
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Exophiala spinifera
                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 463
                                                                                                                          311 WREQGFSG 318
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50.0%;
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Pred. No.
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Pred. No. 2.
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2.6e+02;
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2.6e+02;
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335

WREQGFSG 342

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; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; OTHER INFORMATION: K:trapao translational fusion with barley alpha
; OTHER INFORMATION: amylase signal sequence, for expression and
; OTHER INFORMATION: secretion of the mature trapao in maize.
US-09-352-168-21
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                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 487
TYPE: PRT
                                                              Query Match
Best Local :
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LENGTH: 487
                                         Matches
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Folkerts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT APPLICATION NUMBER: US/092,936
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
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Best Local Similarity
Matches 4: Consert
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                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 46 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Duvick, Jonathan P. APPLICANT: Gilliam, Jacob T. APPLICANT: Maddox, Joyce R.
                                                                                                                                                                                                                                                                                   ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                              Local Similarity
1 wrxxsfxg 8
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50.0%;
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50.0%;
                                       Score 26; DB Pred. No. 2.7e 0; Mismatches
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Pred. No.
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                                                            DB 4;
2.7e+02;
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2.7e+02;
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                                                                              Length 487
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CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 554
TYPE: PRT
ORGANISM: Exophiala spinifera
                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 554
TYPE: PRT
ORGANISM: Exophiala spinifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09352168A
Patent No. 6211435
GENERAL INFORMATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Folkerts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
APPLICANT: Maddox, Joyce R.
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; NAME/KEY: SIGNAL
; LOCATION: (1)...(89)
US-09-352-159-17
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                                                                                                              ; NAME/KEY: SIGNAL ; LOCATION: (1)...(89) ; OTHER INFORMATION: yeast alpha mating factor secretion signal. US-09-352-168-17
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Query Match 74.3
Best Local Similarity 50.0
Matches 4; Conservative
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Best Local Similarity
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APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
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                       74.38;
50.08;
  Score 26; DB 4; |
Pred. No. 3.1e+02;
0; Mismatches 4
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 44
LENGTH: 591
TYPE: PRT
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LENGTH: 591
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                                                                         Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                    APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/092,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Amino Polyol Amine Oxidase TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use FILE REFERENCE: 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gilliam, Jacob T APPLICANT: Maddox, Joyce R.
                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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442 WREQGESG 449
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50.0%;
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                                                                       Score 26; DB
Pred. No. 3.3e
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3.3e+02;
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3.3e+02;
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CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEO ID NOS: 46
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 40
LENGTH: 598
LENGTH: 598
LENGTH: 598
LENGTH: 598
LENGTH: 598
COTARNISM: Exophiala spinifera
FEATURE:
NAMEKEY: VARIANT
LOCATION: (216)...(216)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-352-159-40
                 QΥ
                                         Query Match
Best Local Similarity
Thes 4; Conserve
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; TYPE: PRT
; ORGANISM: Rhinocladiella atrovirens
US-09-352-159-42
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US-09-352-159-42
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US-09-352-159-40
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APPLICANT: Duvick, Jonathan P.

APPLICANT: Gilliam, Jacob T.

APPLICANT: Gilliam, Jacob T.

APPLICANT: Gilliam, Jacob T.

APPLICANT: Gilliam, Jacob T.

APPLICANT: Maddox, Joyce R.

TITLE OF INVENTION: Amino Polyol Amine Oxidase

TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use

FILE REFERENCE: 1134

CURRENT APPLICATION NUMBER: US/09/352,159A

CURRENT FILING DATE: 1999-07-12

EARLIER APPLICATION NUMBER: 60/92,936

EARLIER APPLICATION NUMBER: 60/93,391

EARLIER APPLICATION NUMBER: 60/135,391

EARLIER FILING DATE: 1999-05-21

NUMBER OF SEO IT NOS. 46
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Patent NO. 6211434
GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 42
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Pred. No. 3.3e
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Pred. No. 3.3e+02;
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3.3e+02;
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Search completed: January 14, 2002, 07:23:45 Job time: 76 sec

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| 50 | 49 | 48 | 47 | 46 | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 |
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| 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 |
| 74.3 | 74.3 | | | | 74.3 | | | 74.3 | | 74.3 | 77.1 | 77.1 | 77.1 | | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 | 77.1 |
| 286 | 262 | 261 | 260 | 245 | 232 | 224 | 212 | 171 | 169 | 154 | 1083 | 733 | 513 | 396 | 386 | 381 | 381 | 381 | 379 | 379 |
| N | N | N | N | N | N | N | N | N | N | N | N | 1 | _ | N | μ | ν | N | ب | ш | ب |
| D64235 | F82959 | A64066 | F82120 | C85682 | E70830 | A85742 | S72873 | H75017 | B71454 | E70971 | S54293 | S33643 | A35742 | S31959 | S31140 | T04164 | T03289 | JN0447 | S71244 | S51357 |
| hypothetical prote | permease of ABC zi | probable membrane | zinc ABC transport | hypothetical prote | hypothetical prote | probable tail comp | hypothetical prote | hypothetical prote | hypothetical prote | probable rRNA meth | regulator protein | transforming prote | aqualysin (EC 3.4. | acyl-(acyl-carrier | alcohol dehydroger | formaldehyde dehyd | formaldehyde dehy | alcohol dehydroge | alcohol dehydroger | alconol denydroger |

ALIGNMENTS

A;Cross-references: GB:J02459; GB:M17233; GB:M24325; GB:V00636; GB:X00906; NID:g21510 A;NOte: there are two possible initiation sites for gene K translation, the codon for C;Comment: Gene K protein is involved in the assembly of the initiator complex for ta C;Genetics: tail assembly protein K - phage lambda C;Species: phage lambda C;Species: phage lambda C;Date: 13-Jun-1983 *sequence_revision 13-Jun-1983 *text_change 23-Jul-1999 C;Date: 13-Jun-1983 *sequence_revision 13-Jun-1983 *text_change 23-Jul-1999 C;Accession: H43009; G43013; A04355 R;Daniels, D. Submitted to the Nucleic Acid Sequence Database, September 1982 A; Map position: C; Superfamily: | A; Molecule type: DNA A; Residues: 1-199 <SAN> A; Molecule type: DNA A; Residues: 1-199 < DAN> A; Residues: 1-199 < DAN> A; Residues: 1-199 < DAN> Mol. Biol. 162, 729-773, 1982 J. Mol. Biol. 162, 729-773, 1982 A; Title: Nucleotide sequence of bacteriophage lambda DNA. A; Reference number: A92891; MUID:83189071 A; Accession: G43013 A; Gene: K A; Accession: H43009 A; Reference number: TJBPKL : 29.43-30.66 phage lambda A94614 tail assembly protein

A; Title:

Genome sequence of

enterohemorrhagic Escherichia

O157:H7

Burland, V.; Mau, B.; Glasner, J.D.; Rose, N.W.; Lim, A.; Dimalanta, E.; Potamousis,

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Query Match Best Local Matches

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Conservative

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91.4%;

Score 32; DB Pred. No. 3.3; 0; Mismatches

DB . 3; 1.

Length 199;

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Gaps

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A;Title: Isolation and characterization of A;Reference number: A39484; MUID:92130000 A;Accession: A39484
A;Molecule tvoo
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C;Species: phage SPP1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 11-May-2000
C;Accession: S43804; T42337; S41178
C;Accession: S43804; T42337; S.; Lueder, G.; Alonso, J.C.
R;Pedre, X.; Weise, F.; Chai, S.; Lueder, G.; Alonso, J.C.
J. Mol. Biol. 236, 1324-1340, 1994
A;Title: Analysis of cis and trans acting elements required for the initiat A;Reference number: S43798; MUID:94172631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-224 <STO>
A; Cross-reference
A; Molecule type: mRNA
A; Residues: 1-280 <BR
A; Cross-references: Gl
                                                                                                androgen-withdrawal apoptosis protein RVP1, C;Species: Rattus norvegicus (Norway rat) C;Date: 03-Aug-1992 #sequence_revision 03-Au C;Accession: A39484 R;Briehl, M.M.; Miesfeld, R.L. Mol. Endocrinol. 5, 1381-1388, 1991
                                                                                                                                                                                                   RESULT
A39484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X67865; NID:9472886; A;Note: the nucleotide sequence was submitted R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and 1 A;Reference number: Z22137; MUID:98094274
A;Accession: T42337
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A; Accession: B85584
A; Status: preliminal
A; Molecule type: DNA
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A; Residues: 1-159 <A
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A; Residues: 1-159 <PE2>
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C;Superfamily: phage lambda tail assembly protein
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Best Local :
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Experimental source: strain O157:H7, substrain EDL933
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5; Conser
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GB:M74067;
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62.5%;
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                                                                acterization of MUID:92130987
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NID:g205857;
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PIDN: AAA41760.1;
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7.6;
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3.6;
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PID:g205858
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C;Genetics:
A;Gene: RVP.1
C;Superfamily: 1
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R;Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
                                                                                          A;Gene: adhC; PA3629
C;Superfamily: alcohol
                                                                                                                                                                                                                                                                                                          alcohol dehydrogenase class III PA3629 [imported] - Pseudomonas C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                      RESULT
B83191
                                                                                                                                 A;Cross-references: GB:AE004783; GA;Experimental source: strain PA01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Saunders, D.C.; Harris, D.; submitted to the EMBL Data Lil A; Reference number: Z21563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
T34972
                                                                                                                       C; Genetics:
                                                                                                                                                                                                   A;Title: Complete genome
A;Reference number: A829
A;Accession: B83191
                                                                                                                                                                                                                                            .; Lory, S.; Olson, M.V. Nature 406, 959-964, 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AL109663; A;Experimental source: strain A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T34972
                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-370 <STO>
                                                                                                                                                                             A; Molecule
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                          Matches
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                                                                                                                                                                                                                    A82950;
                                                                                                                                                                                                                                              2000
                                                                                          dehydrogenase;
                                                                                                                                                                                                                   sequence of Pseudomonas 50; MUID:20437337
                                      85.7%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.; James, K.D.;
Library, August
                                                                                                                                                                                                                                                                      Erwin,
L.L.; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor
                                                                                                                                               GB:AE004091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              score 30; DB
Pred. No. 15;
0; Mismatches
                          0;
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                            Mismatches
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                                                                                          long-chain
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                                                                                                                                                                                                                                                                    Mizoguchi, S.D.;
r, S.N.; Folger,
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1999
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13;
                                                                                                                                               NID: g9949786;
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                          Gaps
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Larbig,
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CS3 pilin synthesis protein, 104K - Escherichia coli N:Contains: CS3 pilin synthesis protein, 104K; CS3 pilin synthesis protein, C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 21-Jul-2000 C;Accession: S78561; S07900; S07901; S07902; S07903 R;Jalajakumari, M.B.; Thomas, C.J.; Halter, R.; Manning, P.A. Mol. Microbiol. 3, 1685-1695, 1989
                                                                                                                                                                                                                                RESULT
S78561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable gcvT protein - Mycobacterium tuberculosis (strain H37RV)
c;Species: Mycobacterium tuberculosis
c;Species: Mycobacterium tuberculosis
c;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
c;Acccssion: D70786
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Best Local Similarity
5; Conserv
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C;Superfamily: aminomethyltransferase
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A;Authors: Sqraes, R.; Sulston, J.E.; Taylor, K.; A;Title: Deciphering the biology of Mycobacterium A;Reference number: A70500; MUID:98295987
A;Accession: D70786
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A; Residues: 1-198 <STO>
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A;Experimental source: strain |
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A; Residues: 1-379 <COL>
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62.5%;
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H37Rv
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Pred. No.
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K.; Apodaca
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A;Map position
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Best Local Similarity
Matches 4; Conserv
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C;Accession: H75258
C;Accession: H75258
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey,
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A; Residues: 1-206 <WHI>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A; Reference number: A75250; MUID: 20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M.; Shen, M.; Vamathevan, J.J.; Lam, P.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable 3-demethylubiquinone-9 3-methyltransferase - Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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A;Residues: 572-753 <AJAZ>
A;Cross-references: EMBL:X16944; NID:g41155; PIDN:CAA34819.1;
A;Experimental source: Strain PB176
C;Function:
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A; Residues: 451-753 <JAA>
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A; Residues: 317-753
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A; Residues: 181-753 <JAW>
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A; Experimental source: strain PB176
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A; Residues: 1-937 <JAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S07900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: H75258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   595 WRGRAFIG 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                        GB:AE002085;
ce: strain R1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.9%;
                               80.0%;
Score 28; DB Pred. No. 28; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB Pred. No. 72; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                           GB:AE000513;
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28;
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                                                                                                                                                                                                                                                                                                                                    NID:g6460383;
                                                                          <u>ب</u>
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                                                                      Length 206
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                                                                                                                                                                                                                                                                                                                                           PIDN: AAF12100.1;
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T.; Zalewski,
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Conservative

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A;Cross-references: EMBL:AL0315;
A;Experimental source: strain 9
C;Genetics:
A;Gene: SPDB:SPCC13B11.04c
A;Map position: 3; IIIR
A;Introns: 9/3
A;Note: SPCC777.01c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Brucel
C; Date: 03-Oct-19
C; Accession: A561
R; de Wergifosse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain 972h-; cosmid c13B11 R; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; submitted to the EMBL Data Library, August 1998 A; Reference number: Z17318 A; Accession: T11707 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                   A;Note: intron positions not resolved (incomplete sequence) C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydroge C;Keywords: NAD; oxidoreductase; zinc E;50,72,179/Binding site: zinc, catalytic (Cys, His, Cys) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alcohol dehydrogenase (EC 1.1.1.1) class III [similarity] - fission yeast (Schizosacchar N;Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 08-Dec-2000 C;Accession: T40965; T11707 R;Purnelle, B; Goffeau, A.; Lyne, M.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A56152;
A; Accession: A56152
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-213 <DEA>
                          VО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-380 < PUR>
A; Cross-references: EMBL: AL032681; PIDN: CAA21785.1; GSPDB: GN00068; SPDB: SPCC13B11.04c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;de Wergifosse, P.; Lintermans, P.; Limet, J.N.; Cloeckaert, A.
J. Bacteriol. 177, 1911-1914, 1995
A;Title: Cloning and nucleotide sequence of the gene coding for the major 25-kilodalton
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-61 <SEE>
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A; Accession: T40965
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A;Cross-references: GB:X79284; NID:g769744; PIDN:CAA55872.1; PID:g769745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Brucella abortus
pate: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change
Accession: A56152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                             Query Match
Best Local
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Best Local
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                                                                       Local Similarity
les 5; Conserv
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4; Conservative
                                                                       Conservative
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                                                                                             80.0%;
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Pred. No. 29;
1; Mismatches
                                                                       0;
                                                                                             Score 28;
Pred. No.
                                                                       Mismatches
                                                                                                                  DB
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                                                                       ω,.
                                                                                                                  Length 380;
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                                                                       Indels
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                                           probable tail component of prophage CP-9330 Z2143 [imported] - Escherichia C;Speciles: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Accession: E85718
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
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A;Gene: Z3314
C;Superfamily: phage lambda tail assembly protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unspecific monooxygenase (EC 1.14.14.1) - common tobacco N;Alternate names: cytochrome p450 homoLog TBP C;Species: Nicotiana tabacum (common tobacco) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: G85842
                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: cTBP
C;Keywords: monooxygenase; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-530 <SUG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 1308, 231-240, 1996
A;Title: Cloning and expression in Escherichia coli
A;Reference number: Z14816; MUID:96404975
A;Accession: T02995
                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005174; NID:g12516364; PIDN:AAG57203.1; GSPDB:GN00145; UWGP:A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-224 <STO>
                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Genome sequence of enterohemorrhagic Escherichia A; Reference number: A85480; MUID:21074935; PMID:11206551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Sugiura, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
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205
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hes 5; Conserv
                                          1 wrxxafxg 8
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WHASAFTG 212
                                                                                                          Similarity
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                                                                                   Conservative
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                                                                                                     77.1%;
50.0%;
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                                                                                                       Score 27; Pred. No.
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53;
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                                                                                                                            Length 224;
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                                                                                                                                                                                                                                                                                                                                                                                                                  coli 0157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.D.; Rose, Potamousis,
                                                                                   0;
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                                                                                   Gaps
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K.; Apoda
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Potamousis, J.D.; Rose,

D.J.;

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A;Title: Purification, characterization, and partial sequence of the glutathlone-domine of the glutathlone-domine of the glutathlone of A;Reference number: A42015; MUID:92118844
A;Accession: A42015
                                                                                                                     A; Residues: 1-24, 7X', 26-40, E', 42-45, 'G', 47 < GUT>
A; Residues: 1-24, XY', 26-40, 'E', 42-45, 'G', 47 < GUT>
A; Note: this enzyme also has hemithiolacetal dehydrogenase activity
R; Nashimoto, H; Salto, N.
Submitted to the EMBL Data Library, May 1996
A; Description: Kohara library: 8F10.
A; Reference number: $78608
A; Reference number: $78608
A; Reference number: $78608
A; Molecule type: DNA
A; Residues: 'MIPLHIL', 11, 'VNRWKSLKLTLHHR', 26-369 < NAS>
A; Residues: 'MIPLHIL', 11, 'VNRWKSLKLTLHHR', 26-369 < NAS>
A; Residues: 'MIPLHIL', 11, 'NOTE REMBL: 885613
A; Experimental source: strain R12
C; Comment: Class III alcohol dehydrogenases are pyrazole-insensitive, are not very C; Genetics:
A; Genetics:
A; Genetics:
C; Complex: homodimer
C; Complex: homodimer
C; Function: ABDH>
A; Description: catalyzes oxidation of primary and secondary alcohols to aldehydes if C; Function: APDH>
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C; Function:
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F; 189-218/Region: beta-alpha-beta NAD nucleotide-binding fold F; 40,62,169/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted F; 92,95,98,106/Binding site: zinc, noncatalytic (Cys) #status predicted
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Nichtenate names: class III alcohol dehydrogenase
Nichtenate names: class III alcohol dehydrogenase
Nichtenate formaldehyde dehydrogenase
Nichtenate formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1)
Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cispecies: Date: 10-Jul-1992 #sequence_revision 01-May-1998 #text_change 11-Jun-1999
Ciscession: S57525
Nichtenate in S57525
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Pred. No. 85;
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Pred. No. 85;
1; Mismatches
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Matches 4; Conservative
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Best Local Similarity
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                                        A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85718
A;Status: preliminary
A;Rolecule 'type: DNA
A;Residus: 1-293 <STO>
A;Residus: 1-293 <STO>
A;Cross-references: GB:ABC05174; NID:g12515097; PIDN:AAG56209.1; GSPDB:GN00145; UWGP:Z21
A;Experimental source: strain O157:H7, substrain EDL933
A;Genetics:
A;Genetics:
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A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-293 <STO>
A;Residues: 1-293 <STO>
A;Residues: 1-293 <STO>
A;Cross-references: GB:AE005174; NID:g12516098; PIDN:AAG56997.1; GSPDB:GN00145; UWGP:23G
A;Experimental source: strain O157:H7, substrain EDL933
A;Gene: Z3081
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: A85817
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
111er, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
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C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 11-Jun-1999

C; Accession: D64763; A42015; S78608

R; Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUID:97426617
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A;Reference number: A85480; MUID:21074935; PMID:11206551
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N;Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1)
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68;
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68;
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Pred. No.
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A; Residues: 1-369 <BLAT>
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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Nature 405,
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N; Contains: formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1)
C; Species: gaus caballus (domestic horse)
C; Species: gaus caballus (domestic horse)
C; Date: 31.Mar-1991 #sequence_revision 31-Mar-1991 #text_change 01-May-1998
C; Accession: A33419
R; Aislear, R.; Holmquist, B.; Vallee, B.L.; Joernvall, H.
B; Natiesr, R.; Holmquist, B.; Vallee, B.L.; Joernvall, H.
B; Afference number: A33419; MUID: 90105360
A; Accession: A33419
A; Molecule type: protein
A; Residues: 1-373 *AKAI>
C; Comment: Class III alcohol dehydrogenases are pyrazole-insensitive, are not very active comment: class III alcohol dehydrogenases are pyrazole-insensitive, are not very active cypnex: homodimer; does not form heterodimers with the class I alcohol dehydrogenase cypneriment alcohol dehydrogenase cypneriment alcohol dehydrogenase cypneriment alcohol dehydrogenase homology C; Function: catalyzes the oxidation by NAD+ of formaldehyde and glutathione to S-form C; Superfamily: alcohol dehydrogenase; long-chain alcohol metabolism: homodimer: metalloprotein; NAD; ox C; Superfamily: alcohol dehydrogenase homology C; Keywords: acetylated amino end; alcohol metabolism: homodimer: alcohol dehydrogenase homology C; Keywords: acetylated amino end (Ser) #status experimental chain slong-file site: acetylated amino end (Ser) #status predicted
F; 17, Modified site: acetylated amino end (Ser) #status predicted
F; 44,66,173/Binding site: zinc, noncatalytic (Cys) #status predicted
                                                                                                                                                                                                                                                                                                               hypothetical protein adhC [imported] - Escherichia coli (strain O157:H7)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Diana coli
C;Accesion: G85530
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamcusis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUD:21074935; PMID:11206551
A;Residues: Dralminary
A;Molecule type: DNA
A;Residues: 1-369 <STO>
A;Cross-references: GB:AE005174; NID:g12513195; PIDN:AAG54707.1; GSPDB:GN00145; UMGP:204
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Genetics:
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Pred. No. 86;
1; Mismatches 3; Indels
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Pred. No. 85;
1; Mismatches 3; Indels
Indels
3;
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1;
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50.08;
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Matches 4; Conservative
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4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Search completed: January 14, 2002, 07:37:32 Job time: 902 sec
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313 WKGTAFGG 320
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RESULT
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Best Local
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PROSTIE; PSO1346; CLAUDIN: 1.
Tight junction; Transmembrane.
TRANSMEM 10 30 PO
TRANSMEM 82 102 PO
TRANSMEM 118 138 PO
TRANSMEM 161 181 PO
SEQUENCE 209 AA; 22029 MW;
                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CLAUDIN-4 (CLOSTRIDIUM PERFRINGENS ENTEROTOXIN
RECEPTOR) (CPE-R).
CLDN4 OR CPETRI OR CPER.
                                                                                                                                                                                                                                                   LHUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KBETANITA J., Inoue N., Horiguchi Y., Matsuda M., Su
Molecular cloning and functional characterization
Clostridium perfringens enterotoxin.";
J. Cell Biol. 136:1239-1247(1997);
II PUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRA-
I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
II SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDILINE-97242441; PubMed-9087440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecus aethlops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence
30-MAY-2000 (Rel. 39, Last annotati
CLAUDIN-4 (CLOSTRIDIUM PERFRINGENS
RECEPTOR) (CPE-R).
                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
                                                                                                                                                                                                                    CLD4_HUMAN
014493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Claudin
Pfam; PF00822; PMP22_Claudin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D88492; BAA22781.1; -
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NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLDN4 OR CPETR1 OR CPER
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30-MAY-2000
                                                                       NCBI_TaxID=9606;
                                            QUENCE FROM N.A
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SUE-Fetal brain;
INF-97476271; PubMed-9334247;
INF-9 J., Suglyama H., Inoue N.,
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5; Conserv
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39, Last sequence update)
39, Last annotation update)
39, Created)
(CPE-
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62.58;
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POTENTIAL.
POTENTIAL.
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                                                                                     Craniata; Vo
Catarrhini;
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                                                                                                                                                                                                                                  209
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5.9;
                                                                                   Vertebrata; Euteleostomi;
i; Hominidae; Homo.
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                                                                                                                                                         RECEPTOR) (CPE-
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Horiguchi Y., Matsuda

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Brachydanio rerio (Zebrafish) (Zebra danio).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.

NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM SEQUENCE
                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Keen T.J., Inglehearn C.F.;

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases

-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugimoto N.; "Clostridium perfringens enterotoxin utilizes two structurally mambrane proteins as functional receptors in vivo.";
                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001832; Claudin.
InterPro; IPR000729; pmp22_Claudin.
Pfam; pF00822; pmp22_Claudin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane proteins as functional receptors in vivo.";
J. Biol. Chem. 272:26652-26658(1997).
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
              EMBL; AJ011790; CAA09778.1; InterPro; IPR001832; Claudi InterPro; IPR000729; PMP22_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
Tight junction; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 602909;
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-!- SIMILARITY: BÉLONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
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nes 5; Conserv
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118
161
209 AA;
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PMP22_Claudin;
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                            Claudin
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               _Claudin
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0659A93AA5F0E4C5 CRC64;
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Pred. No. 5.9;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2002, 07:40:40; Search time 37.71 Seconds (without alignments) 7.778 Million cell updates/sec

Title:
Perfect score:
Sequence: 09-185908-1H 35 1 wrxxafxg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters:

100059

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 33 33 33 33 | 10 10 10 10 10 10 10 10 10 10 10 10 10 1 | 13 14 15 16 17 | 6 7 9 10 11 | Result No. 1 2 2 3 4 |
|---|---|--|--|---|
| 227 27 27 | 28 28 27 27 27 | 22888888888888888888888888888888888888 | 30 30 30 30 30 30 | Score 32 30 30 30 |
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| P25437 escherichia P25437 escherichia P39450 pasteurella P19854 equus cabal P11766 homo sapien P28474 mus musculu O19053 oryctolagus P12711 rattus norv | | brucella brucella brucella brucella brucella brucella gadus mor | mus ratt homo homo myco esch | Description P03729 bacteriopha O19005 cercopithec O14493 homo sapien O99yh90 brachydanio O35054 mus musculu |

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| RESULT 2 CLD4_CERAE ID CLD4_CERAE | 1 wrxxafxg 180 WRASAFTG | Query Match Best Local Similarity Matches 5; Conser | Z TA | This SWISS-PROT ent: between the Swiss the European Bioinfe use by non-profit modified and this seentities requires a or send an email to | SEQUENCE FROM N.A SEQUENCE FROM N.A SEQUENCE FOR COLLSON MEDLINE-83189071; Sanger F., Coulson Nucleotide sequency Mol. Biol. 162 -i- FUNCTION: GENI IN THE MATURE IN THE MATURE -i- CAUTION: IT II | AMBD TAK_LAMBD TAK_LAMBD 03729; 1-JUL-1986 1-JUL-1986 1-APR-1993 AIL AGSEMBL AIL AGSEMBL LTUSES AUTHORNOO ACTETIOPHAG LTUSES AUTHORNOO ACTETIOPHAG ACT | |
| STANDARD; | 8 187 | 91.4%; larity 62.5%; Conservative | AAA96551.1; TJBPKL. R000064; NLPC_P60 7; NLPC_P60; 1. 99 AA; 23011 MW; | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). | MEDLINE-83189071; PubMed-6221115; MEDLINE-83189071; PubMed-6221115; MINICHOSTIAN A.R., Hong G.F., Hill D.F., Petersen G.B.; "Nucleotide sequence of bacteriophage lambda DNA."; J. MOL. Biol. 162:729-773(1982). J. MOL. Biol. 162:729-773(1982). INITIATOR COMPLEX FOR TAIL POLYMERIZATION. IT HAS NOT BEEN FOUND IN THE MATURE PHAGE. IN THE MATURE PHAGE. | reat ast ast | |
| PRT; | | Sco Pre 0; | • | y is copyright. It is present the of Bloinformat rematics Institute. The institutions as long atement is not removed. License agreement (See license@isb-sib.ch). | 221115; Hill tteriophage lan 982) INVOLVED ALL POLYMERIZ. | PRT; 199 A sequence update annotation upda RNA stage; Tail | |
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CLAUDIN-4 (CLOSTRIDIUM PERFRINGENS ENTEROTOXIN RECEPTOR) (CPE-RECEPTOR) (CPE-R).
CLDN4 OR CPETRI OR CPER.
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Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration bottween the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cutilles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-97476271; PubMed-9334247;
Katahira J., Sugiyama H., Inoue N.,
Sugimoto N.;
                                                       Pfam; PF00822; PMP22_Clau
PRINTS; PR01077; CLAUDIN
PROSITE; PS01346; CLAUDIN
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J. Biol. Chem. 272:20
                                                                               MGD: MGI:1313314; Cldn4.
InterPro; IPR0001832; Claudin.
InterPro; IPR000729; pMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
                                                                                                                            EMBL; AB000713; BAA22985.1; -. EMBL; AF087822; AAD09757.1; -.
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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J. Biol. Chem. 272:26652-26658(1997).
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CLAUDIN-3 (CLOSTRIDIUM PERFRINGENS ENTEROTOXIN
RECEPTOR 2) (CPE-R 2).
CLDN3 OR CPETR2.
Mus muscult
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                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                             Paperna T., Peoples R., Wang Y.K., Kaplan P., Francke U.; "Genes for the CPE receptor (CPETR1) and the human homolog (CPETR2) are localized within the Williams-Beuren syndrome Genomics 54:453-459(1998).
                                                                                                                                                                            EMBL; AF087821; AAD09756.1; MGD; MGI:1329044; Cldn3.
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                                                                                                           PRINTS; PRO1077; CLAUDIN.
PROSITE; PSO1346; CLAUDIN; 1.
Tight junction; Transmembrane
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InterPro; IPR000729; PMP22_C
Pfam; PF00822; PMP22_Claudin
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Sciurognathi; Muridae; Murinae; Mus
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Pfam; PF00822; PMP22_Claudin; 1.
PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN; 1.
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InterPro; IPR001832; Claudin.
InterPro; IPR000729; PMP22_Clau
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CLAUDIN-3 (VENTRAL PROSTATE.1 PROTEIN) (RVP1).
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MEDLINE=92130987; PubMed=1723140;
Briehl M.M., Miesfeld R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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Metazoa; Chordata;
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                                                                                                                                                   29 WRVSAFIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M74067; AAA41760.1; -.
                                                                                                                                                                                                                                                 Similarity 62.5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         AA;
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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101
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182
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                                                                                                                                                                                                                                                                      Score 30;
Pred. No.
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G -> S (IN REF. 1).

MISSING (IN REF. 1).

DYV -> TTSERPGARTPHHHHYQPSMYPTRPACSLASETT

PPSRRLQTPRSLLARLEEDRQPGVPFSPVAT (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                      820CC6BFC20D122D CRC64;
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                                                                                                                                                                                                                                                                                               DB 1;
                            AA
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                                                                                                                                                                                                                                                                                               Length 219;
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Best Local :
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                                                        CLDH_HUMAN
P56750;
30-MAY-2000
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20-AUG-2001
                               CLAUDIN-17.
CLDN17.
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000729; PMP22_Claudin. Pfam; PF00822; PMP22_Claudin; 1. PRINTS; PR01077; CLAUDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane proteins as functional receptors in vi
J. Biol. Chem. 272:26652-26658(1997).
-i- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ)
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PRO-
-i- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Katahira J., Sugiyama H., INOUE N., Sugimoto N.;
Sugimoto N.;
"Clostridium perfringens enterotoxin utilizes two structurally "Clostridium perfringens enterotoxin receptors in vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CLAUDIN-3 (CLOSTRIDIUM PERRETINGENS ENTEROTOXIN RECEPTOR 2)
RECEPTOR 2) (CPE-R 2) (VENTRAL PROSTATE.1 PROTEIN HOMOLOG)
CLDN3 OR CPETR2.
    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01346; CLAUDIN; Tight junction; Transmembra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF007189; AAC78277.1; -. EMBL; AB000714; BAA22986.1; -.
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                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97476271; PubMed=9334247;
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39, Last sequence update)
40, Last annotation updat
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Chordata; Craniata; Vertebrata; Euteleostomi;
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62.5%;
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                                                                                                                   PRT;
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                                                         update)
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RA Hattori M., Fujlyama A., Taylor T.D., Watanabe H., Yada T.,

RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,

RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,

RA Menzel U., Delabbr J., Kumpf K., Lehmann R., Patterson D.,

RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,

RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,

RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,

RA Rosenthal A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,

RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,

RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,

RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,

RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,

RA Lehrach H., Reinhardt R., Yaspo M.-L.;

"The DNA sequence of human chromosome 21.";
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Best Local :
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TRANSMEM
SEQUENCE
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PROSITE: PS01346; CLAUDIN: 1.
Tight junction; Transmembrane.
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-I- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ)
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PRO-I- SIMILARITY: BELONGS TO THE CLAUDIN FAMILY.
                                                                                                                                                                                                        GCST_MYCTU STANDARD; PRT; 367 AA GCST_MYCTU STANDARD; PRT; 367 AA G10376; O1-OCT-1996 (Rel. 34, Creuted) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
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InterPro; IPR000729; PMP22_Claudin.
Pfam; PF00822; PMP22_Claudin; 1.
                                                             Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                           GCVT OR RV2211C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ250712; CAB60616.1; -. EMBL; AP001707; BAA95566.1; -.
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   Actinomycetales; Corynebacterineae; NCBI_TaxID-1773;
                                                                                                                                                                            PROBABLE AMINOMETHYLTRANSFERASE (EC
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NCBI_TaxID=9606;
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185 P
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62.5%;
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2.1.2.10)
                                 Mycobacteriaceae;
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                                                                                                                                                                               (GLYCINE CLEAVAGE SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 224;
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__ECOLI STANDARD; PRT; 937 AA
P15484; P15485; P15486; P15487;
01-APR-1990 (Rel. 14, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Cast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnler T., Churcher C., Harris Gordon S.V., Biglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamiin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory Strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002536; GCV_T. pfam; pF001571; GCV_T; 1. Transferase; Aminotransferase; SEQUENCE 367 AA; 38317 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE007072; AAK46553.1; TIGR; MT2267; -. TubercuList; Rv2211c; -.
                                    KDA PROTEIN) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 393:537-544(1998).
   Bacteria; Proteobacteria;
                   Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            263 WRKDAFFG 270
                                                                                                                                                                                                                                                                               1 wrxxafxg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCINE (BY SIMILARITY).

CATALYTIC ACTIVITY: (6S)-TETRAHYDROFOLATE +

CAMINOMETHYLDHYDROLIPOYLPROTEIN = (6R)-5,10-

METHYLENETETRAHYDROFOLATE + NH(3) + DIHYDROLIPOYLPROTEIN.

SUBUNIT: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS:

P, T, L, AND H (BY SIMILARITY).

SIMILARITY: BELONGS TO THE GCVT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z70283; CAA94254.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                   Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                   82.9%;
62.5%;
gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALT_INIT
                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                   Score 29; DB Pred. No. 17; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. 47CD3E1FFE46B321 CRC64;
                                                        PRECURSOR
                                                                                                                                                   Ã.
   Enterobacteriaceae
                                                        (CS3
                                                                                                                                                                                                                                                                                                                                                    Length 367
                                                        PILI SYNTHESIS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris
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OM25.
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Best Local S
Matches 5
STRAIN=63/290;
STRAIN=66239016; PubMed=8675306;
MEDIZINE=96239016; PubMed=8675306;
Cloebkaert A., Verger J.M., Grayon M., Zygmunt M.S., Grepinet O.
"Nucleottide sequence and expression of the gene encoding the maj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90158116; PubMed-2576094;
Jalajakumari M.B., Thomas C.J., Halter R., Manning P.A.;
Jalajakumari M.B., Thomas C.J., Halter R., Manning P.A.;
"Genes for biosynthesis and assembly of CS3 pili of CFA/II
enterotoxigenic Escherichia coll: novel regulation of pilus
production by bypassing an amber codon.";
Mol. Microbiol. 3:1685-1695(1989).

-i-FUNCTION: THIS PROTEIN IS ESSENTIAL FOR THE BIOGENESIS C
MATURE CS3 PILI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
CHAIN
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CHAIN
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                                                                                                                                                                                                                                                                      OM25_BRUOV
Q45335;
                                                                                                                                                                                                                                                                                                        BRUOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                Bacteria; Proteobacteria;
Brucellaceae; Brucella.
                                                                                                                                                                                              OMP25
                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
25 KDA OUTER-MEMBRANE IMMUNOGENIC PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00577; Usher; 1
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NCBI_TaxID=562;
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=236;
                                                                                                                                                                              Brucella ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative initiation.
                                                                                                                                                                                                                                                                                                                                                                  595
                                                                                                                                                                                                                                                                                                                                                                                              1 wrxxafxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS: FIVE PROTEIN ARE PRODUCED BY ALTERIATION. THE FIFTH PROTEIN REQUIRES THE SUPPRESSION OF READTHROUGH OF AN INTERNAL AMBER CODON IN POSITION 754.
SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                  WRGRAFIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X16944; CAA34817.1; -.
X16944; CAA34816.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 62. 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01151;
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317
451
572
937
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753
753
753
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                                                                                                                                                              alpha
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CS3 PILI SYNTHESIS 104 KDA PROTEIN.

CS3 PILI SYNTHESIS 63 KDA PROTEIN.

CS3 PILI SYNTHESIS 48 KDA PROTEIN.

CS3 PILI SYNTHESIS 33 KDA PROTEIN.

CS3 PILI SYNTHESIS 30 KDA PROTEIN.

CS3 PILI SYNTHESIS 20 KDA PROTEIN.

CS3 PILI SYNTHESIS 20 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB Pred. No. 40; 0; Mismatches
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                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                            subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                        201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 937;
                                    Grepinet O.; ding the major
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                           for
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RESULT 13
OM25_BRUAB
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15-DEC-1998
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                                                                                                         use by non-profit institutions as Long to sage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                         de Wergifosse P., Lintermans P., Limet J.N., Cloeckaert A.; "Cloning and nucleotide sequence of the gene coding for the major kilodalton outer membrane protein of Brucella abortus."; J. Bacteriol. 177:1911-1914 (1995).

-i- SUBCELLULAR LOCATION: OUTER MEMBRANE.

-i- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM25_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infect.
                                                                                                                                                            between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01389; OmpA_membrane; Antigen; Outer membrane; Signa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigenic shift, compared with other Brucella species, deletion in the gene."; Infect. Immun. 64:2047-2055(1996).
                           SIGNAL
                                      Antigen;
                                                      Pfam; PF01389; OmpA_membrane;
                                                                                 EMBL;
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  Brucella abortus
                                                                                                                                                                                                                                                                                                                                                                                                               OMP25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q44664;
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                                                                                                                                                                                                                                                                                                 MEDLINE=95204367; PubMed=7896724;
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=235;
                                                                                                                                                                                                                                                                                                                                                                                                                            25 KDA OUTER-MEMBRANE
                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 WKAGAFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 wrxxafxg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: OUTER MEMBRANE. SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY. HAS A C-TERMINAL DELETION COMPARED TO THAT OF OTHER BRUCELLA SPECIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRUAB
                                                                               X79284; CAA55872.1;
                                                                                                        an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                         Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                 IPR000498; OmpA_tmem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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50.0%;
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Last annotation update)
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PROTEIN.
              25 KDA OUTER-MEMBRANE IMMUNOGENIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
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                                                                                                                                                               There are no re
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RESULT 15
0M25_BRUME
ID 0M25_B
AC Q45321
DT 15-DEC
DT 15-DEC
DT 15-DEC
DT 15-DEC
DT 25 KDA
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Best Local
OM25_BRUME STANDARI
Q45321;
15-DEC-1998 (Rel. 37, C
15-DEC-1998 (Rel. 37, I
15-DEC-1998 (Rel. 37, I
25 KDA OUTER-MEMBRANE )
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                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                             Pfam; PF01389; OmpA_membrane; 1.
Antigen; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-i- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
                                                                                                                                                                                                                                                                                                                                       EMBL; U39358; AAB36692.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloeckacrt A., Verger J.M., Grayon M., Zygmunt M.S., Grepinet O. "Nucleotide sequence and expression of the gene encoding the mages the statement of the sequence and expression of Brucella ovis: Evidence 25-kilodalton outer membrane protein of Brucella ovis: Evidence antigenic shift, compared with other Brucella species, due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM25_BRUCA
Q45110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deletion in the gene
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SIGNAL
                                              -1- SUBCELLULAR LOCATION: OUTER MEMBRANE.
-1- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
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"Nucleotide sequence and expression of the gene encoding the major
25-kilodalton outer membrane protein of Brucella ovis: Evidence for
antigenic shift, compared with other Brucella species, due to a
deletion in the gene.";
Infect. Immun. 64:2047-2055(1996).
                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Brucellaceae; Brucella.
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-!- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
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RESULT 19
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ID FADH_PICPA
AC 074685;
DT 20-AUG-2001
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-i- SIMILARITY: BELONGS TO THE ZINC-CONTAINING
FAMILY. CLASS-III SUBRAMILY.
InterPro: IPR002328; ADH_Zinc.
InterPro: IPR002328; ADh_Zinc.
Pfam; PF00107; adh_Zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
PROSITE; PS00059; ADH_ZINC; 1.
CX:dorrductase; Zinc; NAD; Multigene family; Accoxidorrductase; Accoxidorrductase; Accoxidorrductase; Accoxidorrductase; Accoxidorrductase; Accoxid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY
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50.0%;
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HETERODIMER WITH L
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BY FATTY ACIDS (BY SIMILARITY).
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C (CATALYTIC).
C (SECOND ATOM).
C (SECOND ATOM).
C (SECOND ATOM).
C (SECOND ATOM).
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HSSP: P11766; 1TEH.

INTERFO: IPR002328; ADH_zinc.

R InterPro; IPR002085; Adh_zinc.

R InterPro; IPR00205; NAD_binding.

R InterPro; IPR000205; NAD_binding.

R Pfam; PF00107; adh_zinc; 1.

DR PROSITE; PS00059; ADH_ZINC; 1.

DR PROSITE; PS00059; ADH_ZINC; 1.

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Best Local S
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20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
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20-AUG-2001
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"A strong nitrogen source-regulated promoter for controlled expression of foreign genes in the yeast Pichia pastoris.";
Gene 216:93-102(1998).
-!- CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE + NAD(+) = S-FORMYLGLUTATHIONE + NADH.
-!- COPACTOR: REQUIRES ZINC FOR ITS ACTIVITY (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY. CLASS-III SUBFAMILY.
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Eukaryota; Fungi; Ascomy
Saccharomycetales; Sacch
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20-AUG-2001 (Rel. 40,
GLUTATHIONE-DEPENDENT
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Last annotation update)
FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1) (FDH)
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Pred. No. 29;
0; Mismatches
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NC (CATALYTIC) (BY SIMILARITY).
NC (SECOND ATOM) (BY SIMILARITY).
NC (SECOND ATOM) (BY SIMILARITY).
NC (SECOND ATOM) (BY SIMILARITY).
NC (SECOND ATOM) (BY SIMILARITY).
NC (SECOND ATOM) (BY SIMILARITY).
NC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                   380
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Interfo.,
Interpo.,
Interpo.,
Interpo.,
Interpo.,
Pfam. pF00107; adh_zinc; 1.

R PROSITE; PS00059; ADH_ZINC; 1.

W Hypothetical protein; Oxidoreductase; Zinc; NAD.
M Hypothetical protein; Oxidoreductase; Zinc; NAD.
M Hypothetical protein; Oxidoreductase; Zinc; NAD.
FT METAL 50 50 ZINC (CATALYTIC) (BY
FT METAL 102 102 ZINC (SECOND ATOM) (F
FT METAL 105 105 ZINC (SECOND ATOM) (F
METAL 108 108 ZINC (SECOND ATOM) (F
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1: CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE + NAD(+) = S-FORMYLGLUTATHIONE + NADH.

5: FORMYLGLUTATHIONE + NADH.

1: COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
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Q1-MAR-2001 (TrEMBLrel. 17, La:
Q1-JUN-2001 (TrEMBLrel. 17, La:
PUTATIVE ENOYL-COA HYDRATASE.
2SCK31.11C.
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cr
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and pl
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL512667; CAC21620.1; -
Interpro; IPR001753; Enoyl_CoA_hydrtse.
Pfam; PF00378; ECH; I.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.
SEQUENCE 266 AA; 28121 MW; C07F9346B82E0451 CRC64;
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Cerdeno A.M., Parkhill J., F
Submitted (JAN-2001) to the
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Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
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e EMBL/GenBank/DDBJ databases.
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  SEQUENCE FROM N.A. TISSUE-QORSAL LIP;
                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
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MEDIJINE-94172631; PubMed-8126723;

MedDring-94172631; PubMed-8126723;

Pedre X., Weise F., Chai S., Lueder G., Alonso J.C.;

"Analysis of cis and trans acting elements required for the initiation of DNA replication in the Bacillus subtilis bacteriophage SPP1.";

Mol. Biol. 236:1324-1340(1994).
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Alonso J.C., Luder G.,
Submitted (JAN-1998) t
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Viruses; dsDNA viruses,
Lambda phage group.
NCBI_TaxID=10724;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
REQUIRED FOR REPLICATION INITIATION.
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PF00436; SSB; 1.
NCE 159 AA; 17088
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Pipidae;
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Q98SR2;
Q1-JUN-2001
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Q9S2V4;
01-MAY-2000
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CLDN3.
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InterPro; IPR001729; PMP22_Claudin.
Pfam; Pf00822; PMP22_Claudin; 1.
PRINTS; PR01077; CLAUDIN.
PROSITE; PS01346; CLAUDIN. UNKNOWN_1.
PROSITE; PS01346; CLAUDIN. UNKNOWN_1.
SEQUENCE 214 AA; 23151 MW; 3F0D65E3ADE311E6 CRC64;
       STRAIN=A3(2);
Saunders D.C., Harris
Submitted (AUG-1999) t
                                                                                          Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                          Reardon E., Kojima S., Rizzolo L.J.;
"Sequence of chick claudin-3 cDNA.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF334677; AAK20876.1; -.
SEQUENCE 214 AA; 23090 MW; A2540116CBD53978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                        NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brizuela B.J., Wessely O., De Robertis E.M.;
"Overexpression of Xenopus Claudin Tight Junction Protein Affects
Adhesion and Causes Randomization of the Left-Right Body Axis.";
                                           SEQUENCE FROM N.A.
                                                                              Actinomycetales; Streptomycineae;
                                                                                                                    SC4A10.35C
                                                                                                                               PUTATIVE MEMBRANE PROTEIN.
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EMBL: AF224712; AAG44257.1; -.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redenbach M., Kleser H.M., Denapalte D., Elchner A., Cullum J., Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL109663; CAB52011.1;

SEQUENCE 330 AA; 35177 MW; DB21004753E11700 CRC64;
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SEQUENCE
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Jumes K.D., Parkhill J.,
Submitted (AUG-1999) to
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                                                                                                                                                                                                                                                                                     --- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY)
--- SIMILARITY: TO THE ZINC CONTAINING ALCOHOL DEHYDROGENASE
EMBL; AE004783; AA607017.1; --
INTERPRO; IPR0022085; Adh_zinc.
InterPro; IPR0022085; Adh_zinc.
InterPro; IPR002328; Adh_zinc.
Pfam; PF00107; adh_zinc.
1.

PROSITE; PS00059; ADH_ZINC; 1.
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Bacteria; Proteobacteria;
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370 AA; 39208 MW; 5B48DC94FB45DE10 CRC64;
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the EMBL/GenBank/DDBJ databases
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III.
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"Molecular characterization of genes of Pseudomonas sp. strain HR195
involved in bioconversion of vanillin to protocatechuate.";

J. Bacteriol. 179:2595-2607(1997).

-i- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).

-i- SIMILARITY: TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY.
EMBL, AJ243941; CAB64351.1;
-HSSP; P11766; ITEH.
InterPro; IPR002328; ADH_zinc.
InterPro; IPR002328; ADH_zinc.
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE FORMALDEHYDE DEHYDROGENASE (GLUTATHIONE-DEPENDENT).
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                                                                 enterotoxigenic Escherichia coli: novel
by bypassing an amber codon.";
Mol. Microbiol. 3:1685-1695(1989).
EMBL; X16944; CAA34819.1;
InterPro: IPRO00015; Fimb_usher.
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PROSITE; PS00059; ADH_ZINC; 1.
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       SEQUENCE
                                                                                                                                                                                                                                             Jalajakumari M.B., Thomas C.J., Halter R., "Genes for biosynthesis and assembly of CS:
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Jalajakumari M.B., Thomas C.J., Halter R., Manning P.A.;
Jalajakumari M.B., Thomas C.J., Halter R., Manning P.A.;
"Genes for biosynthesis and assembly of CS3 pili of CFA/II
enterotoxigenic Escherichia coli: novel regulation of pilus
by bypassing an amber codon.";
Mol. Microbiol. 3:1685-1695(1989).
EMBL; X16944; CAA34818.1; -.
InterPro; IPR000015; Fimb_usher.
Pfam; PF00577; Usher; 1
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Best Local :
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09QQN6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE APHID TRANSMISSION FACTOR (FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
  Moonan F.,
"Sugarcane
                                                                                                                                  Unassigned Luteoviridae
NCBI_TaxID=94290;
                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                     sugarcane yellow leaf virus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
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SEQUENCE 206
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EMBL; AE002085; AAF12100.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20036896;
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NCBI_TaxID=1299;
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InterPro; IPR000051; SAM_bind.
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Molina J.J., Mirkov T.E.; yellow leaf virus is a new virus with a
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06 AA; 22186 MW; 6F63E1369E12D870 CRC64;
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STRAIN:CV. CP65-357;

STRAIN:CV. CP65-357;

MEDLINE-20318675; PubMed::10859394;

MEDLINE-20318675; PubMed::10859394;

MEDLINE-20318675; PubMed::10859394;

MITCHARD BOTG Z., Lockhart B.E.L., Braithwaite K

Smith G.R., Borg Z., Lockhart B.E.L., Braithwaite K

Smith G.R., Borg Z., Lockhart B.E.L., Braithwaite K

Sugarcanc yellow leaf virus: a novel member of the

Probably arose by inter-species recombination.";

J. Gen. Virol. 81:1865-1869(2000).

EMBL, AJ249447; CAB75437.1; ".

InterPro; IPR000893; Luteo_ORF6.

InterPro; IPR002929; PLRV_ORF5.

InterPro; IPR002929; PLRV_ORF5.

InterPro; IPR002929; PLRV_ORF5.

R PINTS; PRO0910; LVIRUSORF6.

R PRINTS; PRO1217; PRICHENTENSN.
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Best Local Similarity
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AR157029; AAA45687.1; -.
InterPro; IPR000893; Luteo_ORF6.
InterPro; IPR002929; PLRV_ORF5.
InterPro; IPR002929; PLRV_ORF5.
InterPro; IPR002965; P_rich_extensn.
Pfam: PF001690; PLRV_ORF5; 1.
PRINTS; PR00910; LVIRUSORF6.
PRINTS; PR01217; PRICHEXTENSN.
Q9BRR6; ...
Q9BRR6; ...
Q1-JUN-2001
Q1-JUN-2001
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09JH75;
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Viruses; ssRNA positive-strand viruses,
Unassigned Luteoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrembLrel. 15, Last sequence update) 01-JUN-2001 (TrembLrel. 17, Last annotation update) PUTATIVE APHID TRANSMISSION FACTOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-94290;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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(TremBLrel. 17, (TremBLrel. 17,
                                                                                                                                                                                                                                                         Conservative
                                                              PRELIMINARY;
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Pred. No. 2.3e+02;
1; Mismatches 3
  Created)
Last sequence update)
                                                                                                                                                                                                                                                         Score 28; DB 12;
pred. No. 2.3e+02;
1; Mismatches 3;
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PRELIMINARY; PRT; 530 AA.
004892;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOCHROME P450 LIKE_TBP (EC 1.14.14.1).
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TISSUE-KIDNEY ADENOCARCINOMA;
Strausberg R.;
Submitted (APR-2001) to the F
Submitted (APR-2001) AAH05112.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last annotation update) SIMILAR TO RIKEN CDNA 2610017G09 GENE.
                                                                    Q9BUQ2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SELENOPHOSPHATE SYNTHETASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRIGHT YELLOW 2;
MEDLINE-96404975; PubMed-8809115;
Sugiura M., Sakaki T., Yabusaki Y., Ohkawa H.;
"Cloning and expression in Escherichia coli and Saccharomyces
"Cloning and expression in Escherichia coli and Saccharomyces
cerevisiae of a novel tobacco cytochrome P-450-like cDNA.";
Biochim. Biophys. Acta 1308:231-240(1996).

EMBL; D64052; BAA10929.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                  Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase.
SEQUENCE 530 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTBP.
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                                                                                                                                                            Q9BUQ2
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mendel; 23988; Nicta; 3078; 23988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                   254 WRPDAFVG 261
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BC006112; AAH06112.1; -.
NCE 497 AA; 54088 MW; B758E977CDA88F8F CRC64;
                                                                                                                                                                                                                                                                                                                      Similarity
5; Conserv
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                      Primates; Catarrhini;
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                                   Chordata; Craniata; Vertebrata;
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Pred. No. 2.6e
0; Mismatches
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No.
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2.6e+02;
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                        Hominidae;
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Best Local
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Q9EYE4;
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NON_TER
SEQUENCE
                         STRAIN=0157:H7;
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Q30824;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MHC CLASS I ANTIGEN (FRAGMENT).
PubMed=11111050;
                                                                                                               Escherichia
                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                      Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (FEB-2001) to the
EMBL; BC002381; AAH02381.1;
SEQUENCE 59 AA; 5897 MW;
                                                                                    NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mazon L.I., Estomba A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
EMBL; U26008; AAA67310.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-LATXA BREED; TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001039; MHC_I.
Pfam; PF00129; MHC_I; 1.
ProDom; PD000050; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vicario A., Jugo B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     56 WRASAWSG
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nes 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 wrxxafxg 8
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Pred. No.
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EMBL; AP000400; BAB19565.1; -.

InterPro; IPR000555; Mov34.

InterPro; IPR000064; NLPC_P60.

Pfam; PP00877; NLPC_P60; 1.

SMART; SM00232; JAB_MPN; 1.

SEQUENCE 247 AA; 28045 MW; 1
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MEDLINE-97046307; PubMed-8891129;

Kuemmerle N., Feucht H., Kaulfers P.M.;

"Plasmid-mediated formaldehyde resistance in Escherichia col
characterization of resistance gene.";

Antimicrob. Agents Chemother. 40:2276-2279(1996).

-i-CATALYTIC ACTIVITY: FORMALDEHYDE + GLUTATHIONE + NAD(+)
FORMYLGUUTATHIONE + NADH.
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002328; ADH_zinc. Pfam; PF00107; adh_zinc; 1. PROSITE; PS00059; ADH_ZINC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
-:- SIMILARITY: TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY.
EMBL; X7835; CAA52057.1; -.
HSSP; P11766; 1TEH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           059399 PRELIMINARY; PRT; 369 AA. 059399; Ol-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) FORMALDEHYDE DEMYDROGENASE (EC 1.2.1.1) (FORMALDEHYDE (GLUTATHIONE)) (FORMIC DEHYDROGENASE).
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                      309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002085; Adh_zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yokoyama K., Makino K., Kubota Y., Watanabe M., Kimura S.,
Yutsudo C.H., Kurokawa K., Ishii K., Hattori M., Tatsuno I
Yoh M., Iida T., Ohnishi M., Hayashi T., Yasunaga T., Hond
Sasakawa C., Shinagawa H.;
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Pred. No. 3e+02;
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Pred. No.
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DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 17, Last annotation update)
DT 01-JUN-2001 (TrEMBLE) 17, Last annotation update)
DT 01-JUN-2001 (TREMBLE) 17, Last annotation update)
DT 01-JUN-2001 (TREMBLE) 17, Last annotation update)
DT 01-JUN-2001 (TREMBLE) 17, Last annotation update)
DT 01-JUN-2001 (TREMBLE) 17, Last annotation update)
DE GLUTAHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1).
GN AND ABORDE DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1).
RN (11] TaxID-1164;
RN (11] TaxID-1164;
RN (11] TaxID-1164;
RN (12] TaxID-1164;
RN (13] Submitted (FEB-1978) to the EMBL/GenBank/DDBJ databases.
CC (-1- SIMILARITY: TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY.
CC (-1- SIMILARITY: TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY.
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CONTAINED THE CONTAINING ALCOHOL DEHYDROGENASE FAMILY.
CC (-1- SIMILARITY: TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE FAMILY.
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/SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*

/SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*

/SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:*

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ALIGNMENTS

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RESULT
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Claudin-3 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer; graft rejection.
                                      03-NOV-1998;
30-MAR-1999;
                                                                                                                                                                Claudin-3 cell adhesion recognition sequence SEQ ID
        Blaschuck OW,
                       (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                03-NOV-1999;
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The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-3 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery
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                                                                                                                   The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-4 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery
                                                                                    Sequence
                                                                                                                                                                                                        Claim 58; Page 100; 121pp; English.
                                                                                                                                                                                                                                       Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous sys
                                                                                                                                                                                                                                                                                                                                         03-NOV-1998;
30-MAR-1999;
                                                                                                        to the desired target site.
                                                                                                                                                                                                                               and across the skin -
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99US-0282029
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         Claudin-3 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer; graft rejection; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin - {\sf vasopermiss}
                                                          Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO:
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                                                                                    28-SEP-2000
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The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-3 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases,
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    Claudin-4 modulating
                           Claudin-4 cyclic cell adhesion recognition sequence SEQ ID NO: 172.
                                                                                                         AAB06654 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-4 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
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                                03-NOV-1998;
30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAR sequence; aut graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claudin-4 modulating agent; cell adhesion recognition sequence; CAR sequence; autoimmune disease; inflammatory disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claudin-4 cyclic cell adhesion recognition sequence
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The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-4 group of proteins are cadherins,
                                                                                                                                                            Claim 61; Page 101; 121pp; English.
                                                                                                                                                                                                                                                             Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous systand across the skin -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}
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                                       The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-4 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases, inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
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Query Match Best Local S Matches

Similarity 5; Conserv

Conservative

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Indels

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Score 30; DB Pred. No. 3; 0; Mismatches

DB 21;

Length 10;

85.7%; 62.5%;

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RESULT 1
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ID AAW8
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XX AABC
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Thehes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the use of peptides as claudin-mediated cell adhesion modulators. The claudin-4 group of proteins are cadherins, which are membrane glycoproteins involved in cell adhesion. In some situations, cell adhesion occurs at abnormal levels, and these peptides can be used to modulate these levels, and thus treat autoimmune diseases. Inflammatory diseases and cancer, and aid wound healing and implant adhesion. In addition, they can also be used to facilitate drug delivery to the desired target site. The present sequence has a cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody modulation of claudin-mediated cell adhesion for increasing vasopermiability, for delivering drugs to tumors and the nervous system and across the skin - {\sf constant}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-NOV-1998;
30-MAR-1999;
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                       01-MAR-1999
                                                                             AAW88629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 61; Page 101; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blaschuck OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-NOV-1999;
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                                                                                                                             AAW88629 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                          (first entry)
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99US-0282029
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                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                               85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell adhesion recognition sequence;
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzhelmer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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Secreted protein encoded

by gene

96 clone HRDFB85

06-JUN-1997 06-JUN-1997 06-JUN-1997 06-JUN-1997 06-JUN-1997 06-JUN-1997 06-JUN-1997 06-JUN-1997 06-JUN-1997 06-JUN-1997 05-SEP-1997 06-JUN-1997 05-SEP-1997 18-DEC-1997;
06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
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06-JUN-1997;
06-JUN-1997; 04-JUN-1998; 10-DEC-1998 W09854963-A2 Homo sapiens 970S-0057765. 970S-0057771. 970S-0057776. 970S-0048876. 970S-0048880. 970S-0048883. 970S-0048893. 970S-0057642. 970S-0057648. 970S-00576548. 970S-0057651. 970S-0057662. 970S-0057668. 970S-0057762. 97US-0048885 97US-0048894 97US-0048897 97US-004890 97US-0048916 97US-0048962 97US-0048970 97US-0057647. 97US-0057650. 97US-0057667. 97US-0057667. 97US-0057761. 97US-00577764. 97US-0057770. 97US-0057775. 97US-0048875. 97US-0048878. 97US-0048882. 97US-0048964. 97US-0048972. 97US-0049020. 97US-0049375. 97US-0057584 97US-0057629 97US-0048974 97US-0049373 97US-0057778 97US-0057635 97US-0057644 97us-0057628 97US-0048915 97US-0048949 97US-0048899 97US-0048896 97US-0048884 97US-0048893 97US-0070923 97US-0048881. 98WO-US11422

06-JUN-1997; 06-JUN-1997;

s-0048901 s-0048917

-0048898

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Вþ
                                    δÃ
                                                                                                                                                                             CC The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
CC encoding human secreted proteins (AAW88534 to AAW88756). The secreted control gene sequences are deposited with the ATCC under deposit numbers are deposited with the ATCC under deposit numbers are deposited with the ATCC under deposit numbers are deposited with the ATCC under deposit numbers are deposited with the ATCC under deposit numbers are deposited with the ATCC under deposit numbers are deposited and an are described acid are deposited and are used for the recombinant production of the secreted are used for the recombinant production of the secreted are used for the recombinant production of the secreted are useful for are used for the recombinant production of the secreted are useful for are useful for are useful for are useful for are useful for are useful for are useful for are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also as a product of the polynucleotides in a sample are described for each of the new polypeptides in a sample are described for each of the polynucleotides, based on an are described for each of the polynucleotides, based on a products for the diagnosis or treatment of cancer, neurodegenerative accombination and the polynucleotides are also developmental abnormalities and foetal deficiencies, blood alsorders, tumours, leukemias, diseases of the immune system, autoimmune accombination and accombination and accombination are therefore.

CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, archeres are also useful for identifying their binding narrhers.

CC colvered are also useful for identifying their binding narrhers.
                                                                          Matches
                                                                                               Query Match
Best Local
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05-SEP-1997;
05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA; Fan P, Feng P, Ferrie AM, Fischer CL, Florence C; Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW; Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM; Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 533; 772pp; English.
                                                                                                                                                                                                              polypeptides are also useful for identifying their binding partners. The present sequence represents human secreted protein (see descript line for gene number and clone identification).
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05-SEP-1997;
                                                                                                                                                                           Sequence
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                                                                              Local Similarity
nes 5; Conserv
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Wrytafig 29
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97US-0057769.
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97US-00577777.
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97US-0057760
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97US-0057654
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97US-0057627
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97US-0049374.
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s-0048971
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62.5%;
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                                                                                               Score 30;
Pred. No.
                                                                              Mismatches
                                                                                               DB 49;
                                                                                                                   20;
                                                                                                                   Length 202;
                                                                              Indels
                                                                            0;
                                                                                                                                                                                                                                    descriptor
                                                                            Gaps
                                                                            0;
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CC human secreted proteins AAB52012 - AAC95570 represent cDNA encoding 50 CC human secreted proteins AAB52012 - AAB52161. Sequences AAB52062 - CC AAB52103 represent alternative polypeptides encoded by the genes, and CC amino acid sequences with which they share homology. The genes and CC proteins have activities dependent on the tissues and cells in which they immunosuppressive, nootropic; neutroprotective; antiviral; antiallergic; cc immunosuppressive; nootropic; natiinflammatory; antiulcer; vulnerary; cc anticonvulsant; antibacterial; antiinflammatory; antiulcer; vulnerary; cc anticonvulsant; antibacterial; antifungal; antiparasitic; and cardiant. CC The secreted proteins, polypeptides, antagonists and agonists and because and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital. Immune disorders such as Addison's disease, colitergies, autoimmune haemolytic anemia, autoimmune thyroiditis, cc diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid cc arthritis and ulcerative colitis; cardiovascular disorders such as coretial, fungal and parasitic infectious diseases such as creebral anoxia and epilepsy; and infectious diseases such as creebral anoxia and epilepsy; and infectious diseases such as viral, bacterial, fungal and parasitic infections may also be treated using the created and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC95520 and AAC
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AAB52100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-1999; 99US-0128703.
20-JAN-2000; 2000US-0176068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; cancer; immune disease; allergy;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 83; 505pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-611865/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM, Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2000; 2000WO-US08983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 48 human secreted protein homologous amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB52100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB52100 standard; Protein;
                                                                                                      the proteins and polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200061596-A1
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208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #149
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Query Match
Best Local Similarity
Thehas 5; Conserve

Conservative

85.7%;

Score 30; DB Pred. No. 51; Mismatches

DB 21;

Length 208; Indels

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Gaps

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RESULT 1
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                                                                                                        antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinfiammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1999;
02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiAnflammatory; antiviral; antibacterial; antiungal; antiIneumatic; antiAnflammatory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; sollergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant
hypertension, erythematosus,
                                 nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthitis, graft vs host disease, cardiovascular disease, diabetes mellitus,
                                                                                                                                                                                                                                                            AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ORFX ORF2897 polypeptide sequence SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB43133;
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                                                                                                                                                                                                                                                                                                                                                                            neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                       11; Page 4961; 5507pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0540763
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                   hypothyroidism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0127607.
99US-0127636.
99US-0127728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209
                                                                                                                                                                                                                                                                                                                                         English.
cholesterol ester d immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO:5794
storage, (SCID), P
systemic lupus
AIDS, viral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiant;
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(KIM) protein. KIM proteins can be administered therapeutically considered the promote growth and/or compressing KIM encoding polynucleotides, to promote growth and/or compressing KIM encoding polynucleotides, to promote growth and/or compressing KIM encoding polynucleotides, to promote growth and/or compressing KIM encoding polynucleotides. Since the KIM proteins can also be used therapeutically, e.g. these or the KIM proteins may be included with an companient of conditions associated with disfunction/disregulation of comphylaxis of conditions associated with disfunction/disregulation of comphylaxis of conditions associated with disfunction/disregulation of comphylaxis of conditions associated with disfunction/disregulation of compositions, especially renal diseases or impairments of renal compositions in humans (e.g. acute renal failure, acute nephritis). The collinaries of internalised into cells, can disrupt expression of a cellular KIM gene, compositions. The proteins and polynucleotides are consected in the proteins and polynucleotides are useful diagnostically e.g. to block the growth of tumours dependent on compositions. The proteins and polynucleotides are consected in the proteins and polynucleotides are useful diagnostically e.g. to detect and quantify renal injury/disease consected in the consecution of the proteins and polynucleotides are consecutive of increased risk, or presence of, renal injury or impaired consecution), or abnormal responses to tissue injury (indicative of
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial or fungal infection, malaria, autoimmune disorders, as allergies, aplastic anaemia, burns, wounds, bone and cartilage concturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour.
                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 46-47; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth and regeneration, especially to treat renal conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAY-1997;
23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kidney injury associated molecule; kidney injury related molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kidney injury associated molecule HW014 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW86307 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                        present sequence represents a kidney injury associated mole present KIM proteins can be administered therapeutically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-045312/04
DB; AAV80582.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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97US-0047490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sanicola-Nadel M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders, asthma,
                                                                                                                                                                                                                                                                                                                                            molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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999999888
                                           CC cancer-associated nucleic acid molecules (N) and proteins (P), where cc the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene cc therapy and vaccine production. N and P may be used in the prevention, cc diagnosis and treatment of diseases associated with inappropriate P cc expression. For example, N and P may be used to treat disorders cc in a patient's genome that affect the activity of by expressing cc inactive proteins or to supplement the patients own production of P. additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell cto express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB37789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      increased risk, or presence of, an autoimmune response or abnormal tissue growth arising from/affecting renal tissue). The proteins can also be used to locate KIM producing cells (especially specific loci, e.g. tissue masses abnormally producing/expressing KIM such as tumours arising from/affecting renal tissue), by contacting cells with an
                  N.B. Pages
                                   present invention.
                                                                                                                                                                                                                                                                                                         Claim 11; Page 7681; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-235357/24.
N-PSDB; AAH34872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-1999;
03-NOV-1999;
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 666\ to\ 682 and page 7053\ of\ the\ sequence\ listing\ were\ time\ of\ publication,\ meaning\ no\ sequences\ are\ present
                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tight junction-constituting membrane protein clodin family - useful in the medical field % \left( 1\right) =\left( 1\right) +\left(                                                                                                                                                                                                                                                                                                                                                            Sequence
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Query Match
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| 50 | 4.0 | 47 | 46 | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 8 | 37 | 36 | 35 | 34 | ယ | 32 | 31 | 30 | 29 | 28 |
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| 255 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 |
| 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | 71.4 | | | | | 74.3 | | | | | 74.3 | 74.3 |
| 455 455 | 455 | 455 | 455 | 455 | 455 | 283 | 164 | 164 | 159 | 58 | 58 | 58 | 1205 | 1205 | 1196 | 1196 | 1000 | 1000 | 991 | 991 | 829 |
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| US-08-457-335A-18 US-08-729-214-18 | -08-458 | US-08-457-646A-18 | US-08-457-342-18 | US-08-456-837-18 | US-08-258-261B-18 | US-08-807-151-1 | US-09-352-619-1 | US-08-911-319A-1 | US-09-518-046-24 | PCT-US96-03180-43 | US-08-985-499-43 | US-08-405-647B-43 | US-09-352-168-29 | US-09-352-159-29 | US-09-352-168-31 | US-09-352-159-31 | US-09-352-168-25 | US-09-352-159-25 | US-09-352-168-27 | US-09-352-159-27 | US-09-352-168-33 |
| Sequence 18, Appl | 18, | Sequence 18, Appl | ` | Sequence 18, Appl | Sequence 18, Appl | Sequence 1, Appli | | Seguence 1, Appli | Sequence 24, Appl | Sequence 43, Appl | Sequence 43, Appl | Sequence 43, Appl | Sequence 29, Appl | Sequence 29, Appl | Sequence 31, Appl | Sequence 31, Appl | Sequence 25, Appl | • | Sequence 27, Appl | • | • |

ALIGNMENT

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; MOLECULE TYPE: US-08-608-241-2
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US-08-608-241-2
                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION UNBER: 27,386
REFERENCE/DOCKET NUMBER: 9602:
TELEPHONE: 608-251-5000
TELEPHONE: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATENT NO. J.....
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08608241 Patent No. 5747328
                                                                                                                                                                                                                                                                                                                                                                ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                   TYPE: ami
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1 Sout
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Quarles & Brady STREET: 1 South Pinckney Street
                                                                       LENGTH:
                                     : 376 amino acids
amino acid
GY: linear
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Similarity

77.18; 50.08;

Score Pred.

27; No.

DB 1; 1.2e+02;

Length 376;

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US-08-919-953-2
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Best Local Similarity
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                                                                                                          Sequence 2, Application US/08919953
Patent No. 5837481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Applic
Patent No. 5834300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
             GENERAL INFORMATION:
APPLICANT: Donohue, Timothy J
APPLICANT: Barber, Robert D
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
TITLE OF INVENTION: SENSING AND REMEDIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                             316 WKGSAFGG 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/922,182 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
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VENTION: MICROBIAL SYSTEM FOR FORMALDEHYDE
                                                                                                                                                                                                                                                                            Conservative
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Barber, Robert D
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 SENSING AND REMEDIATION
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pred. No. 1.2e+02;
1; Mismatches 3; Indels
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; TYPE: PRT; ORGANISM: Rhodobacter sphaeroides US-09-192-983-2
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Best Local Similarity
Thes 4; Conserve
                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
 Matches
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09192983A Patent No. 6242244
                                                                                                                                                                                                                                                                                                               APPLICANT: Donohue, Timothy
APPLICANT: Barber, Robert
APPLICANT: Witthuhn, Vernon
TITLE OF INVENTION: Microbial System for Formaldehyde Sensing and
TITLE OF INVENTION: Remediation
FILE REFERENCE: 960296,95505
                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/192,983A CURRENT FILING DATE: 1998-11-16 EARLIER APPLICATION NUMBER: 08/919,953 EARLIER FILING DATE: 1997-08-29 EARLIER FILING DATE: 1997-08-29 EARLIER APPLICATION NUMBER: 08/608,241 EARLIER FILING DATE: 1996-02-28 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                         ENGTH: 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/608,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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1 South Pinckney Street
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 Conservative
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                77.1%;
50.0%;
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50.0%;
Score 27; DB 4; Le
Pred. No. 1.2e+02;
1; Mismatches 3;
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1.2e+02;
3;
                                Length 376;
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 Gaps
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; LENGTH: 462
; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-159-8
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US-09-352-159-8
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                                                                                                                                                                                                                                                                 APPLICANT: Duvick, Jonathan P.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Haddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 74.3%;
Best Local Similarity 50.0%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 6 LENGTH: 462
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                                                                    Query Match
Best Local Similarity
Matches 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICANT: Maddox, Joyce R.
APPLICANT: Maddox, Joyce R.
APPLICANT: Maddox, Joyce R.
APPLICANT: Maddox, Joyce R.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
NUMBER OF SEQ ID NOS: 46
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1 wrxxafxg 8
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                                                                       4; Conservative
                                                                    74.3%; Score 26; DB 4;
50.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 4
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TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-168-6
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                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Exophiala spinifera
US-09-352-168-8
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APPLICANT: Crasta, Oswald R.
APPLICANT: Duvick, Jonathan P.
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 462
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Best Local Similarity 50.0
Matches 4; Conservative
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APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 607/092,936
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
                                                                              Matches
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            APPLICANT: Crasta, Oswald R.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1998-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09352168A Patent No. 6211435
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                                                                                               Score 26; DB 4;
Pred. No. 2.4e+02;

 Mismatches

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Pred. No. 2.
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Sequence 11, Application US/09352168A
Patent No. 6211435
GENERAL INFORMATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Folkerts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Pol
FILE REFERENCE: 0875
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                                                                                                                                                                       ; OTHER INFORMATION: ; OTHER INFORMATION: US-09-352-168-11
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Best Local Similarity
Thes 4; Conserv
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US-09-352-168-11
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; TYPE: PRT
; ORGANISM: Exophiala
US-09-352-159-11
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                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/352,168A CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 463
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APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
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                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Exophiala spinifera
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311 WREQGFSG 318
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                                                                            Conservative
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Pred. No. 2.4e+02;
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Pred. No. 2.4e+02;
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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; OTHER INFORMATION: K:trapao translational fusion with barley alpha
; OTHER INFORMATION: amylase signal sequence, for expression and
; OTHER INFORMATION: secretion of the mature trapao in maize.
US-09-352-168-21
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Best Local Similarity
"hes 4; Conserva
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; LOCATION: (1)...(24)
US-09-352-159-21
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Query Match
Best Local Similarity
Matches 4; Conserv
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Folkerts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/352,168A CURRENT FILING DATE: 1999-07-12 EARLIER APPLICATION NUMBER: 60/092,936 EARLIER FILING DATE: 1998-07-25
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TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Crasta, Oswald R. APPLICANT: Duvick, Jonathan P.
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EARLIER FILING DATE: 1998-07-25
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
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APPLICANT: Maddox, Joyce R.
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TYPE: PRT
                                                                                                                                                                                                                                                 ORGANISM: Unknown
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Conservative
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                   74.3%;
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50.0%;
Score 26; DB 4;
Pred. No. 2.6e+02;
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Pred. No. 2.
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Indels
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335 WREQGFSG 342

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APPLICANT: Cristin, Oswald R.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Divick, Jonathan P.
APPLICANT: Folkerts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Oscillation Polyol Amine Oxidase
TITLE OF INVENTION: Mimber: US/09/352,168A
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/092,936
SEARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 554
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Best Local Similarity
Thehes 4; Conserve
; NAME/KEY: SIGNAL ; LOCATION: (1)...(89) ; OTHER INFORMATION: yeast alpha mating factor secretion signal. US-09-352-168-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: SIGNAL ; LOCATION: (1)...(89) US-09-352-159-17
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EARLIER FILING DATE: 199-05-21
NUMBER OF SEO ID NOS: 46
SOFTWARE: FASTSEO for Windows Version 3.0
SEO ID NO 17
LENGTH: 554
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09352168A Patent No. 6211435 GENERAL INFORMATION:
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
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CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
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                                                                                                                 TYPE: PRT
ORGANISM: Exophiala spinifera
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Pred. No. 2.
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Query Match Best Local Similarity

74.3%; 50.0%;

Score 26; Pred. No.

DB 4; 3.1e+02;

Length 591;

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; ORGANISM: Rhinocladiella atrovirens US-09-352-159-46
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                                      NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 46
LENGTH: 591
TYPE: PRT
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SEQ ID NO 44
LENGTH: 591
TYPE: PRT
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Best Local Similarity 50.0
Matches 4; Conservative
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APPLICANT: Duvick, Jonathan P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44, Application US/09352159A Patent No. 6211434
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Matches 4; Conservative
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                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/352,159A CURRENT FILING DATE: 1999-07-12 EARLIER APPLICATION NUMBER: 60/092,936 EARLIER FILING DATE: 1998-07-25 EARLIER APPLICATION NUMBER: 60/135,391 EARLIER FILING DATE: 1999-05-21
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TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1998-07-21
EARLIER FILING DATE: 1998-07-21
NUMBER: 07-25
EARLIER FILING DATE: 1999-05-21
NUMBER: 07-25
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NUMBER: 07-25
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TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
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EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 40
LENGTH: 598
TYPE: PRT
ORGANISM: Exophiala spinifera
                                                                                                                                                                                                  APPLICANT: DUVICK, Jonathan P.
APPLICANT: MINISTER STATEMENT OF THE REFERENCE: 1134
FILE OF INVENTION: Amino Polyol Amine Oxidase
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/035,391
EARLIER APPLICATION NUMBER: 60/135,391
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; Sequence 42, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
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Matches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 42
LENGTH: 598
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Query Match.
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                                                     TYPE: PRT
ORGANISM: Rhinocladiella atrovirens
-09-352-159-42
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LOCATION: (216)...(216)
OTHER INFORMATION: Xaa = Any Amino Acid
-09-352-159-40
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APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
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Query Match
Best Local Similarity
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LENGTH: 600
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LENGTH: 600
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Patent No. 6211434
                Query Match
Best Local Similarity
Matches
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TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
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TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
EARLIER FILING DATE: 1998-07-25
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
NUMBER: OSEO ID NOS: 46
COLUMBER: OSEO ID NOS: 46
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EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
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                                                                                                                                     TYPE: PRT
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ALIGNMENTS

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dnaZX-like protein - Bacillus subtilis (fragment)
C:Species: Bacillus subtilis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: 140469
R;Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.
Mol. Gen. Genet. 215, 478-482, 1989
A;Fittle: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.
A;Reference number: 140469; MUID:89218958
A;Accession: 140469
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-5 <RES
A;Cross-references: EMBL:X14796; NID:g40130; PIDN:CAA32902.1; PID:g4376204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phenol 2-monooxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (frag C;Species: Pseudomonas sp. C;Accession: A37832 | #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993 | C;Accession: A37832 | R;Powlowski, J.; Shingler, V. J. Bacteriol. 172, 6834-6840, 1990 | A;Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydro A;Accession: A37832 | MUID:91072231 | A;Accession: A37832 | A37832; MUID:91072231 | A;Status: preliminary A;Molecule type: protein A;Residues: 1-4 <POWP C;Keywords: oxidoreductase
C;Genetics:
A;Start codon: GTG
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Query Match Best Local Similarity

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Length

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hypothalamic heptapeptide - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_chan
C:Accession: A01417
R:Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy
Horm. Metab. Res. 13, 228-232, 1981
A;Title: Isolation, structure and synthesis of a heptapeptide
A;Reference number: A01417; MUID:81213980
A;Accession: A01417
A;Molecule type: protein
A;Residues: 1-7 <CHA>
C:Superfamily: hypothalamic heptapeptide
C;Keywords: hypothalamic heptapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                           fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 22-Jan-1993 *sequence_revision 22-Jan-1993 *text_change 26-May-2000
C;Accession: A60139
C;Accession: A60139
R;Hardie, D.G.; Dewart, K.B.; Altken, A.; McCarthy, A.D.
Biochim. Biophys. Acta 828, 380-382, 1985
A;Fitle: Amino acid sequence around the reactive serine residue of the thioesterase doma
A;Reference number: A60139; MUID:85175165
A;Reference number: A60139; MUID:85175165
A;Residues: 1-7 <HAR-
C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homo
C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] S-
C;Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enz
F;5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) *status experimental
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              R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K. FEBS Lett. 323, 104-108, 1993
A:Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from A:Reference number: $33244; MUID:93265912
A:Accession: $33244
                                                                                                           neuromodulatory peptide WWamide-1 - giant African snail C;Species: Achatina fulica (giant African snail) C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #texic,Accession: S33244
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hypothetical L2 protein (mistranslated) - human papillomavirus type 16 (c;Species: human papillomavirus type 16 (c;Species: human papillomavirus type 16 (c;Species: human papillomavirus type 16 (c;Species: human papillomavirus type 16 (c;Species: human papillomavirus type 18-Feb-2000 (c;Accession: 156695 (c;Schneider-Maunoury, S.; Croissant, O.; Orth, G. J. Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3295-3298, 1987 (l) Virol. 61, 3
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A;Molecule type: protein
A;Residues: 1-7 <MIN>
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A;Accession: S33246
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glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - C:Species: Pichia jadinii, Candida utilis c:Date: 30-Jun-1991 #sequence_revision 30-Sep-1991 #C:Accession: S11078 C:Accession: S1078 Danielsson, O.; Persson
                                                                                                                                                RESULT
S11078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M30709; NID:g190253; PIDN:AAA65995.1; PID:g553616 C;Comment: This is the hypothetical translation of a viral sequence integ C;Comment: It is translated in an incorrect, -1, reading frame of the L2
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                                                                   30-Sep-1991 #text_change 05-Aug-1994
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                 Persson,
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                                                                                                                           yeast (Pichia jadinii) (fragment)
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FEBS Lett. 269, 194-196, 1990
A:Title: Fast atom bombardment mass spectrometry and chemical analysis in determinations A:Reference number: S11074; MUID:90353571
A:Accession: S11078

A; Molecule type: protein A; Residues: 1-8 <EGE>

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                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
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A:Title: Preferential utilization of specific immuno A:Reference number: PT0222; MUID:91108337
A:Accession: PT0238
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PT0238
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A;Cross-references: FlyBase:FBgn0003944
C;Keywords: DNA binding; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homeotic protein Ultrabithorax - fruit fly (Drosophila melanogaster) (fragment) c;Species: Drosophila melanogaster C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 23-Feb-1997 C;Accession: B27867 R;Saari, G; Bienz, M. EMBO J. 6, 1775-1779, 1987 A;Title: The structure of the ultrabithorax promoter of Drosophila melanogaster. A;Reference number: A91072 A;Molecule type: mRNA A;Residues: 1-8 <SAA>
                                                                                                                                                                                                                                                                                     Ig heavy chain CRD3 region (clone 2-94B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C:Accession: PT023B
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C:Keywords: acetylated amino end; oxidoreductase; pentose phosphate pathway
F:1/Modified site: acetylated amino end (Ser) #status experimental
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A; Molecule type: protein A; Residues: 1-9 <LAK> C; Keywords: aldehyde-lyase;
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                                                                                                                                                       R:Lacko, A.G.; Brox, L.W.; Gracy, R.W.; Horecker, B.L. J. Biol. Chem. 245, 2140-2141, 1970
A;Title: The carboxyl-terminal structure of rabbit liver A;Reference number: A28924; MUID:70166720
A;Accession: A28924
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C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
C:Accession: I46016
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J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity A; Reference number: PT0222; MUID:91108337
A;Accession: PT0324
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-9 <-YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
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c;Speciles: Homo sapiens (man)
c;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0324
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Similarity 2; Conserv

Score 2; DB 2; Pred. No. 2.2 0; Mismatches

2; Le 2.2e+05; 0;

Length 9;

Indels

0

Gaps

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gonadoliberin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Species: 13-Jul-1981 #sequence_revision 13-Jul-
C:Accession: A01411
R:Baba, Y:, Matsuo, H.; Schally, A.V.
Biochem. Biophys. Res. Commun. 44, 459-463, 19
A:Title: Structure of the porcine LH- and FSH-
A;Reference number: A90172; MUID:72114303
A;Accession: A01411
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S36850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: G41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma A;Reference number: A41946; MUID:92049316
A;Accession: G41946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A; Description: In situ Studies on the primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S25024
A; Accession: S36850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-9 <WHEP C;Keywords: T-cell receptor
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A; Residues: 1-9 < JAC>
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A;Residues: 1-10 <BAB>
R;Matsuo, H.; Arimura,
Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                          В
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Best Local S
Matches 2
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Species: Sus scrofa domestica (domestic pig)

pate: 13-Jul-1981 #sequence_revision 13-Jul-1981

Accession: A01411
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ilarity 100.0%;
Conservative
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A.; Nair, R.M.G.; Schally, Commun. 45, 822-827, 1971
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100.0%;
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A; Note: the synthetic and many, A.V. R; Babba, Y.; Arimura, A.; Schally, A.V. Biochem. Biophys. Res. Commun. 45, 483-487, 1971
A; Title: On the tryptophan residue in porcine LH and FSH-releasing hormone a: Reference number: A90175; MUID:72117544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: gonadoliberin C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid F;L/Modified site: pyrolidone carboxylic acid (Gln) #status experimental F;10/Modified site: amidated carboxyl end (Gly) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: the natural and synthetic hormones have C; Comment: This hypothalamic hormone stimulates C; Superfamily: gonadoliberin
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C;Species: Ovis orientalis aries, Ovis ammon aries
C;Date: 31-Dec-1991 *Sequence_revision 31-Dec-1991
C;Accession: A93780; A01411
C;Accession: A93780; A01411 Morss, M.; Ling, N.; Mor
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C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1/Modlfied site: pyrrolldone carboxylic acid (Gln) #status experimental
F:10/Modlfied site: amidated carboxyl end (Gly) #status experimental
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A;Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing A;Reference number: A93780; MUID:72094314
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A; Molecule type: protein
A; Residues: 1-10 <LOV>
C; Superfamily: gonadoliberin
C; Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experiment
                                                                                                            R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.I
Regul. Pept. 33, 105-116, 1991
A;Title: Primary structure of two forms of
A;Reference number: A60066; MUID:91352338
A;Accession: A60066
                                                                                                                                                                                                                                                   N;Alternate names: gonadotropin-releasing hormone I
C;Species: Alligator mississippiensis (American alligator)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
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#text_change 18-Mar-1997
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F; 10/Mod1fled

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RESULT
A49187
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                                 RESULT
A21114
                                                                                                                                                                                                                                                                          R:Sower, S.A.; Chiang, Y.C.; Lovas, S.; Conlon, J.M. Endocrinology 132, 1125-1131, 1993
A:Title: Primary structure and biological activity of a A;Reference number: A49187; MUID:93178316
A:Accession: A49187
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SOW>
                                                                                                                                                                                                                                                                                                                                                                                                           gonadotropin-releasing hormone III - sea lamprey
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C;Accession: A49187
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A; Residues: 1-10 <SHE>
C; Comment: This hormone was isolated from the brain
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R:Shorwood, N.M.: Sower, S.A.; Marshak, D.R.; Fraser, B.A.; Brownstein, M.J.
J. Biol. Chem. 261, 4812-4819, 1986
A;Title: Primary structure of gonadotropin-releasing hormone from lamprey brain.
A;Reference number: A01412; MUID:86168192
A;Accession: A01412
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C;Species: Petromyzon marinus (sea lamprey)
C;Datc: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 18-Mar-1997
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gonadoliberin - chum salmon
C; Species: Oncorhynchus keta
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A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:126381)
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C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 18-Jun-1993 C;Accession: A21114
C;Accession: A21114
R;Sherwood, N.; Biden, L.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W. Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983
A;Title: Characterization of a teleost gonadotropin-releasing hormone. A;Reference number: A21114; MUID:83195140
A;Accession: A21114
transgelin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Oct-1997
C;Accession: A40693
R;Shapland, C: Hsuan, J.J.: Totty, N.F.: Lawson, D.
J. Cell Biol. 121, 1065-1073, 1993
A;Title: Purification and properties of transgelin: a transformation and shear, Reference number: A40693; MUID:93273790
A;Reference number: A40693; MUID:93273790
A;Residues: 1-11 <SHA>
A;Experimental source: aorta
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A; Residues: 1-10 <GO3>
A; Accession: PH0899
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A; Accession: PH0948
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C;Date: 09-Oct-1992 #sequence_revision 19-Oct-1995 #text_change 30-May-1997
C;Accession: PH0948; PH0897; PH0999; PH0899
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experime A;Reference number: PH0891; MUID:92078857
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A; Residues: 1-10 <GO2>
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A; Residues: 1-10 <GOl>
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A; Residues: 1-10 <GO4>
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A; Molecule type: DNA
A; Residues: 1-11 <RES>
A; Cross-references: EMBL
C; Genetics:
A; Gene: NF68
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I60434
R;Reeben, M.; Neuman, T.; Palgi, J.; Palm, K.; Paalme, V.; Saarma, M.
J. Neurosci. Res. 40, 177-188, 1995
A;Title: Characterization of the rat light neurofilament (NF-L) gene promoter and idential;Reference number: I60434; MUID:95264348
A;Recession: I60434
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                                                                                                                                                                                                                                                                                   T-cell receptor beta chain V-D-J region (clone 12) - rat (fragment)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rottus norvegicus (Norway rat)
C; Species: Rottus norvegicus (Norway rat)
C; Species: Rottus norvegicus (Norway rat)
C; Accession: PH0941
R; Gold, D.D.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A; Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi A; Accession: PH0941
A; Accession: PH0941
A; Accession: PH0941
A; Molecule type: mRNA
A; Accession: PH0941
A; Experimental source: complete Freund's adjuvant-immunized lymph node
C; Keywords: T-cell receptor
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Search completed: January 14, 2002, 07:58:36 Job time: 386 sec
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| HEPTAPEPTIDE. |
| Chordata: Craniata: Vertebrata: |
| Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. |
| D=9823; |
| SEQUENCE, AND SYNTHESIS. |
| MEDLINE=81213980; PubMed=6263778; |
| A., Redding |
| ton J.W., Cohn D.V., Schally A |
| ACTH-releasing activity from porcing beneathing. |
| Horm. Metab. Res. 13:228-232(1981). |
| PIR: A01417; NYPG7. |
| SEQUENCE / AA; 957 MW; 632B45B1FB5059A0 CRC64; |
| Query Match 25.0%; Score 2; DB 1; Length 7; Best Local Similarity 100.0%; Pred. No. 1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps |
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| WWA2_ACHFU STANDARD; PRT; 7 AA. P35920; |
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| 01-00T-1994 (Rel. 30, Last annotation update) WWAMIDE-2. |
| Achatina fulica (Giant African snail). |
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| NCB1_10X1D=6330; [1] |
| SEQUENCE. |
| TissuE=Gangilon; MEDLINE=93265912; PubMed=8495720; |
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01-JUN-1994
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Minakata H., Ikeda T., Muneoka Y., Kobayashi
"Wimamide-1, -2 and -3: novel neuromodulatory
ganglia of the African giant snail, Achatina
FEBS Lett. 332:104-108(1993).
PIR: S33244; S33244.
Neuropeptide; Amidation.
MOD_RES. 7
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MIDATION.
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Achatina fulica (Giant African snail).
Achatina; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Achatinacea; Achatinidae; Achatina.
ACBI_TaxID=6530;
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MOD_RES 7 7
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                                                                                               Eukaryota; Metazoa; Arthropoda; Cruste Eumalacostraca; Eucarida; Decapoda; Pl Eubrachyura; Portunoidea; Portunidae; NCBI_TaxID=6759;
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Visolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Blochem. 250:727-734(1997).
                                                     TISSUE-Cerebral ganglion, and Thoracic MEDLINE=98121193; PubMed=9461295;
                                                                                                                                            Carcinus maenas (Common shore crab) (Green crab)
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Decapoda; Pleocyemata; Brachyura;
Portunidae; Carcinus.
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RESULT 5

GONI_ALLMI STANDARD; PRT; 10 AA.

ID GONI_ALLMI STANDARD; PRT; 10 AA.

P37041; P20407;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE GONADOLIBERIN I (GONADOTROPIN-RELEASING HORMONE I) (

GONADOLIBERIN I).

OS Alligator mississippiensis (American alligator).

OC Entaryota; Metazoa; Chordata; Craniata; Vertebrata;

OC Entaryota; Metazoa; Chordata; Craniata; Vertebrata;
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Matches 2
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Matches 2; Conserv
                                                                                                                                          GONI_PETMA STANDARD; PRT; 10 AA.
GONI_PETMA STANDARD; PRT; 10 AA.
P04378;
20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
GONADOLIBERIN I (GONADOTROPIN-RELEASING HORMO
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Petromyzontiformes;
NCBI_TaxID=7757;
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InterPro; IPR002012; GNRH.
                                                                       Eukaryota; Metazoa;
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Petromyzon man
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PROSITE; PS00473; GNRH; 1.
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SIMILARITY: BELONGS TO THE ALLATOSYATIN FAMILY.
ropeptide; Amidation; Multigene family.
RES 8 8 AMIDATION.
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                                                     Petromyzon
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). 1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 10;
. 1.1e+03;
                                                                          Vertebrata;
                                                                                                                                                    HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alligator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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                                                                            Hyperoartia;
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RESULT
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                                                                                  REPECIES:C. pallus11; TISSUE-Brain, and Pituitary;

K SPECIES:C. pallus11; TISSUE-Brain, and Pituitary;

K MEDLINE-20114351; PubMed=10650929;

A Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,

A Chang J.P., Rivier J.E., Sherwood N.M.;

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A Chang J.P., Rivier J.E., Park
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Best Local S
Matches 2
             MOD_RES
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MOD_RES
MOD_RES
SEQUENCE
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P20367; P81751;
01-FEB-1991 (Rel. 17, Created)
01-FEB-991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GONADOLIBERIN III (GONADOTROPIN-RELEASING HORMONE III) (GNRH-III) (LH-
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 83195140; PubMed-6341999;
Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Va
"Characterization of a teleost gonadotropin-releasing hormone.
Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncorhynchus keta (Chum salmon), and Clupea pallasii (Pacific herring). Clupea pallasii (Pacific herring). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncc NCBI_TaxID~8018, 30724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR;
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TISSUE-Brain;
TISSUE-Brain;
MEDLINE-86168192; PubMed-3514603;
Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A.,
"Primary structure of gonadotropin-releasing hormone f
                                                      MOD_RES
                                                                           Hormone;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ONCKE
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1- FUNCTION: STIMULATES THE SECRETION OF BOTH
FOLLICLE-STIMULATING HORMONES.
1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
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erPro; IPR002012; GnRH.
m; PF00446; GnRH; 1.
SITE; PS00473; GNRH; 1.
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                                                                         Amidation; Hypothalamus
             10 AA;
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             1230
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100.0%; Pr
100.0%; Pr
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1 PYRROLIDONE CARBOXYLIC
10 AMIDATION.
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284B3233786B45A3 CRC64;
                                                    PYRROLIDONE CARBOXYLIC ACID
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red. No. 1.1
Mismatches
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). 1.1e+03;
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                                                                                                                                                                                                                                                                      teleost, herring.";
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RLA2_MOUSE STANDARD; PRT;
P99027;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence uprocedule)
15-DEC-1998 (Rel. 37, Last annotation and a company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the compan
                                             TISSUE-Liver;
Sanchez J.-C., Rouge V.,
Hoogland C., Appel R.D.,
     Cowthorne M.;
Submitted (AUG-1998)
-!- FUNCTION: PLAYS
                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                      RPLP2
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MOD_RES
MOD_RES
SEQUENCE
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                                                                                                        SEQUENCE.
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01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GONADOLIBERIN III (GONADOTROPIN-RELEASING HOR
                                                                                                                                     NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sower S.A., Chiang Y.-C., Lovas S., Conlon Primary structure and biological activity
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P30948;
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2; Conser
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g Y.-C., Lovas S
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                                                    Frutiger S.
Binz P.-A.,
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Pred. No. 1.1
0; Mismatches
                                                                                                                                                  Craniata; Ver
Sciurognathi;
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284B36237AA1F5A3
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(FRAGMENT).
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thi; Muridae; Murinae; Mus
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   bank.
E ELONGATION
                                                                   G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10;
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P04559;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update
20-AUG-2001 (Rel. 40, Last annotation upda
20-ROTENSIN IIB (U-IIB) (UIIB).
Matostomus commersoni (White sucker).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Actinopterygii; Neopterygii; Teleostei; El
                                                                                                                                                                                                                                                                                                                                                            **MCMaster D., Lederis K.;

**Tsolation and amino acid sequence of two urotensin II peptides from Catostomus commersoni urophyses.";

Peptides 4:367-373(1983).

-i- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETOR: SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A CORTICOTROPIN-RELEASING FACTOR.

-I- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
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-i- SIMILARITY: BELONGS TO THE L12P FAMILY OF SWISS-2DPAGE; P99027; MOUSE.
Ribosomal protein; Phosphorylation.
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SEQUENCE
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13-AUG-1987
13-AUG-1987
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VARIANT
SEQUENCE
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DISULFID
SEQUENCE
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                                                                                                                                                                                      Munekata E., Ohtaki T., Ichikawa T., McMaster D., Lederis K.;
(In) Rich D.H., Gross E. (eds.);
Proceedings of the 7th american peptide symposium, pp.69-72,
Pierce Chemical Co., Rockford II. (1981).
-i- FUNCTION: URCTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CORTICOTROPIN-RELEASING FACTOR.
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
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13-AUG-1987 (Rel. 05,
20-AUG-2001 (Rel. 40,
UROTENSIN II-BETA.
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-i- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A CORTICOTROPIN-RELEASING FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cypriniformes; Catostomidae; Catostomus.
NCBI_TaxID=7971;
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                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY InterPro; IPR001483; Urotensin_II. Pfam, PF02083; Urotensin_II; 1.
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DISULFID
SEQUENCE
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TISSUE-Spinal cord;
MEDLINE-96051494; PubMed-8536944;
MEDLINE-96051494; PubMed-8536944;
Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;
"Urotensin II from the river lamprey (Lampetra fluviatilis),
lamprey (Petromyzon marinus), and the paddlefish (Polyodon spathala).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
UROTENSIN II (U-II) (UII).
POLYOdon spathula (North American paddlefish).
Eukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordrostel; Acipenseriformes; Polyodontidae;
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21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UROTENSIN II (U-II) (UII).
61111chthys mirabilis (Long-jawed mudsucker).
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PO1147;
                                                                -i- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY InterPro; IPR001483; Urotensin_II. Pfam; PF02083; Urotensin_II; 1.
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Proc. Natl. Acad. Sci. U.S.A. 77:5021-5024(1980).

-I- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CORTICOTROPIN-RELEASING FACTOR.
-I- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.

PIR: A01409; UGGM2.
                            PROSITE;
                                                                                                                                                                                                                                                                                                       Gen.
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Pfam; PF02083; Urotensin_II; 1.
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FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN
                                                                                                                                                                                 MUSCLE STIMULATION.
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                            PS00984; UROTENSIN_II; 1.
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DT 01-NOV-1995 (Rel. 32, Created)
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SEQUENCE
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01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UROTENSIN II (U-II) (UII).
Scyliorninus canicula (Spotted dogfish) (Spotted catshark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorninidae; Scyliorninus.
NCBI_TaxID-7830;
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SEQUENCE
                                                                                                                                                                                                                  Anolis carolinensis (Green anole) (American chameleon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis
NCBI_TaxID-28377;
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Pfam; PF02083; Urotensin_II; 1.
PROSITE; PS00984; UROTENSIN_II; 1.
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Conlon J.M., O'Harte F., Smith D.D., Balment R.J., Hazon N.;
Conlon J.M., O'Harte F., Smith D.D., Balment R.J., Hazon N.;
Purification and characterization of urotensin II and parvalbumin from an elasmobranch fish, Scyliorhinus canicula (common dogfish).'
Neuroendocrinology 55:230-235(1992).
Neuroendocrinology 55:230-235(1992).
-i- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
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SIMILARITY: BELONGS TO THE UROTENSIN
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Pred. No. 1.2
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7551E9DBB879CEBB CRC64;
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   Jankelow L.,
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   yk D.L.;
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01-NOV-1995
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SEQUENCE
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MOD_RES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus NCBI_TaxID=9838, 9796;
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21-JUL-1986 (Rel. 01, Last sequence updat
20-AUG-2001 (Rel. 40, Last annotation upd
MELANOTROPIN ALPHA (ALPHA-MSH).
Camelus dromedarius (Dromedary) (Arabian
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P01198;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dixon J.S., Li C.H.;
"The isolation and structure of alpha-melanocyte-stimulating hormone from horse pituitaries.";
J. Am. Chem. Soc. 82:4568.4572(1960).
-!- SIMILARITY: BELONGS TO THE POMC FAMILY.
PIR; A01464; MTCMAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.

SPECIES-C.dromedarius;

MEDLINE-75146434; PubMed-1125179;

Li C.H., Danho W.O., Chung D., Rao A.J.;

"Isolation, characterization, and amino acid melanotropins from camel pituitary glands.";

Biochemistry 14:947-952(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolated from the intermediate pituitary of the reptile, Anolis carolinensis.";
Peptides 12:1261-1266(1991).
-!- SIMILARITY: BELONGS TO THE POMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hormone; Amidation.
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ST_VESXA STANDA:

MAST_VESXA STANDA:

P01515;
21-JUL-1986 (Rel. 01,
21-JUL-1999 (Rel. 38,

MASTOPARAN X (MP-X).
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MAST_POLJA STANDARD
POLSTJ;
21-JUL-1986 (Rel. 01, C
21-JUL-1986 (Rel. 01, C
21-JUL-1996 (Rel. 23, D
01-AUG-1992 (Rel. 23, D
POLISTES MASTOPARAN.
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Pterygota; Neoptera;
Vespoidea; Vespidae;
NCBL_TaxID=31921;
                                                                                                                                                                                                                                  PIR; A01780; QMWAPP.
Mast cell degranulati
MOD_RES 14 1
SEQUENCE 14 AA; 16
                                                                                                                                                                                                                                                                                                                                                                                             Polistes jadwigae (Paper wasp).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ac
Vespoidea; Vespidae; Polistinae; Polistes.
NCBI_TaxID=7457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and sequential analysis of parapolybia indica."; Eisei Dobutsu 39:105-111(1988).
-i- FUNCTION: MAST CELL DEGRANULATING THAT COUPLE TO PHOSPHOLIPASE C.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apovernoidea; Vespidae; Polistinae; Parapolybia.
                                                                                                                                                                                                                                                                                  Hirai Y., Ueno Y., Yasuhara T., Yoshid
"A new mast cell degranulating peptide
venom of Polistes jadwigae.";
biomed. Res. 1:185-187(1980).
-!- FUNCTION: MAST CELL DEGRANULATING
THAT COUPLE TO PHOSPHOLIPASE C.
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14 14 AMIDATION.

14 AA; 1636 MW; 26472A53BF4778D8 CRC64;
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01-FEB-1991 (Rel. 1
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SOMATOSTATIN I.
                                                                                     SEQUENCE.

SPECIES-M.scorpius; TISSUE-Pancreas;

MEDLINE-88029486; PubMed-2889597;

Conlon J.M., Davis M.S., Falkmer S., Thim L.;

"Structural characterization of peptides derived from prosomatostatins I and II isolated from the pancreatic islets of species of teleostean fish: the daddy sculpin and the flounder.";
                                                                                                                                                                                                                                                                                                                                                                                                 Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin), oncorrhynchus kisutch (Coho salmon), and Anguilla anguilla (Biropean freshwater eel). Eukaryota; Metazoa; Chordata; Cranilata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes; Cottoidei; Cottidae; Myoxocephalus. MCBI_TaxID~8097, 8019, 7936;
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-!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTION THAT COUPLE TO PHOSPHOLIPASE C.
       SEQUENCE
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H1rai Y., Kuwada M., Yasuhara T., Yoshida H., Nakajima
"A new mast cell degranulating peptide homologous to me
the venom of Japanese hornet (Vespa xanthoptera).";
Chem. Pharm. Bull. 27:1945-1946(1979).
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PDB; 1A13; 16-FEB-99.
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MEDLINE-92304942; Pu
Wakamatsu K., Okada
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Eukaryota; Metazoa; Archropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
Vespoldea; Vespidae; Vespinae; Vespa.
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                                                                         J. Biochem.
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llarity 100.0%;
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                                                                      168:647-652(1987).
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da_A., Miyazawa T.,
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MEDLINE-89065329; PubMed=2904391.

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"Isolation and structural characterization of insulin, somatostatin from the turtle, Pseudemys scripta.";
Peptides 11:461-466(1990).
                                                                                                 -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS TO PIR; C60414; C60414.
                                                                                                                                                                                                                                                                                                                                                    SPECIES-T.scripta;
MEDLINE-90341082; PubMed-1974347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alligator mississippiensis (American alligator), and Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Crocodylidae; Alligatorinae; Alligator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Neuroendocrine peptides (NPY, GRP, and stomach of the alligator."; peptides 14:573-579(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
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MEDLINE-87055212; PubMed=2877919;
Plisetskaya E.M., Pollock H.G., Rouse J.B., Han Kimmel J.R., Andrews P.C., Gorbman A.;
"Characterization of coho salmon (Oncorhynchus somatostatins,";
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01-BC-1992 (Rel. 24, Last annotation update)
MALTASE (EC 3.2.1.20) (ALPHA-GLUCOSIDASE I) (FRAGMENT).
Bacillus thermoamyloliquefaciens.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Pacillus/Staphylococcus group; Bacillus.
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Olivera B.M., McIntosh J.M.;
"Alpha-conotoxin AulB selectively blocks alpha3 beta4 nicotinic
"Alpha-conotoxin AulB selectively blocks alpha3 beta4 nicotinic
acetylcholine receptors and nicotine-evoked norepinephrine release.";
J. Neurosci. 18:8571-8579(1998).

-i- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
-i- MASS SPECTROMETRY: MW=1572.5; METHOD=ELECTROSPRAY.
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Conus aulicus (Court cone).

Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;

Neogastropoda; Conoidea; Conidae; Conus.

NCBI_TaxID=89437;
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DISULFID
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MEDLINE-92209510; FUNDER AND ACTION OF TAKIN Y.;

Suzuki Y., Yonezawa K., Hattori M., Takii Y.;

"Assignment of Bacillus thermoamyloliquefaciens KP1071

*Ripha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence
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                                                                                                                                                                                                                                                                                                                                              Bacillus/Staphylococcus group; NCBI_TaxID=1425;
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                                                                                                                                                                                                MEDLINE=92209510; PubMed=1555585;
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STRAIN=KP1071 / FERM P8477;
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84EFE95FDC700155 CRC64;
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-! CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING
-! 1,4-LINKED D-GLUCOSE RESIDUES WITH RELEASE OF D-GLUCOSE.
-! SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES,
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PH2_PERAM STANDARD; PRT; 15 AA P82695; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation updat PEPTIDE HORMONE 2 (PEA-VEAACID 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
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SEQUENCE 15 AA;
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Best Local Similarity
Matches 4; Conserv
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GENERAL INFORMATION:
APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Brevican, A Glial Cell Proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 552 anino acids
TYPE: anino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEO ID NO: 28:
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03747
FILING DATE: 27-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Imbra Richard J.
REGISTRATION NUMBER: 37,643
REFERENCE/DOCKET NUMBER: FP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,544
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,899
FILING DATE: OG-FEB-1997
CLASSIFICATION: 800
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 SFXG 281
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ADDRESSEE: Burns, Do
                                                                                                                                                                                                                                                                                                 STREET: 4370 La JC
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mouth, Donna M
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States ZIP: 22313-1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
STATE: Virginia
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.O. Box 1404
                                                                                                                                                                                                                                                                                      USA
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  FP-LJ 1453
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              Query Match
Best Local Similarity
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; ORGANISM: HIV
US-08-889-841B-6
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Best Local Similarity
Whiches 2; Conserve
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; LENGTH: 2
; TYPE: PRT
                                                                                                                                                                    NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 2
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TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
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Best Local
                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE FILE REFERENCE: 14918-703CIP CURRENT APPLICATION NUMBER: US/08/889,841B CURRENT FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Berman, Phillip W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
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5 sf 6
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                            25.0%; Score 2; DB 3; Length 2; ilarity 100.0%; Pred. No. 1.6e+05; Conservative 0; Mismatches 0; Indel
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100.0%; Pred. No.
tive 0; Mismatc
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100.0%; Pred. No.
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o. 1.6e+05;
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o. le+03;
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; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-17
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; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-13
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Best Local Similarity
Thes 2; Conserve
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Best Local Similarity
Thes 2; Conserv
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US-08-889-841B-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/08889841B
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 17
                                                                                                                     Sequence 20, Application US/08889841B GENERAL INFORMATION:
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CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
                           APPLICANT: Berman, Phillip W.

TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
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TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
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PRIOR APPLICATION NUMBER: US 60/676,737 PRIOR FILING DATE: 1996-07-08
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100.0%;
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Pred. No. 1.6e+05;
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Best Local Similarity
Tatches 2; Conservi
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; ORGANISM: HIV
US-08-889-841B-20
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                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 37 LENGTH: 2
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GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
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SOFTWARE: FastSEQ for
SEQ ID NO 20
LENGTH: 2
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Best Local Similarity
Matches 2; Conserv
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   Best Local Similarity Matches 2; Conserv
                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BEZMAN, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
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PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
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       Conservative
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100.0%; Pred. No. 1.
Live 0; Mismatches
                                      25.0%; Score 2;
100.0%; Pred. No.
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          Mismatches
No. 1.6e+05;
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RESULT 15
US-07-657-769B-14
; Sequence 14, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
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APPLICANT: Co. Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEO ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 405
LENGTH: 3
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GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
UNMBER OF SEO ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 40
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Best Local Similarity
Conserv
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Patent No. 62777.
Patent INFORMATION:
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TYPE: PRT
ORGANISM: HIV
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US-07-714-540-11
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US-07-657-769B-14
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Irell & Manella
STREET: 545 middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                              APPLICANT: Almquist, Ronald G.
APPLICANT: Toll, Lawrence
TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING
TITLE OF INVENTION: ENZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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               APPLICATION NUMBER: U. FILING DATE: 19910607 CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 415-327-2951
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FILING DATE: 19910219
CLASSIFICATION: 435
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CITY: MENLO PARK
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM.PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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545 MIDDLEFIELD ROAD, SUITE 200
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INFORMATION
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100.0%; Pr
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                                                   US/07/714,540
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                                                                                        Version #1.25
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RESULT 17
US-07-714-540-12
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Query Match 25.0%; Score 2; DB 1; Ler Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 42; Conservative 0; Mismatches 0;
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APPLICANT: Almquist, Ronald G.
APPLICANT: Toll, Lawrence
TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING
TITLE OF INVENTION: ENZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                           NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/07/714,540
FILING DATE: 199.0607
CLASSIFICATION: 530
CRESSIFICATION: 530
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Reed, Dianne E.
REGISTRATION NUMBER: 31,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
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TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
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TELEFAX: 706141
                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                           TELLETAX: 41.
TELEFAX: 706141
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STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
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                                                                                                                              TOPOLOGY:
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100.0%; Pred. No.
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US-07-828-450-38
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                                                                                                                                                                                        RESULT 19
                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 2
                                                Sequence 3, Application US/08079445
Patent NO. 5440016
GENERAL INFORMATION:
APPLICANT: Blondelle, Sylvie E.
APPLICANT: Pinilla, Clemencia
APPLICANT: Eichler, Jutta
APPLICANT: Houghten, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/07828450 Patent No. 5434133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TANAKA, SHOJI
APPLICANT: MINAMITAKE, YOSHIH
APPLICANT: KITAJIMA, YASUO
APPLICANT: FURUYA, MAYUMI
APPLICANT: MATSUO, HISAYUKI
TITLE OF INVENTION: CNP ANALO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: ADDRESSEE: CUSHMAN,
 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US FILING DATE: 19920131
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CITY: WASHINGTON
STATE: D.C.
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2 SF 3
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nes 2; Conserv
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TOPOLOGY: li
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HOUGhten, Richard A.
VENTION: PEPTIDES HAVING ANTI-MICROBIAL,
VENTION: HEMOLYTIC, ANTI-MELITTIN OR ANTI-ENZYMATIC ACTIVITY
EQUENCES: 15
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100.0%; Pred. N
tive 0; Misma
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o. 1.6e+05;
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ADDRESSEE: CAMPBELL AND FLORES

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US-07-840-077A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                       APPLICANT: Zamora, Paul O.
APPLICANT: Rhodes, Buck A.
TITLE OF INVENTION: Pharmaceutical
TITLE OF INVENTION: Pharmaceutical
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhomed Incorporated
STREET: 4261 Balloon Park
                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-HP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
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                                       STREET: 4261 Ballo
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 4370 La
CITY: San Diego
                              STATE:
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OTHER INFORMATION:
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FILING DATE: 18-JUN-1993
CLASSIFICATION: 514
                COUNTRY:
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87109-5802
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                                                                                                                          Pharmaceutical Preparation and Method
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100.0%; Pred. No.
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amidated"
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/note- "Xaa=KFmoc"
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/note "xaa any amino acid"
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RESULT 21
US-08-127-904-11
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Sequence 11, App...
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Eugene Roberts
TITLE OF INVENTION: Method
TITLE OF INVENTION: Annesti
TITLE OF INVENTION: Quality
TITLE OF INVENTION: With Al
                                                     SOFTWARE: Microsoft
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,904
FILING DATE: 29 September 1993
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4" diskette
COMPUTER: Wang PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Deborah A. Peacock REGISTRATION NUMBER: 31,649 TELECOMMUNICATION INFORMATION: TELEPHONE: (505) 242-9677
FILLING DATE: 29 September 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: NO. 5470951e
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: City of Hope
STREET: 1500 East Duarte Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
FILING DATE: 03-JAN-1992
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-D SOFTWARE: Worder
                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                   CITY: Duarte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/840,077A FILING DATE: 20-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC/XT/AT, IBM PS/2 or COMPUTER: compatibles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
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: United States of America
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                                                                                                                            MS DOS Version 3.20
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                        Method For Antagonizing
Amnestic Effects of Amyloid n
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1.6e+05;
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               Query, Match
Best Local
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   Matches
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TELEX: NO. 5470951e
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                TELEX: NO. 5470951e INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                 SOFTWARE: Microsoft
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,904
FILING DATE: 29 September 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: No. 5470951e
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3M Double Density 5 1/4 " diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: City of Hope
STREET: 1500 East Duarte Road
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: NO. 5470951e
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                       TYPE: Amino Acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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Similarity
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                                                                                                                                                                                              : (202) 783-60
(202) 783-6031
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25.0%; Score 2; I ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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100.0%; pr
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Amnestic Effects of Amyloid n
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   Mismatches
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               DB 1; Le
o. 1.6e+05;
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                            Length 4;
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 0;
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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-405-933-14
                                                                                                                                                                                                                                                    US-08-461-611-12
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
"hes 2; Conserva
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                                                                                               Sequence 12, Application US/08461611

Sequence 12, Application US/08461611

Patent No. 5635477

Patent No. 5635477

Patent No. 5635477

Patent InfoRMATION: GENERAL INFORMATION: William Frank DeGrado, Sharon Anne Jackson, Shaker Ahmed Mousa, Anju APPLICANT: Parthasarathy, Michael Sworin, Maria Rafalski
TITLE OF INVENTION: Cyclic Compounds Useful as
TITLE OF INVENTION: Inhibitors of Platelett Glycoprotein IIb/IIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: Usa
ZIP: 22313-1404
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PLOPS/MS-DOS
MS-DOS/MS-DOS
MS-DOS/MS-DOS
MS-DOS/MS-DOS
MS-DOS/MS-DOS
MS-DOS/MS-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                   CORRESPONDENCE ADDRESS:
ADDRESSEE: The DuPon
ADDRESSEE: Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 21-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 02
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moore, Graham J
TITLE OF INVENTION: Synthet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                5 sf 6
1 SF 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Washingt
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Dillahunty, Mary Ann REGISTRATION NUMBER: 34,57
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STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Burns, Doane, Swecker & Mathis Washington & Prince Streets, P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hollenberg, Morley D. Matsoukas, John M.
1007 Market Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415)854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                       The DuPont Merck Pharmaceutical
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100.0%; Pred. No. 1.
tive 0; Mismatches
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Legal Department
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CITY: Wilmington STATE: DE COUNTRY: U.S. ZIP: 19898

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 25
US-07-789-184-109
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REGISTRATION NUMBER: 34,329
REFERENCE/DOCKET NUMBER: BP-6543-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-1676
TELEFAX: 302-892-1676
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
ORIGINAL SOURCE: synthetic
FEARINES:
                                                                                                                                                                                                                                                                                                                                                 Sequence 109, Application US/07789184
Patent No. 5688768
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.0%; Score 2; DB 1; Le Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 Inch disk
COMPUTER: Apple MacIntosh
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: Apple MacIntosh
SOFTWARE: MICROSOft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,611
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA: none
APPLICATION UMBER: 08/038,448
FILING DATE: March 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FERGUSON, Blair, 0
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,184
FILING DATE: 19911107
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                            STREET: 755 Page M
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94304-1018
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Search completed: January 14, 2002, 07:57:31 Job time: 376 sec
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                                                                                                                          Query Match
Best Local Similarity
Matches 2; Conserv
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INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 01.
TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                   TYPE: AMINO ACID
STRANDEDNESS: sin
                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                         SF 2
                                                                                         _sf 6
                                                                                                                                 Conservative
                                                                                                                                                                                                                                   single
                                                                                                                            25.0%; Score 2; DB: 100.0%; Pred. No. 1.0 tive 0; Mismatches
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b. 1.6e+05;
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Result
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
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                                                                                                                                                                                                                    Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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F85630
E86739
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A61304
S36662
S31240
S33246
S37141
A46306
S37141
A46306
S37147
S566607
S566607
S563491
S363491
S363491
S363491
S363491
S36363
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A60753
A85797
                                                                                                                                                                                                                                          SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search time 45.4 Seconds (without alignments)
13.423 Million cell updates/sec
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ferredoxin - F
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                                                                                   spasmogenic toxin
leucokinin VII - |
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dermorphin (Lys-7)
dermorphin (Trp-4,
                                                                                                                                                 hypothetical prote
blood cell protein
locustakinin - mig
                                                                                                                                                                hypothetical
hypothetical
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                                                                                                                                                                                                    class II histocomp
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                                                        ribosomal protein
                                                                             cardioacceleratory
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|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|
| N | 2 | N | N | N | 2 | 2 | 2 | 2 | 2 | 2 | ນ | Ν | 2 | N | 2 | 2 | 2 | ۵ | 2 | 2 |
| 25.0 | 25.0 | 25.0 | 25.0 | 25.0 | 25.0 | 25.0 | 25.0 | | 25.0 | 25.0 | 25.0 | 25.0 | • | ٠ | | 25.0 | | 25.0 | 25.0 | 25.0 |
| 13 | 13 | 13 | 13 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 11 | 11 | 11 | 11 | 11 | 11 | 10 | 10 |
| ν | N | N | N | N | N | N | N | Ν | N | N | ν | Н | 4 | ν | N | N | Н | L | N | N |
| S63492 | PC1008 | S01119 | PQ0445 | S47393 | JS0424 | A35585 | S01122 | 869123 | S29479 | JS0423 | S42765 | UOGM2 | S52252 | E57789 | A35594 | S07203 | EOOC | E00CC | A49187 | C61440 |
| dissimilatory sulf | 40K extracellular | photosystem II pro | urotensin II - lau | T-cell antigen rec | urotensin II-B pep | cytokinin-binding | photosystem II 3.7 | proton-translocati | hypothetical prote | urotensin II-A pep | urotensin II - tel | urotensin II - lon | hypothetical prote | gallbladder stone | buccalin - Califor | uperolein - frog (| eledoisin - musky | eledoisin - curled | gonadotropin-relea | polygalacturonase |

ALIGNMENTS

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Class II histocompatibility antigen HLA-DR beta chain - human (fragments) C;Species: Homo sapiens (man) C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 30-May-1997 C;Accession: B18955 R;Wiman, K.; Claesson, L.; Rask, L.; Tragardh, L.; Peterson, P.A. Blochemistry 21, 5331-5338, 1982 A;Reference number: A90403; MUID:83075335 A;Accession: B18955
                 οy
                                                                                                                                                                                                C;Accession: A60753
R;von Tigerstrom, R.G.; Boras, G.J.
J. Gen. Microbiol. 136, 521-527, 1990
A;Title: beta-Lactamase of Lysobacter enzymogenes: induction, purification and charac A;Reference number: A60753; MUID:90362037
A;Accession: A60753
                                                                                                                                                                                                                                                                                                    beta-lactamase (EC 3.5.2.6) - Lysobacter enzymogenes (fragment)
C;Species: Lysobacter enzymogenes
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
B18955
                                                                                                                                         A;Molecule type: protein
A;Residues: 1-41 <VON>
C;Keywords: antibiotic resistance; hydrolase;
                                                                                                                                                                                                                                                                                                                                                                   RESULT
A60753
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A;Residues: 1-31 <WIM>
C;Superfamily: class II histocompatibility antigen;
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Matches
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Best Local Similarity
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5 afxg 8
                                                                      Local Similarity
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100.0%; F;
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                                                                    Score 3;
Pred. No.
                                                     Mismatches
                                                                    DB 2; Le
5. 2.2e+02;
                                                                                                                                               monomer
                                                                                    Length 41
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Accession: A85797
C;Accession: A85797
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                    hypothetical protein yhjG [imported] - Escherichia coli (strain 0157:H7) C;Specites: Escherichia coli (C;Specites: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2. C;Accession: E86025 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Ro
                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain C; Genetics: A; Gene: Z1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: A85797
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A; Residues: 1-122 <STO>
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A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Z1373 [imported] - Escherichia coli (strain O157:H7) C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Accession: F85630
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                   iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
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A; Residues: 1-260 <STO>
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                                  N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; A
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5.9e+02;
es 0; Indels
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A; Residues: 1-3
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A;Reference number: A85480; MUID:21074935;
A;Accession: E86025
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-691 <5TO>
                                                                                                                                                                                                                                                                 blood cell protein A - Molgula manhattensis (fragment)
C;Species: Molgula manhattensis
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change
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A;Residue: 1-879 <STO>
A;Cross-references: GB:AE005174; NID:g12515319; PIDN:AAG56379.1;
A;Cross-reference: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
C;Accession: G85739
C;Accession: G95739
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
Nature 409, 529-533, 2001
                                                                                                                                                                                     R;Taylor, S.W.; Ross, M.M.; Waite, J.H. Arch. Biochem. Biophys. 324, 228-240, 1995
A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: ydbH
C;Superfamily: Escherichia coli membrane protein ydbH
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C;Superfamily: Escherichia coli hypothetical 75.1K protein (treF-kdgK region)
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                                                                                                                                                                  A; Reference number: S68325;
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Best Local Similarity 100.
4; Conservative
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4; Conservative
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100.0%;
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100.0%;
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DB 2; L., NO. 2.2e+05; 0;
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dermorphin (Lys-7) [validated] - two-colored leaf frog C;Species: Phyllomedusa blcolor (two-colored leaf frog) C;Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000 C;Accession: S36662 R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G. R;Mignogna, G.; 151-154, 1992 R;BS Lett. 302, 151-154, 1992 A;Title: Identification and characterization of two dermorphins from skin extracts of the A;Reference number: S21152; MUID:92339502 A;Accession: S36662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dermorphin - Rohde's leaf frog
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 17-Jul-1994 #sequence_revision 05-Aug-1994 #text_cha
C;Accession: A61324
R;Montecucchi, P.C.; De Castiglione, R.; Erspamer, V.
Int. J. Pept. Protein Res. 17, 316-321, 1981
A;Ritle: Identification of dermorphin and Hyp(6)-dermorphin
A;Reference number: A61324; MUID:82029915
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Regul. Pept. 37, 49-57, 1992
A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation,
A;Reference number: A61068; MUID:92262851
A;Accession: A61068
  A; Molecule type: protein A; Residues: 1-7 <MIG> C; Superfamily: dermorphi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Molecule type: protein
A:Residues: 1-7 RON>
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
C:Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; sk:
F:2/Modified site: D-alanine (Ala) #status experimental
F:6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F:7/Modified site: amidated carboxyl end (Ser) #status experimental
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C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
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                                                             A; Status: preliminary
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R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K. FEBS Lett. 323, 104-108, 1993
A:Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia A; Reference number: S33244; MUID:93265912
A; Accession: S33244
A; Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia A; Reference number: S33244; MUID:93265912 A; Accession: S33246
                                                                                                                             C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuromodulatory peptide WWamide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
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S33244
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C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 19-Mar_1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
                                                             R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, FEBS Lett. 323, 104-108, 1993
                                                                                                              C; Accession: S33246
                                                                                                                                                       neuromodulatory peptide WWamide-3 - giant African snail C: Species: Achatina fulica (giant African snail)
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A; Accession: S21230
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A;Title: Identification and characterization of two dermorphins from skin extracts of A;Title: Tentification and characterization of two dermorphins from skin extracts of
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o. 2.2e+05;
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RESULT
S68004
                    spasmogenic toxin PNV1 - spider (Phoneutria nigriventer) (fragment)
C;Species: Phoneutria nigriventer
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
C;Accession: A46306
                                                                       RESULT
A46306
                                                                                                                                                                                                                                                                                                                                                           rpsA protein - Erwinia chrysanthemi
C;Species: Erwinia chrysanthemi
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
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S37141
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C; Date: 15-Feb-1997 #sequence
C; Accession: S68004
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A;Molecule type: prot
A;Residues: 1-7 <MIN>
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A;Molecule type: DNA
A;Residues: 1-8 <DOU>
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A; Accession: S37141
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R;Doulllie, A.; Toussaint, A.; Faelen, M.
submitted to the EMBL Data Library, August 1993
A;Description: Identification of the integration
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A;Molecule type: protein
A;Residues: 1-7 <EDG>
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R; Marangoni, S.; Borges, N.C.C.; Toxicon 31,7377-384, 1993
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5. 2.2e+05;
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           Antunes,
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RESULT
S66607
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C:Species: Leucophaea maderae (Madeira cockroach)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000 C:Accession: JS0317
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A; Residues: 1-8 < HOL>
A; Residues: 1-8 < HOL>
C; Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate C; Keywords: amidated carboxyl end; cephalomyotropic peptide
F; 8/Modified site: amidated carboxyl end (Gly) #status experimental
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JS0317
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A;Accession: A46306
A;Status: preliminary
quinoline 2-oxidoreductase beta chain C; Species: Comamonas testosteroni
                                                                                                                                                                                                                                                                            R;Huesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderek, K.M.; Tublitz, FEBS Lett. 371, 311-314, 1995
A;Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide A;Reference number: S66646; MUID:96013159
                                                                                                                                                                                                                                                                                                                                                 cardioacceleratory protein 2b - tobacco hornworm
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
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A; Status: preliminary
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ribosomal protein S8 - Mycobacterium bovis (fragment)
C;Species: Mycobacterium bovis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C;Accession: S36898
R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
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S36898
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S63491
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A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline A;Reference number: $66606; MUID:96035889
A;Accession: $66607
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                                                                                                                                                                                A;Molecule type: protein
A;Rcsidues: 1-9 <OHA>
C;Keywords: protein biosynthesis; ribosome
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A;Molecule type: protein
A;Residues: 1-9 <STE>
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Eur. J. Blochem. 233, 873-879, 1995
A;Title: Molecular properties of the dissimilatory sulfite reductase
A;Reference number: S63489; MUID:96085152
A;Accession: S63491
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C:Accession: S66607
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A26363

Cardioactive peptide - green crab (fragment)
C;Species: Carcinus maenas (green crab, common shore crab)
C;Date: 25-Oct.1987 #sequence_revision 25-Oct.1987 #text_change 18-Jun-1993
C;Accession: A26363
C;Accession: A26363
C;Stangler, J.; Hilbich, C.; Beyreuther, K.; Keller, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 575-579, 1987
A;Title: Unusual cardioactive peptide (CCAP) from pericardial organs of the
                                                                                                                                                                                                                                                                             cardioactive peptide CCAP - tobacco hornworm (Species: Manduca sexta (tobacco hornworm) (C:Date: 09-Jun-1994 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996 C:Accession: S27233 R:Cheung, C.C.; Loi, P.K.; Sylwester, A.W.; Lee, T.D.; Tublitz, N.J. FEBS Lett. 313, 165-168, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardioactive peptide CCAP - yellow mealworm (Species: Tenebrio molitor (yellow mealworm) (C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 07-May-1999 C;Accession: S39766 R;Furuya, K.; Liao, S.; Reynolds, S.E.; Ota, R.B.; Hackett, M.; Schooley, D.A. Biol. Chem. Hoppe-Seyler 374, 1065-1074, 1993 A;Title: Isolation and identification of a cardioactive peptide from Tenebrio molitor A;Reference number: S39766; MUID:94176032 A;Accession: S39766
                                                                                                                                                                   A; Residues:
C; Keywords:
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A; Accession: S27233
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S39766
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. 84, 575-579, 1987
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-I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
Neuropeptide; Amidation; Multigene family.
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Duve H., Johnsen A.H., Maestro J.-L., Scott A.G.
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CARCINUSTATIN 5.
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyun
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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Eur. J. Biochem. 250:727-734(1997).
-i. FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-i. SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
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-!- FUNCTION: MAY ACT AS A NEUROTRANSITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Multigene family.
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(Rel.
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Decapoda; Pleocyemata;
Portunidae; Carcinus.
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. le+05;
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RESULT 8
AL12_CARMA
ID AL12_C
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DT 30-MAY
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WWA3_ACHFU
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Matches 2
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Achatinacea; Achatinidae; Achat
NCBI_TaxID-6530;
                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 12.
Carcinus macnas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                                                                              AL12_CARMA
P81815;
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SEQUENCE
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MEDLINE-93265912; PubMed-8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi I
"WWamide-1, -2 and -3: novel neuromodulatory
ganglia of the African giant snail, Achatina
FEBS Lett. 323:104-108(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Ganglion;
MEDLINE=93265912;
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Achatinacea; Achatinidae; Achatina.
MCBI_TaxID-6530;
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01-JUN-1994 (Rel.
01-OCT-1994 (Rel.
      Eumalacostraca; Eucarida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuropeptide; Amidation.
MOD_RES 7 7
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P35921;
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Achatina fulica
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1 WK 2
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2; Conserv
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2; Conserv
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      Decapoda;
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sca; Gastropoda;
Achatina.
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7362D5B69B132310 CRC64;
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0; Mismatches
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      Pleocyemata;
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). 1e+05;
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b. 1e+05;
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peptides isolated
fulica.";
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RESULT 10
ALL8_CARMA
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ALT_CARMA

C P81809; P81810; P81804;

P81809; P81810; P81804;

T 30-MAY-2000 (Rel. 39, Created)

T 30-MAY-2001 (Rel. 39, Last sequence update)

T 20-AUG-2001 (Rel. 40, Last annotation update)

T 20-AUG-2001 (Rel. 47) (Last annotation update)

E CARCINUSTATIN 7 [CONTAINS: CARCINUSTATIN 6; CARCINUSTATIN 1

C Carcinus maenas (Common shore crab) (Green crab).

C Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

C Eukaryota; Metazoa; Arthropoda; Pleocyemata; Brachyura;

C Eubrachyura; Portunoidea; Portunidae; Carcinus.

N NCBI_TaxID=6759;
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Best Local
ALL8_CARMA
P81811;
30-MAY-2000
30-MAY-2000
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TISSUE-Cerebral ganglion, and Thoracic MEDLINE-98121193; PubMed-9461295; Duve H., Johnsen A.H., Maestro J.-L., S
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-i- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULAT - SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY. Neuropeptide; Multipene family.

Neuropeptide; Maltigene family.
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Thorpe A.
                                                                                                                                                                                                          Neuropeptide; Amidation; Multigene family.
CHAIN
1 8 CARCINUSTATIN 7.
CHAIN 2 8 CARCINUSTATIN 1.
CHAIN 4 8 CARCINUSTATIN 1.
MOD_RES 8 8 AMIDATION.
SEQUENCE 8 AA; 825 MW; 922879CDCB4775BD CRC64;
                                                                                                                                                                                                                                                                                                                        allatostatin
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NCBI_TaxID=6759;
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2; Conserv
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ilarity 100.0%;
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                                    STANDARD;
39,
39,
Created)
Last sequence
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maenas.";
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Thorpe A.;
                                                                                                                                                                *Isolation and identification of multiple neuropeptides allatostatin superfamily in the shore crab Carcinus maen Eur. J. Biochem. 250:727-734(1997).
-i- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODU-i- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
MOD_RES 8
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781 MW; 7C2879CDCB476878 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               ALL9_CARMA STANDARD; PRT; 8 AA. P81812; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 310-MAY-2000 (Rel. 39, Last annotation update)
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Eubrachyura; Portunoidea; Portunidae; Carcinus.
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  LCK1_LEUMA
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01-MAY-1991 (Rel. 1
01-MAY-1991 (Rel. 1
01-MAY-1991 (Rel. 1
LEUCOKININ I (L-I).
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Pterygota; Ne
Blaberoidea;
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P19989;
01-FEB-1991
                                                                                                                                                                                                                                                                   "Isolation, primary structure and synthesis of leucokinins VII and VIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae."; Comp. Blochem. Physiol. 88C:31-34(1987).

-i- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).

-i- SIMILARITY: TO THE OTHER LEUCOKININS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
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01-FEB-1991 (Rel. 17, L
LEUCOKININ VII (L-VII)
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Pterygota; Neoptera; Orthopteroidea; Dictyoptera;
Blaberoidea; Blaberidae; Leucophaea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leucophaea maderae (Madeira cockroach).
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FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
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100.0%; Pr
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DC6365A5B9CDC76A
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20-AUG-2001 (Rel. 40,
20-AUG-2001 (Rel. 40,
ORCOMYOTROPIN (OMT).
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MEDLINE-20411310; PubMed-10952880;

Dircksen H., Burdzik S., Sauter A., Keller R.;

Dircksen H., Burdzik S., Sauter A., Keller R.;

"Two orcokinins and the novel octapeptide orcomyotropin in the hindgut of the crayfish Orconectes limosus: identified myostimulatory neuropeptides originating together in neurones of the terminal abdominal ganglion.";

J. Exp. Biol. 203:2807-2818(2000).

-I- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED BY ABDOMINAL GANGLIONIC NEURONS.

-I- MASS SPECTROMETRY: MW-904.8; METHOD-FAB.

Amidation; Neuropeptide.

BY ADDITION: BEST NEUROPETIDE.

BY ABOMINAL GANGLIONIC NEURONS.

-I- MASS SPECTROMETRY: MW-904.8; METHOD-FAB.

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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacida
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NCBI_TaxID-28379;
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Submitted (DEC-1997) to the SWISS-PROT data bank.
-!- CAUTION: WE ARE UNABLE TO FIND THIS PROTEIN I
THE GENOME OF STRAIN H37RV.
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30 KDA NON-SECRETORY PROTEIN 3 (FRAGMENT)
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-1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
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Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyu
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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MEDLINE=98121193;
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3; PubMed=9461295;
n A.H., Maestro J.-L., S
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MOD_RES SEQUENCE 9 AF
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ALI1_CARMA STANDARD; PRT; 9 AA
P81814;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                            Carcinus maenas (Common shore crab) (Green crab), Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm), Tenebrio molitor (Yellow mealworm), and Spodoptera eridania (Southern armyworm). Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyu Eubrachyura; Portunoidea; Portunidae; Carcinus. NOBI_TaxID=6759, 7130, 7067, 37547;
                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Biochem. 250:727-734(1997).

-I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
Neuropeptide; Amidation; Multigene family.
Neuropeptide; Amidation, Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duve H., J
Thorpe A.;
                                                                                                                                                              01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CARDIOACTIVE PEPTIDE (CCAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carcinus maenas (Common shore crab) (Green crab).

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.
SPECIES=C.maenas; TISSUE=Pericardial organs;
Stangier J., Hilbich C., Beyreuther K., Keller R.;
"Unusua cardioactive peptide (CCAP) from pericardial organs
                                                                                                                                                                                                                                           CARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Cerebral ganglion, and Thoracic MEDLINE=98121193; PubMed=9461295;
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01-OCT-1994
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Pred. No. 1e+05;
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01-FEB-1991 (Rel. 17, C
01-FEB-1991 (Rel. 17, L
01-FEB-1991 (Rel. 17, L
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Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
-i- FUNCTION: THE EFFECT OF CCAP IS BOTH INO-
-i- TISSUE SPECIFICITY: STORED IN PERICARDIAL
INTO THE HEMOLYMDU
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SEQUENCE
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                                                                                                                                                                                                          Echinoidea; Euechinoidea; Clypeasteridae; Clypeasteridae; Clypeaster
                                                                                                                                                                                                                              Clypeaster japonicus (Sand dollar). Eukaryota; Metazoa; Echinodermata;
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FEBS Lett. 313:165-168(1992).
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Suzuki N.,
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S27233; S27233.
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Natl. Acad. Sci. U.S.A. 84:575-579(1987).
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Kurita M.,
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omata; Clypeasteroida;
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01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
CALLITACHYKININ I.
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P04378;
20-MAR-1987
Hormone;
MOD_RES
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SEQUENCE
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                                                                                                                                                  J. B101. Chem. 261:4812-4819(1986).
-I- FUNCTION: STIMULATES THE SECRETION
FOLLICLE-STIMULATING HORMONES.
-I- SIMILARITY: BELONGS TO THE GNRH FAN
PIR: A01412; RHLMGS.
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NCBI_TaxID=27454;
                                                            InterPro: TPR002012; GnRH.
pfam; pF00446; GnRH; 1.
pR0SITE; pS00473; GNRH; 1.
Hormone; Amidation; Hypothalamus.
                                                                                                                                                                                                                                                                                                            Sherwood N.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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20-MAR-1987 (Rel.
01-JUN-1994 (Rel.
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Peptides 15:761-768(1994).
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SIMILARITY: SOME SIMILARITY TO TACHYKININS
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2417C86B59CDC1B7 CRC64;
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AMIDATION.
1E4B36237B1735AB
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Pred. No.
                                         PYRROLIDONE CARBOXYLIC ACID
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Bacteria; Protec
NCBI_TaxID=285;
                                                                                                                            MEDLINE-90033007, retrier S., Lingens F.; Schach S., Tshisuaka B., Fetzner S., Lingens F.; Schach S., Tshisuaka B., Fetzner S., Lingens F.; Quinoline 2-oxidoreductase and 2-oxo-1,2-dlhydroquinoline dioxygenase from Comamonas testosteroni 63. The first two emitnoline and 3-methylquinoline degradation.";
                                                                                                                                                                                                                                                                                                                                                                        Hormone;
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93178316; PubMed-8440174; Sower S.A., Chiang Y.-C., Lovas S., Conlon "Primary Structure and biological activity releasing hormone from lamprey brain."; Endocrinology 132:1125-1131(1993).

-I-FUNCTION: STIMULATES THE SECRETION OF B FOLLICLE-STIMULATING HORMONES.
      quinoline and 3-methylquinoline de
Eur. J. Biochem. 232:536-544(1995)
-i- FUNCTION: CONVERTS (3-METHYL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LULLBERTE TIT),
Petromyzon marinus (Sea lamprey),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GONADOLIBERIN III (GONADOTROPIN-RELEASING HOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _PETMA
GON3__PETMA
                                                                                    STRAIN-63;
                                                                       MEDLINE-96035889; PubMed-7556204;
                                                                                               SEQUENCE
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Pfam; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1.
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NCBI_TaxID=7757;
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01-JUL-1993
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100.0%; Pred. No.
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284B36237AA1F5A3 CRC64;
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Search completed: January 14, 2002, 08:08:22 Job time: 707 sec
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1(2H)-ONE + REDUCED ACCEPTOR.
-i- COPACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
-i- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND
(3-METHYL-)QUINOLINE.
-i- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
TWO GAMMA CHAINS (PROBABLE).
OXIGOREGUCTASE; FLAVOPROTEIN; FAD; MOLYBDENUM.
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SEQUENCE 10 AA; 1241 MW; C2E2C25DD9CDC769 CRC64;
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SEQUENCE
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MEDLINE=97295299; PubMed=9150941;
Mini L., Heid H., Libberatori S., Geier G., Pallini V., Zwilling R.;
Mino-dimensional gel electrophoresis of Caenorhabditis elegans
homogenates and identification of protein spots by microsequencing.";
Electrophoresis 18:557-562(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
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Compugen Ltd
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O9tc61 melanoplus
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O9gy07 leishmania
O4865 lutjanus bu
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| Q9TQB3 | 077912 | 077883 | 060614 | P95518 | Q47451 | Q9QVK8 | Q9XMB4 | Q9R7J8 | 090350 | Q85599 | Q9АХН8 | Q9UMA0 | Q9UQW0 | Q14277 | Q46179 | Q45852 | Q98YK9 | Q9JLD7 | Q62721 | P82689 | 009258 | Q95945 | Q15903 | Q65089 | 021218 | 021210 | Q9TEF8 | 003341 | 003340 | 003302 |
| | 077912 oreochromis | oreoc | 060614 homo sapien | P95518 pasteurella | escherichia | Q9qvk8 mus sp. mep | Q9xmb4 aegilops ta | cte | hepatitis | | h8 mese |) homo | homo sap | | Q46179 clostridium | Q45852 clostridium | • | Q9jld7 mesocricetu | _ | | | sacch | ᠴ | 980 | 218 | 0.1 | f8 o | æ | 40 s | 003302 campephilus |

ALIGNMENTS

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RESULT 1
Q9TRU3
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AC Q9TRU3;
DT 01-MAY-2000 (TrEMBLrel. 13, C:
DT 01-JUN-2001 (TrEMBLrel. 17, L:
DT 01-JUN-2001 (TrEMBLrel. 17, L:
DE FACTOR IX HEAVY CHAIN.
                                                                   ACCOCCART RAX
В
            Qy
                            Query Match
Best Local S
Matches 4
                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                      SEQUENCE
                                                                                                                                                                   NCBI_TaxID=9986;
24
              5 afxg 8
AFXG
                             Similarity 4; Conserv
27
                             Conservative
                            37.5%; Score 3;
100.0%; Pred. No.
Live 0; Mismatc
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o. 5.5e+02;
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Q9GXM2;
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01-MAR-2001 (TrEMBLrel. 16, 1
01-JUN-2001 (TrEMBLrel. 17, 1
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PROSITE; PS50297; ANK_REP_REGION;
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919 MW; 60476
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Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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NCBI_TaxID=5664;
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                                                                                                                                                       Mismatches
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No. 8.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosomatidae;
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                                                                                                                                                                                          Length 66;
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Ann. Entomol. Soc. Amer. 92:617-623(1999).

AL Ann. Entomol. Soc. Amer. 92:617-623(1999).

C: FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
C: FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME IS A
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUDLED TO ATP SYNTHESIS (BY SIMILARITY).

CC -!- COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).

CC --- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC --- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC --- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.

DR EMBL; AF145493; AAD56033.1; --
DR InterPro, IPRO00179; CYt_b_b6.
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Q9TC61;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                             NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane.
NON_TER 1
NON_TER 82
                                                                                                                                                                                                                        O9NNG8 PRELIMINARY; PRT; 88 AA.
Q9NNG8;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PROBABLE HYPOTHETICAL 27.7 KDA PROTEIN (FRAGMENT).
                                                                                                 STRAIN-FRIEDLIN;
Murphy L., Quail M., Harris
Submitted (JUL-2000) to the
EMBL; AL160371; CAC00242.1;
                                                                                                                                                                          Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Cae Acridomorpha; Acridoidea; Acrididae; Melanoplus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOCHROME CYTB.
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                LM15.205
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electron transport; Heme; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chapco W., Kuperus W.R., Litzenberger G.S.; "Molecular phylogeny of melanopline grasshoppers Acrididae). The genus Melanoplus."; Ann. Entomol. Soc. Amer. 92:617-623(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chapco W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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les 4; Conservative
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   Conservative
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9379
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37.5%; 5cc
100.0%; Pr
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100.0%; Pr
''' 0;
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82
                                                                                                                                                                                        Kinetoplastida;
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Last
                                                                                                             D., Rajandream M., EMBL/GenBank/DDBJ
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Pred. No.
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annotation
DB 5; LC.;
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                                                                                                                                                                                        Trypanosomatidae;
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                            Length 88;
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Best Local Similarity 100.0%;
Matches 5; Conservative
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                                                                                                     Submitted (AUG-2000) to the EMBL/GenBank/DDBJ EMBL; AL390114; CAC02042.1; -. InterPro; IPR002202; HMG-COA_red. PROSITE; PS00066; HMG_COA_REDUCTASE_1; UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mulyanto, Hijikata M., Matsushita M., Ing
Sumarsidi D., Kanai K., Ohta Y., Mishiro
"TT virus (TTV) genotypes in native and n
Irian Jaya, Indonesia: implication for no
transmission.";
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                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-FRIEDLIN;
                                                                                                                                                                                             Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE HYPOTHETICAL 77.1 KD PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssDNA viruses;
NCBI_TaxID=68887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TT virus.
                                                                                                                                                                                                                                                                                       Q9GY07
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1999) to the EMBL; AB031728; BAA86191.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-TTV WAM973;
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                                                                                                                                                        L., Quail M.,
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11265 MW;
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                                                                                                                                                                                                                                                                                                                                                                                   37.5%;
                                                                                                                                                         Harris
                                                                                                                                                                                                       Kinetoplastida;
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0; Mismatches
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                                    Score 3; 1
Pred. No.
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                                                                           47230C5CD5456206 CRC64;
                           Mismatches
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iro S.;
                                     DB 5; Le
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). 1.2e+03;
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                                            Length 100;
                           0;
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Best Local
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Q34865;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane.

NON_TER 110

SEQUENCE 110
SEQUENCE FROM N.A.

Lara M.C., Patton J.L.;
"Evolutionary diversification of spiny rats (genus Echimyidae) in the Atlantic Forest of Brazil.";
                                                                                                                                                                                                                                                                                                                 O9T784

O9T7B4;

O1-MAY-2000 (TrEMBLrel. 13,

O1-MAY-2001 (TrEMBLrel. 13,

O1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sarver S.K., Freshwater D., Walsh P.J.;

Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.

FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE

COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2

FERROCYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoide Lutjanidae; Lutjaninae; Lutjanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COV BOUND TO THE PROTEIN (BY SIMILARITY).
-1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
EMBL: U26959; AAA70175.1; -.
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                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                         CYTB OR CYT B.
Trinomys iheringi.
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                                                                                                                                                                                                                                                                                              CYTOCHROME B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTB.
                                                                                                                                        NCBI_TaxID=42830;
                                                                                                                                                                                                                      Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electron transport; Heme; Mitochondrion; Respiratory chain;
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TE; PS00192; CYTOCHROME_B_HEME;
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110 AA;
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12530 MW;
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Rodentia;
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                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Hystricognathi; Echimyidae; Trinomys
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Best Local
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Best Mocal (
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ZOO1. J. Linn. Soc. 0:0-0(2000).

FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-!- COFACTOR: TWO HEME GROUPS (B563 AND B566) WHICH ARE NOT COVALE BOUND TO THE PROTEIN (BY SIMILARITY).

-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.

InterPro; IPR000179; Cyt_b_b6.

Pfam; PF00033; Cytochrome b_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       "Evolutionary diversification of spiny rats (genus Trinomys, Rodentia: Echimyidae) in the Atlantic Forest of Brazil.";

ZOOL. J. Linn. Soc. 0:0-0(2000).

1. Linn. Soc. 0:0-0(2000).

1. - FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

1. COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

1. COPACTOR: TWO HEME GROUPS (B563 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

1. SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
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NON_TER 130
SEQUENCE 130 AA;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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Mammalia; Eutheria;
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01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                         -i - SIMILARITY: BELONGS TO THE CYTOCHROME EMBL; AF194320; AAF16122.1; -. EMBL; AF194319; AAF16121.1; -. InterPro; IPR000179; Cyt_b_b6.
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                                                                                                                                                                                                                                                        Transmembrane
                                                                                                                                                                                                                                                                          Electron transport; Heme; Mitochondrion; Respiratory chain;
                                                                                                                                                                                                                                                                                                         Pfam; PF00033; cytochrome_b_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lara M.C., Patton J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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4; Conservative
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131 AA;
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                                                                           Conservative
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Rodentia;
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17,
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                                                                                                Score 3;
Pred. No
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Pred. No.
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Hystricognathi; Echimyidae; Trinomy
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                                                                                                                                                                                                      F5374EFC940B9EAB CRC64;
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                                                                           Mismatches
                                                                                                   No.
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                                                                                                DB 8; Ler
D. 1.6e+03;
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                                                                                                                        Length 131;
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RESULT
Q59551
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Q9K4Q2
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Best Local Similarity 100.
Conservative
                                                                                                                                                                                                                                                Q59551 PRELIMINARI,
Q59551; O1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ADENOSINETRIPHOSPHATASE (EC 3.6.1.3) (ADENYLPYROPHOSPHATASE) (ATPASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9K4Q2
Q9K4Q2;
01-OCT-2000
01-OCT-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                              MEDLINE=93054343; PubMed=1429453;
Wenzel R., Pirkl E., Herrmann R.;
"Construction of an EcoRI restriction map of Mycoplasma localization of selected genes.";
J. Bacteriol. 174:7289-7296(1992).
-i- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + PHOSPHATE.
                                                                                                                                                                                                                                 Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ388566; CAB96453.1; -. Interpro; IPR003393; AMO. Pfam; PF02461; AMO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Speksnijder A.G.C.L., Kowalchuk G.A.,
"Recovery of a Nitrosomonas-like amoa
habitats.";
Hydrogen ion transport; Hydrolase
NON_TER 1 1 1
NON_TER 151 151
SEQUENCE 151 AA; 16671 MW; A71
                                                 InterPro; IPR000194; ATPase_alpha_beta
Pfam; PF00006; ATP-synt_ab; 1.
                                                                                                                                                                                                           Mycoplasmataceae;
NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unidentified proteobacterium
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                                                                         EMBL;
                                                                                                                                                                         STRAIN=M129;
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2722;
                                                                       -!- SIMILARITY: TO ATPASE ALPHA/BETA CHAINS EMBL; X67653; CAA47895.1; -.
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149 AA;
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16673 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.5%;
100.0%;
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Last annotation update)
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Pred. No.
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  A7FD199618264466 CRC64;
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Query Match
Best Local Similarity

37.5%; 100.0%;

Score 3; Pred. No.

DB 2; Le . 1.9e+03;

Length 151;

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RESULT
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OUTER SURFACE PROTEIN PRECURSOR (FRAGMENT).
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Protrobacteria; alpha subdivision; Rickettsiaceae; Wolbachieae; Wolbachia. NCBI_TaxID-77833;
                                                              Wolbachia sp. wKayLC
                                                                                                                                                                                                                     Q9ZH44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000179; Cyt_b_b6.
Pfam; PF00033; cytochrome_b_N; 1.
PROSITE; PS00192; CYTOCHROME_B_HEME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20458311; PubMed-11005301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17,
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2 2e+03;
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                                              Rickettsiales;
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RESULT
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AC Q9
AC Q9
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DT 0:
CC CC
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01-NOV-1998
01-NOV-1998
01-JUN-2001
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09TEJ6;

01TEMBLTel. 13;

01-MAY-2000 (TrEMBLTel. 13;

01-JUN-2001 (TrEMBLTel. 17;
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SEQUENCE
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                                CYTB.
                                                                                                                                                                                                                                                                                                                                                                                                     Desulfococcus multivorans.
Bacteria; Proteobacteria;
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DISSIMILATORY SULFITE REDUCTASE ALPHA SUBUNIT (FRAGMENT).
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SEQUENCE FROM N.A.
STRAIN-WKAYLC;
   Eukaryota;
           Mitochondri
                    Dicrostonyx torquatus (Arctic
                                                                                                                                                                                                                                                                  Pfam; PF01077; NIR_SIR; 1. PRINTS; PR00397; SIROHAEM.
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-ATCC 33890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=897;
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EMBL; AF071927; AAC77407.1; -
InterPro; IPR002566; Surface_Ag_msp4
Pfam; PF01617; Surface_Ag_2; 1.
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"Phylogeny of the arthropod endosymbiont Wolbachia based
                                                                                                                                                                                                                                                                             InterPro; IPR000660; Nir_Sir.
Pfam; PF01077; NIR_SIR; 1.
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185 AA;
 Metazoa;
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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                                        (FRAGMENT)
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23637 MW;
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19990 MW;
  Chordata;
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100.0%;
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Pred.
 Craniata;
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                    lemming).
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No.
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5. 2.6e+03;
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 Vertebrata;
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                                                  update)
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                                                                                                                                                                                                                                                                                                                                           Stahl D.A
 Euteleostomi;
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RESULT 17
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DT 01-FEE
DT 01-FEE
DT 01-WILL
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C. :- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C EDUCTASE
C. :- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C EDUCTASE
C. :- COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
C. CRESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
C. COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
C. :- COFACTOR: TWO HEME GROUPS (B562 AND 566) WHICH ARE NOT COVALENTLY
C. BOUND TO THE PROTEIN (BY SIMILARITY).
C. :- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
C. :- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
C. :- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE CYTOCHROME B/B6 FAMILY.
C. :- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
C. :- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
C. :- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
C. :- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
C. :- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
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CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
C. :- SIMILARITY: CYTOCHROME B/B6 FAMILY.
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
C. :- SIMILARITY: CYTOCHROME B/B6 FAMILY.
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Best Local
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Bruna E.M., Fisher R.N., Case T.J.;

Bruna E.M., Fisher R.N., Case T.J.;

Proc. R. Soc. Lond., B, Biol. Sci. 263:681-688(1996).

-i- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2
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Q95792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
CYTOCHROME C (FRAGMENT).
                                                                                                         -i- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COY BOUND TO THE PROTEIN (BY SIMILARITY).

-i- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Emoia cyanura (blue-tailed skink).
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"The importance of ice ages in diversification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                          SIMILARITY: BELONGS TO THE CYTOCHROME L; U49347; AAB06601.1; -.
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Scincoidea;
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Best Local
                          Matches
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Q9ZZG1;
Q9ZZG1;
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                             "Phylogenetic relationships and species limits within Phyllotis (Rodentia: Sigmodontinae): concordance between mtDNA sequence and morphology.";
J. Manmal. 79:0-0(1998).

-i- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-i- COPACTOR: TWO HEME GROUPS (B562 AND 8566) WHICH ARE NOT COVALENTLY BOTHER.
                                                                                                                                                                    Steppan S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                        Phyllotis.
NCBI_TaxID=59938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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                                                                                   SEQUENCE
                                                                                                                        Transmembrane.
                                                                                                                                                                                                                   BOUND TO THE PROTEIN (BY SİMILARITY).

1. SUBUNLT: THE MAIN SUBUNLTS OF COMPLEX B-C1 ARE: CYTOCHROME CYTOCHROME AND THE RIESKE PROTEIN (BY SIMILARITY).

1. SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-LCM 638;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phyllotis osgoodi (Osgood's leaf-eared mouse).
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                                   Similarity
                                                                                                                                              00033; cytochrome_b_N; 1.
PS00192; CYTOCHROME_B_HEME; 1.
PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
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PS00192; CYTOCHROME_B_HEME; 1.
PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
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100.0%; Pr
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Rodentia;
                                    37.5%;
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                                                                                                                                   Mitochondrion;
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                         s: Score 3; DB 8
b; Pred. No. 3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Ver
Sciurognathi;
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                                                                                     3E91294031F728ED CRC64;
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b. 3.6e+03;
                                    DB 8; Le
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thi; Muridae; Sigmodontinae;
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                                                                                                                                  Respiratory chain;
                                                Length 311;
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Best Local
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01-MAR-2001
01-JUN-2001
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SEQUENCE
         SEQUENCE FROM N.A. STRAIN-LSU11786;
                                                                                               01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-JUN-2001 (TrEMBLrel. 17, CYTOCHROME B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Renner S.S., Meyer K.; Submitted (MAY-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Renner S.S., Meyer K.;

Renner S.S., Meyer K.;

Melastomeae come full circle: biogeographic reconstruction

molecular clock dating.";
                                                Eukaryota; Metazoa; Chordata; Archosauria; Aves; Neognathae;
                                                                                          CYTB.
                                                                                                                                                                                                                                                                                                                                Pfam; PF00361; oxidored_q1; 1. Pfam; PF01010; oxidored_q1_C; 1. ProDom; PD000531; Bet_v_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; curosids II; Myrtales; Melastomataceae; Rhexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9MRX6
                                      NCBI_TaxID: 56085;
                                                                      Mitochondrion.
                                                                              Campephilus haematogaster.
                                                                                                                                                    003302
                                                                                                                                                                                                                                                                                                                          Chloroplast; NAD;
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000916; Bet_v_I.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR002128; Oxidored_q1_C.
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01-MAR-2001 (TrEMBLrel. 16, La
01-JUN-2001 (TrEMBLrel. 17, La
NADH DEHYDROGENASE (FRAGMENT).
  Moore W.S.,
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ilarity 100.0%;
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Defilippis V.R.;
                                                                                                                                                   PRELIMINARY;
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37082 MW;
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                                                                                                                                                                                                                                                    Score 3; Pred. No.
                                               Craniata; Vertebrata; Euteleostomi; Piciformes; Picidae; Campephilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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ЭВ
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1.8e+03;
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RESULT
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                                                                                COMPLEX (COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
COMPLED TO ATP SYNTHESIS (BY SIMILARITY).
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
COMPLED TO ATP SYNTHESIS (BY SIMILARITY).
COMPLED TO THE PROTEIN (BY SIMILARITY).
COMPLET THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
COMPLET THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
COMPLET THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
COMPLET BELONGS TO THE CYTOCHROME B,
COMPLET BELONGS TO THE CYTOCHROME B/B6 FAMILY.
COMPLET BELONGS TO THE CYTOCHROME B/B6 FAMILY.
COMPLET BELONGS TO THE CYTOCHROME B/B6 FAMILY.
COMPLET BELONGS TO THE CYTOCHROME B/B6 FAMILY.
COMPLET BERODO32; CYTOCHROME_B_C; 1.
CYTOCHROME_B_D; 1.
CYTOCHROME_B_D; 1.
CYTOCHROME_B_D; 1.
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C COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
C RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
C COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
C -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
C BOUND TO THE PROTEIN (BY SIMILARITY).
C -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
C CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
C -1- SIMILARITY: BELONGS TO THE CYTOCHROME B,
C CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
TREMBL; UB3284; AAB53600.1; -.
TREMBL; UB3284; AAB53600.1; -.
TREMBL; UB3284; AAB53600.1; -.
DR PAGM; PF00032; CYTOCHROME B_C; 1.
PF6am; PF00032; CYTOCHROME B_D(; 1.
DR PAGM; PS00193; CYTOCHROME B_D(; 1.)
DR PROSITE; PS00193; CYTOCHROME B_D(; 1.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-WSU86148;
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                        Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore W.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sphyrapicus varius (Yellow-bellied sapsucker).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOCHROME B (FRAGMENT).
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  SEQUENCE
                                                                  Electron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Avian molecular evolution and systematics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moore W.S., DeFilippis V.R., (In) Mindell D.P. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=56079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Electron transport; Heme; Mitochondrion; Respiratory chain;
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Avian molecular evolution and systematics, pp.81-116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 AFXG
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  347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aves; Neognathae;
  AA;
38763 MW;
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                                                                    Heme;
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                                                                  Mitochondrion;
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Pred. No.
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D367AF657218DE0E CRC64;
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drion; Respiratory chain;
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es; Picidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 346
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Sphyrapicus.
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Query Match

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                                                        Q9TEF8 PRELIMINARY;
Q9TEF8;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
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003341;
01-JUL-1997
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01-JUN-2001
                                     CYTB
            Oryctolagus cuniculus (Rabbit). Mitochondrion
                                                                                                                                                                                                                                                                                                                    Interpro; IPR000179; Cyt_b_b6.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
PROSITE; PS00192; CYTOCHROME_B_HEME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moore W.S., DeFilippis V.R.;
(In) Mindell D.P. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOCHROME B
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                              CYTOCHROME B (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-WSU86149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                             FERROCYTOCHROME C.

COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX II OR CYTOCHROME B-C] COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             York (1997)
                                                                                                                                                                                       afxg
                                                                                                                                                                  AFXG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFXG 98
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                                                                                                                                                                                                                                                                                                                                                                  U83296; AAB53614.1;
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                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                          transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 (TrEMBLrel.
7 (TrEMBLrel.
                                                                                                                                                                                                                                                                          347 AA;
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Chordata; Craniata; Vertebrata; Neognathae; Piciformes; Picidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Yellow-bellied sapsucker).
                                                                                                                                                                                                           37.5%; 5c.
100.0%; Pr
                                                                                                                                                                                                                                                                                                           Heme;
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. 17, Last anno
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04,
17,
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Mitochondrion;
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Last annotation update)
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                                                                                                                                                                                                                           Score 3; pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                          50BB475A78C9E28D CRC64
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                                                                                                                                                                                                                 Mismatches
                                                          sequence update;
annotation updat
                                                                                                          355
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0. 4e+03;
                                                                                                                                                                                                                           DB 8;
. 4e+03;
                                                                                                                                                                                                                                                                                                           Respiratory chain;
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                                                                                                                                                                                                                 0;
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Sphyrapicus.
                                                                                                                                                                                                                 0,
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Best Local
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021210;
01-JAN-1998
01-MAY-2000
01-JUN-2001
             from analysis of cytochrome b gene sequences.";
Mol. Phylogenet. Evol. 9:192-203(1998).

-i- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-i- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALE
BOUND TO THE PROTEIN (BY SIMILARITY).

-i- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Verte Actinopterygii; Neopterygii; Teleostei; Eutel Acanthomorpha; Acanthopterygii; Percomorpha; Cichlidae; Parachromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOCHROME B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN_1
Electron transport; Heme; Mitochondrion; Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR000179; Cyt_b_b6.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-:- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

-:- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-:- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.

EMBL; AJ243996; CAB45258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Branco M., Ferrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98224076; PubMed=9562979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parachromis dovii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene.
                                                                                                                                                                                                                                                                                                                                                   Martin A.P., Bermingham E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=63177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [berian peninsula inferred
                                                                                                                                                                                                                                                                                                                    Systematics and evolution of lower Central American cichlids inferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phylogeography
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nitted (JUN-1999) to the EMBL/GenBank/DDBJ databases FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C RICOMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), W
AF009924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 05,
(TrEMBLrel. 13,
(TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and N., of the
AAB64130.2;
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40051
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European rablerred from RFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       821F1AFEAF9A85E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rabbit (Oryctolagus RFLP analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; רבי
ס. 4.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perciformes; Labroidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                  ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REDUCTASE
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SOT TENEDOR

Intempro; IPR000179; Cyt_b_b6.

Pfam; PF00032; cytochrome_b_C; 1.

Pfam; PF00033; cytochrome_b_N; 1.

PROSITE; PS00192; CYTOCHROME_B_HEME; 1.

PROSITE; PS00193; CYTOCHROME_B_OO; 1.

Electron transport; Heme; Mitochondrion; Respiratory chain; Transports of the state

NON_TER NON_TER SEQUENCE

374 374 AA;

1 374 ; 41771 MW;

28E57DD28DCA24D4 CRC64;

Transmembrane.

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                                                                                                                                       C C FERROCYTOCHROME C.

C FERROCYTOCHROME C.

C -1 COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY

C BOUND TO THE PROTEIN (BY SIMILARITY).

C -1 SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,

C CYTOCHROME C1 AND THE RISKE PROTEIN (BY SIMILARITY).

C -1 SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.

DR EMBL; AF009926; AAB64132.1; -

DR Pfam; PF00032; CYTOCHROME_B-B.

DR Pfam; PF00032; CYTOCHROME_B-C; 1.

PROSITE; PS00192; CYTOCHROME_B-N; 1.

DR PROSITE; PS00193; CYTOCHROME_B-OO; 1.

KW Electron transport; Heme: Mitochondrion; Respiratory chain;
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Best Local Similarity
Matches 4; Conserv
                                                           Best Local Similarity
Matches 4; Conserv
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                      Martin A.P., Bermingham E.;

Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-I-CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C · Q + 2
                                                                                                                                    Transmembrane.
NON_TER 379
SEQUENCE 379 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygil; Neopterygil; Teleostel; Euteleostel; Neoteleostel; Acanthomorpha; Acanthopterygil; Percomorpha; Perciformes; Labroide Cichildae; Parachromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2001 (TrEMBLrel. 17, CYTOCHROME B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parachromis loisellei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 021218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 AFXG 128
127 AFXG 130
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                             5 afxg 8
                                                                                                                                       379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.5%; Score 3; DB 8; Le illarity 100.0%; Pred. No. 4.3e+03; Conservative 0; Mismatches 0;
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                    379
42399 MW;
                                                                        37.5%;
                                                          %; Score 3; DB 8
%; Pred. No. 4.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                     2B5895B5481FEBF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379
                                                                        DB 8; Ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
                                                                                      Length 379
                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                           0;
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Search completed: January 14, 2002, 08:07:34 Job time: 764 sec

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20
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first 50 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                  OLIGO Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-185908-1D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      January 14, 2002, 07:56:30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 wkxxafxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp/AA1987.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqp/AA1989, DAT: *
/SIDS2/gcgdata/geneseq/geneseqp/AA1990, DAT: *
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/SIDS2/gcgdata/geneseq/geneseqp/AA1991, DAT: *
/SIDS2/gcgdata/geneseq/geneseqp/AA1992, DAT: *
/SIDS2/gcgdata/geneseq/geneseqp/AA1993, DAT: *
/SIDS2/gcgdata/geneseq/geneseqp/AA1995, DAT: *
/SIDS2/gcgdata/geneseq/geneseqp/AA1996, DAT: *
/SIDS2/gcgdata/geneseq/geneseqp/AA1997, DAT: *
/SIDS2/gcgdata/geneseq/geneseqp/AA1997, DAT: *
                                                                                                                                                                                                          \SIDS2/gcgdata/geneseq/geneseqp/AA1998.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:*
                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search time 81.39 Seconds (without alignments)
7.281 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          522463
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| egult No. | Score | Query Match | Query Match Length DB | DВ | ID | Description |
|--------------|-------|----------------|--------------------------|----|----------|--------------------|
| | w | 37.5 | 5 | 19 | AAW45592 | Substrate #13 for |
| N | ω | 37.5 | 15 | 15 | AAR51894 | Chitin binding pro |
| w | ω | 37.5 | 23 | 21 | AAY84533 | Amino acid sequenc |
| 4 | ω | 37.5 | 65 | 20 | AAY36099 | Extended human sec |
| տ | ω | 37.5 | 91 | 22 | AAG76045 | Human colon cancer |
| 6 | w | 37.5 | 105 | 18 | AAW27978 | Amino acid sequenc |
| 7 | ω | 37.5 | 112 | 20 | AAY13018 | Human secreted pro |
| 8 | w | 37.5 | 127 | 20 | AAY27139 | Vertebrate slit pr |
| 9 | ω | 37.5 | 162 | 22 | AAB63955 | Human prostate can |
| 10 | w | 37.5 | 172 | 22 | AAG73946 | Human colon cancer |
| 11 | w | 37.5 | 181 | 22 | AAG80899 | Lipid degradation |
| | | | | | | |

| 50 | 48 | 47 | 7 4 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 |
|-------------------------------|----------|---------------|------------|--------------|------------|-----------|----------|----------|----------|----------|--------------|-----------|--------------|------------|------------|----------|----------|------------|------------|----------|-----------|-----------|----------|----------|----------|-------------------|--------------------|----------|----------|----------------|------------|----------|----------|--------------------|---------------|--------------------|
| 2 25 2 25 | N | N N | งเ | 2 | N | 2 | N | N | N | N | _ا | 2 | N | N | N | 2 | 2 | 2 | N | N | 2 | 2 | N | 2 | N | 2 | 2 | 2 | N | N | N | w | w | ω | | |
| | 0 | | ٠ | | • | ٠ | | ٠ | • | | ٠ | | • | • | • | | | ٠ | | | | | | - | - | | | ٠ | | | | | | | • | .5 |
| 44 | 4. | 4 4 | 4.4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4. | 4 | 4 | 4 | w | ω | ω | ω | ω | 0 | 1 | 9 | 186 | α |
| 13 14 | 13 | <u>ا</u> د | 3 3 | 12 | 10 | ø | | | | | | | | | | | | | | | | | | | | | | | 19 | 16 | 15 | 21 | 22 | 22 | 22 | 22 |
| AAR30206 AAR41644 | AAR30202 | AAR30195 | AAR20049 | AAR13033 | AAP91623 | AAP81591 | AAP60801 | AAP50545 | AAP50696 | AAP40410 | AAP40746 | AAP20058 | AAP10260 | AAP10270 | AAP10269 | AAP10268 | AAP10267 | AAP10266 | AAP10265 | AAP10264 | AAP10262 | AAP10550 | AAP10548 | AAP10547 | AAP10584 | AAP10545 | AAY49387 | AAW84197 | AAW76946 | AAR85069 | AAR42556 | AAB63190 | AAE04125 | AAE04176 | 4. | AAG83349 |
| -Tyr(1)-beta- ernalisation | Tyr(1)- | -Tyr/1)-beta- | ptide chol | nin deriv. s | f useful i | n specifi | with | of - | | | phine deriv | substrate | de alcohol 2 | ic agonist | ic agonist | agonis | agonist | ic agonist | ic agonist | agonis | c agonist | ic peptid | 5 | lgesic | lqesic | Analgesic peptide | Dermorphin derivat | O | S i | cium ion chann | nhibitor s | secrete | N | Human gene 2 encod | n polypeptide | P patens lipid met |

ALIGNMENTS

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RESULT
AAW45592
AAW45592 standard; peptide;
07-MAY-1996;
               07-MAY-1996;
                               18-NOV-1997
                                                JP09295997-A.
                                                                        Modified-site
                                                                                         Modified-site
                                                                                                         Modified-site
                                                                                                                                  Synthetic.
                                                                                                                                                 Protease activity; pepsin; pepsinogen; substrate; thiol derivative.
                                                                                                                                                                 Substrate #13 for the determination of pepsin enzymic activity.
                                                                                                                                                                                    04-JUN-1998
                                                                                                                                                                                                     AAW45592;
                                                                                                                                                                                                                                      Н
                                                                                                                                                                                   (first entry)
96JP-0112441
               96JP-0112441
                                                                                                                  Location/Qualifiers
                                                               /note= "Gly-4-amino pyridine"
                                                                               /note= "beta-phenylthiolactic acid"
                                                                                                 /note=
                                                                                               "benzyloxycarbonyl-Ala"
                                                                                                                                                                                                                      տ
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PIN PRAKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR51894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 4
                                                 05-OCT-1992;
13-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            norvaline, leucine, isoleucine, norleucine, serine and threonine, or a dipeptide residue consisting of two of these amino acids; B = phenylalanine, paranitrophenylalanine or tyrosine; C = thiol derivative residue constituted by 1 to 30 C atoms which can form thioester bond and H atoms combining with them in which 1 to 10 C atoms can be substituted by O, N and/or S and 2 to 10 H atoms can be substituted by O, N and/or S and 2 to 10 H atoms can be substituted by O, N and/or S and 2 to 10 H atoms can be substituted by O, N and/or S, or its salt. The peptides can be used to determine the presence/activity of pepsin or pepsinogen in a sample by determining the amount of thiol derivative formed due to the action (ie. hydrolysis) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determination of pepsin activity. The invention relates to peptides of the following formula: X-A-B-C (I); X = H, a group masking a termino amino group irreversibly or a protective group for an amino group used usually in peptide chemistry; A = glycine, D- or L-alanine, valine,
                                                                                                                                                                                                                                                                                                                         Chitin binding protein; CBP; antifungal; fungicide; beta-1,3-glucanase; transgenic plant; disease-resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New substrate for the determination of pepsin enzymatic activity -
by allowing the enzyme to hydrolyse the substrate and then measuring
the amount of thiol derivative formed
Apotheker M,
                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                 Nicotiana
                                                                                                                                                                                                                                                                                                                                                                     Chitin binding
                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a peptide substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; Page 8; 12pp; Japanese.
                                                                                                    05-OCT-1993;
                                                                                                                                 14-APR-1994.
                                                                                                                                                               WO9408009-A.
                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR51894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR51894 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                             (MOGE-) MOGEN INT NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NITO ) NITTO BOSEKI CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 afxg 8
||||
2 afxg 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzyme on the peptides
                                                                                                                                                                                                                                                                                                             improvement;
                                                                                                                                                                                                                                                                                 tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.5%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
Bres-vloemans AA,
                                                                                                                                                                                                                                                                                                                                                                      protein internal peptide
                                                         92EP-0203071.
93EP-0201370.
                                                                                                    93WO-EP02790
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                            /note=
                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                               tobacco.
                                                                                                                                                                                       "probably proline or
                                                                                                                                                                                                                      "probably tyrosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 3; DB 19; Le
s; Pred. No. 4.3e+05;
""ematches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
Cornelissen BJC,
                                                                                                                                                                                         arginine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5;
Melchers LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hydrolysis) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT
AAY84533
ID AAY8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SON CCC CXXX PTT PTXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Internal peptides of tobacco cv. Samsun NN chitin binding protein were obtained by digestion with protease V8 (peptide AAR51895) and chlorosuccinimide/urea (peptide AAR51894). CBP can be expressed transgenic plants to improve resistance to fungal pathogens.
               Modified Escherichia coli enterotoxin II signal peptides enhancing protein, especially growth hormone, secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antifungal chitin binding protein from plants - without significant chitinase activity, showing synergistic activity with 1,3-beta-glucanase, also its nucleic acid, vectors, transformed
                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                 Enterotoxin II; signal peptide; peptide secretion; human
                                                                                                                                                                                                                                                                                                                                                                        25-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                          AAY84533;
                                                                                                                                                                                                                                                                                                                                                                                                               AAY84533 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 31;
         recombinant cells
                                              WPI; 2000-271381/23
                                                                                    (HANM-) HANMI PHARM CO LTD.
                                                                                                       15-SEP-1998;
                                                                                                                                              23-MAR-2000
                                                                                                                                                                 WO200015661-A1
                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                     Escherichia coli
                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a modified enterotoxin II toxin signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ponstein AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 afxg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 afxg
                                                                                                                                                                                                                                                                                                                                                                                                                                 ω
                                                               Jung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sela-buurlage MB;
                                                                SY,
                                                                                                       98KR-0038061
                                                                                                                          99WO-KR00547
                                                                                                                                                                                                                                   /label= Ile, Thr, Ser
                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                   /label=
                                                                                                                                                                                                      'label= Ile,
                                                                                                                                                                                                                         /label= Ala,
                                                                                                                                                                                                                                                               /label= Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.5%; 5...
100.0%; Pre
                                                                Shin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54pp; English
                                                                                                                                                                                   Gln,
                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3; I
                                                                                                                                                                                                       Phe,
                                                                                                                                                                                    Asn,
                                                                                                                                                                                                                         Gly, Val,
                                                                                                                                                                                                                                                              Thr, Lys,
                                                                 Choi JD,
                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                      Ala,
                                                                                                                                                                                    Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15; L. No. 3.3e+02; 0;
                                                                                                                                                                                   Lys
                                                                                                                                                                                                        Val
                                                                                                                                                                                                                          Leu,
                                                                                                                                                                                                                                                                GLn
                                                                  Choi
                                                                 Ğ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 15
                                                                  Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                   useful for from
                                                                                                                                                                                                                                                                                                                                  growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                             10-AUG-1998;
17-DEC-1997;
09-FEB-1998;
13-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enterotoxin II from the cell. The modified peptides are characterized in that at least one of the 2nd, 4th, 5th, 12th, 20th and 22nd amino acids of the enterotoxin II signal peptide is replaced by another amino acid, and at least 1 of the 2nd and 4th amino acids of the modified peptide is lysine. The modified signal peptide enhances the efficiency of peptide secretion from the cells. The modified signal peptides may be used according to standard recombinant DNA methodologies to direct the secretion of peptides from microorganisms. In particular, it may be used to direct the secretion of human growth hormone from E. coli
This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treat or controlling a variety of human conditions. The secreted proteins \mathbf{m}
                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                           genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                       cellular differentiation; immune system regulator; anti-inflammatory; haematopolesis regulator; tissue growth regulator; tumour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; human; cytokine; cellular proliferation; cell movement; cellular differentiation; immune system regulator; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells in fermentation culture. note: this sequence does not appear in the specification; it was created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY84533-35 represent modified Escherichia coli enterotoxin II signal peptides. The specification describes modified enterotoxin signal peptides, which are involved in directing the secretion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                         New isolated human secreted proteins
                                                                                                                                                                  Bougueleret L,
                                                                                                                                                                                                                                                                                                                                     24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                  WO9931236-A2
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extended human secreted protein sequence, SEQ ID NO. 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY36099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY36099 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                       17-DEC-1998;
                                                                                                                                                                                                (GEST ) GENSET
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3 kxxaf 7
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DB; AAX97783.
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                                                                                                                                                                                                                                                                                                                                                                                                                            disease.
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5; Conser
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                                                              419;
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97US-0069957.
98US-0074121.
98US-0081563.
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                                                                                                                                                                    Duclert
                                                           516pp;
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                                                            English.
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0; Mismatches
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ed in treating proteins may
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Best Local (
AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify the system of the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases.
                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 4277~{\rm human} colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen
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                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH35450
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                                                                                                                                                                                                                                                                       11; Page 8261-8262;
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99US-0163280.
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100.0%; Pred. No.
Live 0; Mismatc
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                                                                                                                                                                                                                                                                    9803pp; English.
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Best Local
                The present sequence represents a Staphylococcus aureus protein, that, based on homology is believed to be a membrane-associated component of a branched amino acid transport system. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the Control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus protein; ribozyme; Staphylococcal gene; regulatory element; vaccine; Staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infection; food processing the staphylococcal infectio
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N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
a host against invasion by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-424969/39
N-PSDB; AAT83937.
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                                                                                                                                                                                                                                                                                                           Claim 6; Page 385-386; 989pp; English
                                                                                                                                                                                                                                                                                                                                                               aureus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Black MT,
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                                                                                                                                                                                                                                                                                                                                                                                       rel polypeptide(s) from Staphylococcus aureus strain WCUH29 - isolate antimicrobial compounds, and in vaccines against S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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S. aureus, and
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Pred. No.
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, Ward JM;
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bacterial gene expression;
poisoning; scaled skin syndro
conditions relating
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ed skin syndrome;
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                                                                                                                                      human secreted proteins, and encode the proteins given in AAY12987 to AAY13219, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/ chemokinetic activity, haemostatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
              thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                    AAX51787 to AAX52019 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAX12987 to
                                                                                                                                                                                                                                                                                                                                           Claim 3,4; Page 454;
                                                                                                                                                                                                                                                                                                                                                                           which may have cytokine, immune, regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-153782/13.
N-PSDB; AAX51818.
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                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated brain-derived nucleic acids - used to develop products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duclert A,
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                                                                                                                            The Invention relates to a vertebrate-derived protein containing an amino acid sequence shown in ANY27137 and ANY27139. The vertebrate-derived protein has at least 55 % homology to one of sequences shown in ANY27141-Y27143, and has slit protein-like activity. The vertebrate slit proteins encoding nucleic acid sequences have at least 60% homology to nucleic acid sequences ANX89161-163. The vertebrate-derived proteins can be produced recombinantly by transforming host cells with expression vectors comprising the encoding nucleic acids. The proteins of the invention are for diagnosing and treating cancer of the nerves, muscle and/or endocrine system.
                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                             05-DEC-1997;
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Misc-difference
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40 afxg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                     Human; colon cancer; colon cancer antigen; diagnosis;
colorectal carcinoma; chromosome 11.
                                                                           Human colon cancer antigen protein SEQ ID NO:4710
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AAG80899
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SEQ ID N
                                                                      Moss; Physcomitrella patens; lipid metabolism related protein; LMRP; lipid biosynthesis; lipid modification; lipid degradation; cofactor; fatty acid transport; genetic engineering; fatty acid; enzyme; plant; microorganism; polyunsaturated fatty acid; oilseed plant; maize; wheat; biotic stress tolerance; abiotic stress tolerance; rice; barley; soybean; peanut; cotton; rapeseed; canola; manihot; peanut; cotton; rapeseed; canola; manihot; pean; sunflower; tagetes; potato; tobacco; eggplant; tomato; Vicia; pea; alfalfa; coffee; cacao; tea; Salix; oil palm; coconut;
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03-NOV-1999;
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N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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DB; AAH33377.
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o. 1.4e+03;
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RESULT 1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes isolated nucleic acid sequences which encode lipid metabolism related proteins (LMRP). The LMRP nucleic acids can be used to modify lipids and fatty acids, cofactors and enzymes in microorganisms and plants, particularly to produce polyunsaturated fatty acids, and are especially useful in oilseed plants. The nucleic acids may also confer biotic or abiotic stress tolerance, particularly to maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola, manihot, pepper, sunflower, tagetes, potato, tobacco, eggplant, tomato, Vicia species, pea, alifalfa, coffee, cacao, tea, Salix species, oil palm, coconut, perennial grasses and forage crops. AAH50878 to AAH50882 represent primers used in the exemplification of the present invention. AAH50883 to AAH50968 represents LMRP nucleotide sequences, and AAG80843 to AAG80928 represent LMRP protein sequences, given in the present invention.
                                                                                                                                                                                                                                                                                   AAG83349 standard; Protein; 181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding lipid metabolism related proteins from Physcomitrella patens useful to produce fine chemicals in modified organisms, particularly polyunsaturated fatty acids in oilseed plants
             25-NOV-1999;
                                                                                                WO200138541-A1
                                                                                                                           Physcomitrella
                                                                                                                                                                   Moss; LMRP; lipid metabolism related
                                                                                                                                                                                                P patens lipid metabolism related protein #67.
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                                        25-NOV-1999;
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             99WO-EP09108
                                        99WO-EP09108
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Duwenig E,
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100.0%; Pred. No.
tive 0; Mismatc
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Schmidt R,
                                                                                                                                                                      protein; polyunsaturated fatty acid;
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RESULT 13
AAM43545
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116-MAR-2000

117-MAR-2000

18-AFR-2000

19-MAY-2000

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30-JUN-2000

07-JUL-2000

07-JUL-2000

11-JUL-2000

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11-JUL-2000
                                                                                                                                                                                                                                                                Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungloide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antialiergic; hepatotropic; antidiabetic; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of moss ligid metabolism related proteins (LMRPs). The moss Physcomitrella patens is one of the few plants able to produce polyunsaturated fatty acids, and the sequences can be used to create transgenic plants also capable of producing them. They can also be used to identify the presence of P. patens and in the production of fine chemicals. The present sequence is one of the proteins of the invention.
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Frank M,
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           2000US-0184664.

2000US-0189874.

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2000US-0198123.

2000US-029467.

2000US-0214886.

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2000US-0216880.
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Schmidt R,
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08-DEC-2000;
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17-NOV-
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01-DEC-
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05-DEC-
        The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM34497-AAM43660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
                                                                                                                                                                              Claim 11;
                                                                                                                                                                                                       New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders - \,
                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 - NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-
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17-NOV-2000;
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                                                                                                                                                                                                                                                                 2001-488781/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000;
                                                                                                                                                                                                                                                     AAI63851
                                                                                                                                                                                                                                                                                                                      HUMAN GENOME
(c) cardiovascular
                                                                                                                                                                              SEQ ID NO
                                                                                                                                                                                                                                                                                            Barash SC,
                                                                                                                                                                                                                                                                                                                                               2000US-0246611

2000US-0249613

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2000US-0246475.
2000US-0246476.
2000US-0246477.
2000US-0246477.
2000US-0246478.
                                                                                                                                                                              223; 664pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                         SCI INC
disorders such as myocardial ischaemias;
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8×666666
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                   Nucleic acids encoding 24 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease
                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
Disclosure; Page 10; 532pp; English
                                                                                                                                                             12-NOV-1999;
03-AUG-2000;
                                                                                                                                                                                                 08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers Misc-difference 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                           17-MAY-2001.
                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                   WO200134643-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene 2 encoded secreted protein fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
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                                                                                     2001-374441/39
                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                            therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                         culture; chemotaxis; vulnerary; binding partner identification;
                                                                                                             SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted protein; proliferative disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                        mellitus and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76
                                                                                                              Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                              2000US-0222904
                                                                                                                                                                                                   2000WO-US30629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                          99US-0164825
                                                                                                                                                                                                                                                                                                             L-amino acids"
                                                                                                                                                                                                                                                                          /label= Unknown
/note= "xaa equals
L-amino acids"
                                                                                                                                                                                                                                                                                                                                         /label= Unknown
/note= "Xaa equ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.5%; 50
100.0%; Pro
                                                                                                           GA,
                                                                                                             Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 3; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                         any
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                                                                                                                                                                                                                                                                                          of the naturally occurring
                                                                                                                                                                                                                                                                                                                                         of the naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour;
                                       disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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AAD08404-AAD08478 represent cDNAs corresponding to 24 human secreted CC protein genes, and AAE04100-AAE004170 represent the proteins they encode. AAE04172-AAE04197 represent they encode in the conditions and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. CC Pathological conditions can be diagnosed by determining the amount of the conditions can be diagnosed by determining the amount of the conditions can be diagnosed by determining the amount of the conditions in the new genes. Specific uses are described for each of the 24 genes, consear tumours, foetal and developmental abnormalities, themselves concern tumours, foetal and developmental abnormalities, and include disorders, cancer, tumours, foetal and developmental abnormalities, and include conditions of the inmune system, AIDS, autoimmune consideration of the invention, in the condition of the invention, in the condition of the invention   AAE04125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                              Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoletic disorder; Immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; Inflammation; neurological disorder; Alzheimer's disease; food additive;
                      Misc-difference
                                                                                                                                                                                                                                                                                     anglogenic disorder; kidney disorder; gastrointestinal disorder; allergy;
pregnancy-related disorder; endocrine disorder; infection; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene 2 encoded secreted protein HWLFE89, SEQ ID NO:112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE04125 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence represents a human secreted protein to in the disclosure of the invention.
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 afxg 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 afxg 8
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                                                                                                                                                                                                                                                                 culture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                 chemotaxis; vulnerary; binding
                                                                    /label-
27..414
                      /label- Mature_human_secreted_protein 174
                                                                                                                                            Location/Qualifiers
/label≏ Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 3; DB 22; L
100.0%; Pred. No. 2.4e+03;
Live 0; Mismatches 0;
                                                                                      Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 392
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                                                                                                                                                                                                                                                                                                                 allergy;
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AAB63190 ID AAB6

16

0

AAB63190 standard; Protein; 503

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or ameliorating medical conditions, e.g., by protein or gene therapy.

CC or ameliorating medical conditions, e.g., by protein or gene therapy.

CC Pathological conditions can be diagnosed by determining the amount of the conditions of the presence of mutations in the way genes. Specific uses are described for each of the 24 genes, conditions in the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative conditions, cancer, tumours, foetal and developmental abnormalities, conditions (e.g., rheumatoid arthritis), inflammation, allergies, concursionates (e.g., Alzheimer's disease, Parkinson's disease), concursionates (e.g., Alzheimer's disease, Parkinson's disease), conjuitive disorders, schizophrenia, asthma, skin disorders (e.g., conjuitive disorders, schizophrenia, asthma, skin disorders (e.g., prejnancy-related disorders, atherosclerosis, cardiovascular disorders, consideration, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, considerative to modify storage properties. Antibodies specific for a protein of the invention can be used as a food additive or protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., the present sequence represents a human secreted protein of
                                                                                                                                                                          Matches
                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
Misc-difference 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AADO8404-AAD08478 represent cDNAs corresponding to 24 human secreted protein genes, and AAE04100-AAE004170 represent the proteins they encode. AAE04172-AAE04197 represent human secreted protein fragments or variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 24 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 480-482; 532pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetes mellitus and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1999; 99US-0164825
03-AUG-2000; 2000US-0222904
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The secreted proteins and their genes are useful for preventing, treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
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408 afxg 411
                                      5 afxg 8
                                                                                                                                                                                                              present sequence invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-374441/39.
                                                                            4.
                                                                                              Similarity
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                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label≔ Unknown
                                                                      37.5%; Score 3; DB 1
100.0%; Pred. No. 2.4
Live 0; Mismatches
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                                                                                            DB 22; L

D. 2.4e+03;
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                                                                                                              Length 414;
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AAB63190;

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cc antifheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cc cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; cc fungicide; and ophthalmological. The polynucleotides and proteins can be used to prevent, treat or ameliorate a medical condition in e.g. humans, cc mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a cpathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative cd disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. The polypeptides can also be used to disease, infections caused by bacteria, viruses and fungi and ocular cd disorders e.g. corneal infection. The polypeptides can also be used to ading due to sunburn, to maintain organs before transplantation, for caping due to sunburn, to maintain organs before transplantation, for comporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or present invention.

CC preservative to increase or decrease storage capabilities. AAF22364 to the present invention.
                 Query Match
Best Local Similarity
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiovascular disorder; cerebrovascular disorder; angiogenesis; nervous system disorder; hlzheimer's ocular disorder; corneal infection; wound healing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and polypeptides homologous to them. Human secreted proteins have activities based on the tissues and cells the genes are expressed in Examples of activities include: immunosuppressive; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 489-491; 533pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-1999; 99US-0128694.
20-JAN-2000; 2000US-0176931.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF22373 to AAF22421 encode the human secreted proteins given in AAB63134 to AAB63182. AAB63183 to AAB63231 represent more human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben
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                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preventing, treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Komatsoulis
37.5%; Score 3; DB llarity 100.0%; Pred. No. 2. Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein sequence encoded by gene 5 SEQ ID NO:116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection; wound healing; skin aging;
                     DB 21; I
o. 2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiant; vasotropic;
                                         Length 503;
    Indels
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disease; infection;
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RESULT 1
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                                                                                                                                                                AAR85069
                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                   Peptides SP3, SP4 and SP5 have ACE inhibiting activity. They coprepd. easily and in high yield. They are useful for treatment prophylaxis of hypertension.
                                                                                                                   13-JUN-1996
                  24-0CT-1995
                                   JP07278185-A.
                                                                               Calcium ion
                                                                                                 Calcium ion channel blocking peptide fragment #2
                                                                                                                                                         AAR85069 standard;
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 2; 5pp; Japanese
                                                                                                                                                                                                                                                                                                                                                          New tri-, tetra- and penta:peptide(s), e.g. Trp-Lys-Tyr - are ACE inhibitors useful for treatment or prophylaxis of hypertension
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-115194/14.
                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP06065288-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiotensin converting enzyme; ACE; inhibitor; SP5; SP4; SP3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACE inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR42556 standard; peptide; 3 AA
                                                                      therapy
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                                                                               channel; blocking peptide; hypotensive agent; blood pressure;
                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                        peptide;
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100.0%; Pred. No. 4.3e+05;
Live 0; Mismatches 0;
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08-APR-1994;

94JP-0070579

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Best Local
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                                                                                                                                                                                                                                                                                                                                       B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IgH; human immune deficiency virus; HIV; tolerance; treatment; therapy prophylaxis; vaccine; chemotherapy; immune response; modifier; tum microbial infection; autoimmune disease; antibody; apoptosis; antiviral T cell immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR85068 and AAR85069 represent calcium ion channel blocking peptides. This sequence corresponds to residues 10-13 of the peptide represented by AAR85068. The peptides suppress blood pressure by inhibiting the calcium influx into cells. These peptides can be used in a hypotensive
                                                                    New fusion immunoglobulin heavy chain including gpl20 epitopes and related complete antibodies - DNA, vectors and transformed cells, used to induce tolerance to the epitopes for treatment of human immune deficiency virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW76946 standard; peptide; 3
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                                             Disclosure; Page 40; 154pp; English.
                                                                                                                                                                                                         13-FEB-1997;
                                                                                                                                                                                                                                13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW76946;
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                                                                                                                                 WPI; 1998-506315/43.
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                                                                                                                                                                                                                                                                                                      Homo sapiens
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2 af 3
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                            therapy;
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This sequence is an epitope used in the construction of a novel fusion immunoglobulin heavy chain (IgH) protein with a mammalian, especially

n (IgH) protein with a mammaliar frame at its N-terminus to one

or more

human

IgH chain fused in

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AAW84197
ID AAW8
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Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                                     (HALL/) HALL F L.
(HANB/) HAN B.
(NIMN/) NIMNI M E.
(SHOR/) SHORS E C.
(WULL/) WU L.
The present peptide represents a proteinase site used in the creation of the bone morphogenetic fusion proteins of the invention. The bone morphogenetic fusion protein some or all of the following elements: a purification tag, a proteinase site, an ECM/bone binding site, a second proteinase site, and a bone morphogenetic protein active fragment. The fusion proteins of the invention also includes proteins that have transforming growth factor beta active fragments instead of bone morphogenetic protein active fragments. The bone morphogenetic fusion proteins can be used for enhancing wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins can be used against other diseases where an immune response is deleterious, e.g. microbial infection, tumours or autoimmune disease. Induction of tolerance suppresses production of antibodies against gpl20, so prevents or inhibits 'bystander' apoptosis of unifected T cells that are bound to gpl20 protein, maximising induction of protective antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune deficiency virus (HIV) gpl20 epitopes. Fusion Ig proteins and/or transfected cells are used to tolerise subjects to gpl20 epitopes and to maintain this tolerance, particularly for treatment of HIV infection, optionally together with other therapeutic/prophylactic agents such as vaccines, chemotherapeutic agents and immune response modifiers. Such
                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                   New bone morphogenetic fusion proteins - comprising a purification tag and a bone morphogenetic active fragment, used for enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteinase site; bone morphogenetic fusion protein; bone binding site; bone morphogenetic protein; transforming growth factor beta; active fragment; wound healing; bone growth.
                                                                                                                                                                   Claim 8; Page 35; 64pp; English
                                                                                                                                                                                                                                                                                                      Hall FL, Han B,
                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                    and a bone morphogenetic nd healing or bone growth
                                                                                                                                                                                                                                                                       1999-059875/05.
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100.0%; Pred. No. 4.
tive 0; Mismatches
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Best Local :
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15-JUN-1998;
24-MAY-1999;
                                                                                                The invention provides diagnostic markers for a human disorder, comprising either opiate-like peptides or opiate-derived peptides. The novel peptides are used as diagnostic marker, in ex-vivo methods of diagnosing human disorders e.g. autism spectral disorders including autism pervasive developmental disorder. Aspergers syndrome, attention deficient disorder and attention hyperactivity disorder, and multiple sclerosis, Parkinson's disease and Alzheimer's dementia. Sequences AAY49371-413 represent peptide diagnostic markers for the human
                                                                                                                                                                                                                                                                                                                                                                               Diagnostic marker; human disorder; opiate; autism spectral diso autism pervasive developmental disorder; Aspergers syndrome; de attention deficient disorder; attention hyperactivity disorder; multiple sclerosis; Parkinson's disease; Alzheimer's dementia.
                                                                                                                                                                            Claim 6; Page 6; 44pp;
                                                                                                                                                                                             Diagnosing human disorders e.g. autism spectral disorders, multiple sclerosis, Parkinson's disease and Alzheimer's dementia -
                                                                          Sequence
                                                                                                                                                                                                                      WPI;
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                                                                                                                                                                                                                                                                                                       15-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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98US-0089238.
99US-0317702.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                        as diagnostic marker.
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                                  Mismatches
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No. 4.3e+05;
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                                          DB 21; I
                                                                                                                                                                                                                                      Friedman
                                                                                                                                                                                                                                                                                                                                                                                                        autism spectral disorder;
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RESULT 22
AAP10545
RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAY-1980;
20-SEP-1979;
20-SEP-1978;
17-SEP-1980;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Analgesic and antipsychotic polypeptide(s) - also useful in endocrinology and to stimulate liberation of growth hormone
                                                                                                                                                                                                        Sequence
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79GB-0032590.
78GB-0032590.
80GB-0029999.
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "D-Ala"
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1.3e+05;
2s 0; Indels
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AAP10584 standard; peptide; 4

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RESULT 24
AAP10547
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Best Local
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20-SEP-1979;
20-SEP-1978;
17-SEP-1980;
 Synthetic
              Growth Hormone
                                                                                                                                                                                 Peptides covered by this sequence are preferred examples of a highly generic formula for peptides with analyssic and antipsychotic properties. The peptides also have Growth Hormone rel-using and prolactin releasing properties. See also AAP10545-P10583.
                                                                                                                                                                                                                                        Analgesic and antipsychotic polypeptide(s) - also useful in endocrinology and to stimulate liberation of growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth Hormone release;
                           Analgesic peptide #3
                                          22-DEC-1992
                                                        AAP10547;
                                                                   AAP10547 standard; peptide;
                                                                                                                                                                     Sequence
                                                                                                                                                                                                                    Example; Page 11; 41pp; French.
                                                                                                                                                                                                                                     prolactin
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79GB-0032590.
78GB-0032590.
80GB-0029999.
              release; prolactin; painkiller; anti-psychotic
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                                                                                                                                        25.0%; Score 2; DB 2; Le
100.0%; Pred. No. 4.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                     "Gly-NH-NH-Z, -NH-NH-CO-(CH2)2-CH3
Or -NH-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                         "D-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                       "Boc-Tyr"
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20-SEP-1979;
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17-SEP-1980;
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                Modified-site
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                                                                                                                                                                    Growth Hormone release; prolactin; painkiller; anti-psychotic
                                                                                                                                                                                                Analgesic peptide
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                                         Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prolactin
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20-SEP-1979;
20-SEP-1978;
17-SEP-1980;
                                                                                                                                                                                                            Peptides covered by this sequence are preferred examples of a highly generic formula for peptides with analysis and antipsychotic properties. The peptides also have Growth Hormone releasing and prolactin releasing properties. When the N-terminus is not Boc-protected, the peptides are in the form of their hydrochloride (i.e. -NHNHZ) or dihydrochloride (i.e. -NHNHZ) salts.
                                                                                                                                                                                                                                                                                                                                           Analgesic and antipsychotic polypeptide(s) - also useful in neuro endocrinology and to stimulate liberation of growth hormone and prolactin
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Copyright (c) 1993 - 2000 Comp
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US-08-340-045-20
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4.329 Million cell update
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113, Appl
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34, Appl
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34, Appl
302, App
                APPLICATION: 800
FILING DATE:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/411,640
FILING DATE: 05-APR-1995
APPLICATION NUMBER: PCT/EP93/02790
FILING DATE: 05-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-010139-3
FELECHMUNICATION INFORMATION:
TELLEPHONE: (212) 708-1800
TELLEPHONE: (212) 708-1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-08-935-886-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08935886 Patent No. 5994625
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 i
COMPUTER: IBM PC/XT/AT or cc
OPERATING SYSTEM: DOS 6.20
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                              SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ponstein, Anne S.
APPLICANT: Apotheker-de Groot, Marion
APPLICANT: Cornelissen, Bernardus J. C.
TITLE OF INVENTION: Antifungal Chitin Binding Proteins
TITLE OF INVENTION: Coding Therefor
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                               COUNTRY:
ZIP: 100
                                                                                                                                                                                                                                                                                  STREET: 26 West
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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26 West 61st Street
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Anne S.
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                                                                                                                                                                                                                             3.5 inch, 14. or compatibles
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US-08-224-868-7
US-08-338-890B-1
US-08-561-478-4
US-08-561-478-4
US-08-561-63-18
US-08-466-32-8
US-08-466-63-28
US-08-466-177-8
US-08-466-177-8
US-08-466-177-8
US-08-466-177-8
US-08-456-424-23
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А.
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US-08-404-531B-34 ; Sequence 34, Application US/08404531B ; Patent No. 5863724
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Best Local Similarity
Thes 4; Conserve
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US-08-404-531B-34
                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
NAME: Beardell, Lori Y.
NAME: 34,293
                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215.568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ADDITIONATION NUMBER OF CASE AND ASSESSED FOR A STATE OF CASE AND ASSESSED FOR A STATE OF CASE AND ASSESSED FOR A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A STATE OF CASE AND A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO FRAGMENT TYPE: II ORIGINAL SOURCE:
                                                                                                                                                                                                       MOLECULE
HYPOTHETICAL: N
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MEDIUM TYPE: Floppy
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NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRAIN: Samsun NN
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                                                                                                                                                                                                                                                                                                                                        LENGTH:
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E: No. 5863724ris
One Liberty Place 46th. Floor
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                                                                           Score 3; 1; Pred. No.
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                                                   Mismatches
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                                                                                                   Length 24;
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Best Local Similarity
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US-08-488-546A-34
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                                                                                                   APPLICANT: Thomas, G
TITLE OF INVENTION:
Patent No. 6054313
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6031150
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                          Sequence 34, Application US/08488546A Patent No. 6054313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6031150
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                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 6054313ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: BY TELECOMMUNICATION INFORMATION: 215-568-3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: U5/08/476,900A FILING DATE: 07-UN-1995 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Beardell, Lori Y. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6031150ris
STREET: One Liberty Place 46th. Floor
     STREET:
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GY: linear
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  One Liberty Place 46th. Floor
                                                                                                                                                                               Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela Thomas, Gilbert Cote, and Robert Gagel
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                      Sequence Encoding Mammalian Sulfonylurea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-488-546A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.5%; Score 3; DB 3; Best Local Similarity 100.0%; Pred. No. 71; Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 215-568-3190
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,546A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/404,531
FILING DATE: 15-MARCH-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BEATGELI, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0026
ATTORNEY/AGENT INFORMATION:
NAME: Israclsen, Ned A.
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: DueLort, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                          ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 501 West Broadway CITY: San Diego STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Philadelphia
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                                                                                                                                                                                                                                       ZIP: 92101-3505
                                                                                                                                                                                                                                                          COUNTRY: USA
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amino acid
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; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: SCORE 7
; OTHER INFORMATION: SEQ SVMLCLLCYFAFP/FQ
US-08-905-223-302
                                                                                                                                                        ; TOPOLOGY: 11; MOLECULE TYPE: US-08-213-897A-13
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                                                                 Query Match
Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0
FILING DATE: 10-FEB-1992
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/213,897A
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/593,867
FILING DATE: 05-0CT-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                       LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
5 af 6
1 AF 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: sig_peptide LOCATION: -52..-1
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                                                                     25.0%; Score 2;
100.0%; Pred. N
tive 0; Misma
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                                                                     red. No. 1. Mismatches
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o. 1.6e+05;
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RESULT 7 US-08-213-897A-14

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RESULT 8
US-08-470-837-11
; Sequence 11, Application US/08470837
; Patent No. 5800811
; Patent No. 5800811
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Best Local Similarity
Watches 2; Conserva
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FILING DATE: 10-FEB-1992
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
           CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
• NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tuan, Tai-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming
TITLE OF INVENTION: and
TITLE OF INVENTION: Their Use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/593,867 FILING DATE: 05-OCT-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
TELECOMMUNICATION INFORMATION:
                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                        STREET: 11150 Sant
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                         APPLICATION NUMBER: FILING DATE:
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1 AF 2
                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 90025-3395
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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11150 Santa Monica Boulevard, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hall, Frederick L.
Tuan, Tai-Lan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nimni, Marcel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming Growth Factor B Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.0%; Score 2; DB 1; Le 100.0%; Pred. No. 1.6e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                            US/08/470,837
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               30630-1US01
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-470-837-11
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US-07-719-692A-1
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                                                                                                                                                           Sequence 1, Application US/07719692A Patent No. 5250414
GENERAL INFORMATION:
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Best Local
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LENGTH: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 405, Application US/09461697 Patent No. 6277974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
TILE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION UMBER: US/90/461,697
CURRENT FILING DATE: 1999-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COGENT NEUROSCIENCE, Inc. APPLICANT: Lo, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                     APPLICANT: Schwab, I
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                      CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                     STREET: 1155 A
                                                                                                                                                                                                                                                                                                                                Local Similarity les 2; Conserv
               COUNTRY: UZIP: 10036
                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                     ADDRESSEE:
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                                          New York
                                                                        E: Pennie & Edmonds
1155 Avenue of the
                          U.S.A.
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Neurite Growth Regulatory Factors
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100.0%; Pr
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100.0%;
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5. 1.6e+05;
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US-07-719-692A-2
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Best Local Similarity
"arches 2; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/07719692A Patent No. 5250414
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: Schwab
            APPLICATION NUMBER: US/07/719
FILING DATE: 19910624
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4 amino acids
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                     STREET: 1155 AVER CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036
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OTHER INFORMATION: /note= "amide at carboxy terminus"
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FILING DATE: 19910624
CLASSIFICATION: 514
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STREET: 1155 Avenue of the Americas
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               6526-022
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US-07-719-692A-3
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Best Local Similarity
Matches 2; Conserv
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                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                     REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/719,692A
FILING DATE: 19910624
                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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STREET: New York
TTTY: New York
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LOCATION:
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TELEFAX: 212 8698864/9741
LENGTH: 4 am-
                                                                                                                                              NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,8
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end"
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STRANDEDNESS:
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; OTHER INFORMATION:
US-07-719-692A-3
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US-07-805-727-8
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Best Local
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/805,727
FILING DATE: 19911206
CLASSIFICATION: 436
ATTORNEY/ACTION: 436
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: NO. 5424186viel, Vernon A.
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 11509a)1)1)1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPHAX: 415-326-2422
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MEDIUM TYPE: Floppy disk
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nes 2; Conserv
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Read, J. Leighton
VENTION: Very Large Scale Immobilized Polymer
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b. 1.6e+05;
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RESULT 15
US-07-840-077A-7
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/079,44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P-TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn
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LENGTH: 4 amino acids
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                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                              1 wk 2
                                                               2 WK 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08079445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: CAMPBELL AND FLORES 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pinilla, Clemencia
Eichler, Jutta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States
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                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghten,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-1993
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ID NO: 3:
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PEPTIDES HAVING ANTI-MICROBIAL,

HEMOLYTIC, ANTI-MELITTIN OR ANTI-ENZYMATIC ACTIVITY
                                                                                                                                            25.0%;
100.0%;
                                                                                                                                                                                                                     /note= "C-terminal amino acid amidated" % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) ^{2}
                                                                                                                                                                                                                                                                                                                                                                          /label= Xaa
/note= "Xaa=KFmoc"
                                                                                                                                                                                                                                                                                                /note=
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Pred. No.
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                                                                                                                                                                                                                                                                                                "Xaa=any amino acid"
                                                                                                                              Mismatches
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                                                                                                                                                         DB 1;
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                                                                                                                                             1.6e+05
                                                                                                                                                          Length 4;
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Sequence 7, Application US/07840077A Patent No. 5443816

GENERAL INFORMATION: APPLICANT:

Zamora, Paul O.

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Best Local Similarity
Unitednes 2; Conserv
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                                                                                                                                                                                                                                                                                 Sequence 4, Application US/07866018 Patent No. 5470705 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/816,477
FILING DATE: 03-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Peacock
REGISTRATION NUMBER: 31,649
TELECOMMUNICATION INFORMATION:
TELEPHONE: (505) 243-2542
INFORMATION FOR SEQ ID NO: 7:
                                                      STREET: 350 CITY: Palo Alto
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC/XT/AT, IBM PS/2 or COMPUTER: Compatibles
OPERATING SYSTEM: PC-DOS or MS-DOS
SOFTWARE: WordPerfect 6.0a for Windows
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                          APPLICANT: Grossman, Paul D.
APPLICANT: Fung, Steven
APPLICANT: Menchen, Steven M.
APPLICANT: Woo, Sam L.
APPLICANT: Winn-Deen, Emily S.
APPLICANT: Winn-Deen, Emily S.
TITLE OF INVENTION: Probe Composition and Method
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rhodes, Buck A.
TITLE OF INVENTION: Peptide-Metal Ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/840,077A FILING DATE: 20-FEB-1992 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 87109-5802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4261 Ballo
CITY: Albuquerque
STATE: NM
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1 | 1 | 2
2 wk 3
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                                       ZIP: 94306
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100.0%; Pro
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Patent No. 5470951
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TELEX: NO. 5470951e INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 324-09 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                         SOFTWARE: Microsoft
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/127,904
FILING DATE: 29 September 1993
                               TELEFONMUNICATION INFORMATION: TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4" diskette
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: City of Hope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Eugene Roberts
TITLE OF INVENTION: Method
TITLE OF INVENTION: Amnes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA: No. 5470951e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                    NAME: Irons, Edward S. REGISTRATION NUMBER: 16. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fablan, Gary R.
REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                 COMPUTER: Wang PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                        United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein and Improving the Quality of Life in Individuals With Alzheimer Disease
                                                                                                                                                                                                                                                                 MS DOS Version 3.20
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100.0%; Pred. No. 1.
tive 0; Mismatches
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Amnestic Effects of Amyloid n
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SEQUENCE CHARACTERISTICS:

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US-08-390-272-8
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Best Local Similarity
Thes 2; Conserve
                                                                                                               ; MOLECULE TYPE: US-08-390-272-8
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5-489678
                                                 Matches
                                                                        Query Match
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APPLICANT: Fodor, Stephen P.A.
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                               APPLICATION NUMBER: 11509-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/624,120
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Very Large TITLE OF INVENTION: Synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Vernon A. No. 5
STREET: One Market Plaza,
CITY: San Francisco
                                               Local Similarity
nes 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                       TOPOLOGY:
                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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af 6
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AF, 4
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Solas, Dennis W.
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Winkler, James L.
Holmes, Christopher P.
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linear
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100.0%; Pr
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o. 1.6e+05;
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                                                                                                                                              US-08-206-789-5
; Sequence 5, Application
; Patent No. 5580854
; GENERAL INFORMATION:
                                                                                                                                                                                                                  RESULT
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US-08-102-372-4
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                           APPLICANT: Orlowski, Marian
APPLICANT: Cardozo, Christopher
APPLICANT: Vinitsky, Alexander
TITLE OF INVENTION: SUBSTRATE-REL
TITLE OF INVENTION: PEPTIDYL-ALDE
TITLE OF INVENTION: INHIBITORS OF
TITLE OF INVENTION: MULTICATALYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/102,372 FILING DATE: 04-AUG-1993 CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Powers, Vincent M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
CORRESPONDENCE ADDRESS:
                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Powers, Vincent REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                              Application US/08206789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WOO, Sam L.
Winn-Deen, Emily S.
WYENTION: Probe Composition and Method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grossman, Paul D.
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
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                             PEPTIDYL-ALDEHYDE INHIBITORS OF THE PROTEOLYTIC ACTIVITY MULTICATALYTIC PROTEINASE COMPLEX
                                                                                                                                                                                                                                                                                                                              25.0%; Score 2; DB
100.0%; Pred. No. 1.
tive 0; Mismatches
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                                                                                SUBSTRATE-RELATED
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ADDRESSEE:

30 Rockefeller Plaza

BRUMBAUGH, GRAVES, DONOHUE &

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08211070A Patent No. 5585350
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FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Seide, Rochelle K.
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: A29525 - 165/25989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2626
TELEPAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,070A
FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Friedrich, Thomas
APPLICANT: Koerwer, Wolfgang
APPLICANT: Kroeger, Burkhard
APPLICANT: Blalojan, Slegfried
APPLICANT: Blalojan, Slegfried
APPLICANT: Blalojan, Slegfried
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APPLICANT: Common State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State 
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Keil & STREET: 1101 Conn. CITY: Washington STATE: D.C.
CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
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3 AF 4
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TOPOLOGY: linear
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1101 Connecticut Avenue
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C12P 21/02
A61K 37/64
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RESULT 22
US-08-176-938-24
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Best Local Similarity
Matches 2; Conserve
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   Query Match 25.0
Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8783
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: PC'
FILING DATE: 23-SEP-19:

INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schiller, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                 PEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                      LOCATION: 3
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                              OTHER INFORMATION: /label= Tic OTHER INFORMATION: /note= "1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sterner Ph.D., Richard J. REGISTRATION NUMBER: 35,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 04-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1155 A:
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 af 6
                                                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NY
                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: White & Case STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                      Modified-site
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23-SEP-1992
TN NO: 7:
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: 35
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   25.0%; Score 2; DB: 100.0%; Pred. No. 1.0 tive 0; Mismatches
                                                                                                  /label= 2-Nal
/note= "3-(2'-naphthyl)alanine
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No. 1.6e+05;
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o. 1.6e+05;
                                     Length 4;
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Query Match
Best Local Similarity
Whiches 2; Conserve
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                                                                                                                                                                                        RESULT 24
US-08-193-977-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: ; OTHER INFORMATION: US-08-176-938-35
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US-08-176-938-35
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                                                                                            Sequence 20, Application US/08193977 Patent No. 5625031 GEYERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSTETTO:

PC-DOS/MS-DOS

Patentin Release #1.0, Version #1.25

RAPPLICATION DATA:

BILING DATE: 04-TAW

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MEDIUM TYPE: Floppy disk
                                    APPLICANT:
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      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
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REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-080
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llarity 100.0%;
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KEVIN G.
PEPTIDE INHIBITORS OF THE P33CDK2 AND
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/note= "3-(1'-naphthyl)alanine"
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                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5635477
GENERAL INFORMATION:
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Best Local (
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                                                     SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPTTARMTON TONING
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch disk
                                                                                                                                                                                                                                                                                                                APPLICANT: William Frank DeGrado, Sharon Anne Jackson, Shaker Ahmed Mousa, Anju APPLICANT: Parthasarathy, Michael Sworin, Maria Rafalski TITLE OF INVENTION: Cyclic Compounds Useful as TITLE OF INVENTION: Inhibitors of Platelet Glycoprotein IIb/IIIa
                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                             COMPUTER: Apple Macintosh OPERATING SYSTEM: Apple Miscrosoft Word
            APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 514
                                                                                                                                                                 COUNTRY: U
ZIP: 19898
                                                                                                                                                                                                  STATE:
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nes 2; Conserv
                                                                                                                                                                                                              CITY: Wilmington
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STRANDEDNESS: sir
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STATE: CALIFORNIA
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                                                                                                                                                                                                                                 1007 Market Street, Legal Department
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                                                                                                                                                                                U.S.
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100.0%; Pred. No. 1.
Live 0; Mismatches
                                                US/08/461,611
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APPLICATION NUMBER: 08/038,448
FILLING DAYE: March 29, 1993
ATTORNER/AGENT INFORMATION:
NAME: FORGUSON, Blait, 0,
REGISTRATION NUMBER: 34,329
REFERENCE/DOCKET NUMBER: 34,329
REFERENCE/DOCKET NUMBER: 34,329
REFERENCE/DOCKET NUMBER: 39-6543-B
TELECOMMUNICATION INFORMATION:
TELEPAX: 302-892-1856
INFORMATION FOR SEG ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acids
TYPE: amino acids
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TYPE: amino acids
TYPE: ACCURATION: Example Number 12a;
OTHER INFORMATION: Example Number 12a;
OTHER INFORMATION: GPIID/IIIa Inhibitor
US-08-461-611-12

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11: 100.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
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Search completed: January 14, 2002, 07:57:31

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Maximum DB
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14.274 Million cell updates/sec
               Q98824 spinacia ol Q62721 rattus norv Q9uqwO homo sapien Q9umaO homo sapien Q9byf9 homo sapien Q28093 bos tanro-
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Ogym9 leishmania
Ogmzel bos taurus
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Og1947 oryzias lat
Ogym52 leishmania
O27953 balaenopter
O9nz74 homo sapien
O9pyv3 trypanosoma
O9bb52 schoenoceph
O95945 saccharomyc
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   Q9qwt0
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RESULT
Q9GVM9
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   Query Match
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Q9GVM9;
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                 Q9UR79 PRELIMINARY; PRT; 38 AA.
Q9UR79;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CELLOBIOHYDROLASE II CORE PROTEIN, CBH II CP=3.2.1.91.
Trichoderma reesei (Hypocrea jecorina).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Hypocreaceae; Hypocrea.
MCBI_TaxID=51453;
                                                                                             MEDLINE-94250349; PubMed-8192865; Moodward J., Brown J.P., Evans B.R., Affholter K.A.; Moodward J., Brown J.P., Evans B.R., Affholter K.A.; "Papain digestion of crude Trichoderma reesel cellulase: purification and properties of cellobiohydrolase I and II core proteins."; Biotechnol. Appl. Biochem. 19:141-153(1994). HSSP, P07987; ICB2.
HSSP, P07987; 1CB2.
                                                                                                                                        SEQUENCE
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Q9UCQ5
Q83139
Q9UEE3
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0; Mismatches
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Q9MRF6
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Q9FYT0
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Q9uc46 homo sapien
Q77876 oreochromis
Q77883 oreochromis
Q77912 oreochromis
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Q77912 papalura fl
Q9g359 japalura fl
Q9g359 japalura fl
Q9g359 japalura fl
Q9g166 rattus norv
Q9ucq5 homo sapien
Q8x139 barley stri
Q9uee3 homo sapien
Q9x112 bemisia tab
Q9thr8 bryopsis sp
Q64813 autographa
Q9x165 burkholderi
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Q9x166 burkholderi
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O9mrv4 allium porr
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P82433 nicotiana t
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RESULT
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Q91947;
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01-OCT-2000 (TrEMBLrel 15, Last si
01-JUN-2001 (TrEMBLrel 17, Last ai
GLUTATHIONE PEROXIDASE (FRAGMENT).
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Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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01-MAR-2001 (TrEMBLrel. 16, I
07-MAR-2001 (TrEMBLrel. 16, I
HYPOTHETICAL 8.1 KDA PROTEIN
LM12.1312.
                                                                                                                                                                                                                                   "Cow glutathione peroxidase.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ
EMBL; AF236854; AAF74253.1; -
InterPro; IPR000889; Glut_peroxidase.
                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2000) to the EMBL; AL390114; CAC02854.1;
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Murphy L., Quail M.,
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Lussier J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                          Q9MZE1;
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Q27953;
Q1-NOV-1996 (TrEMBLrel. 01, C1
01-NOV-1996 (TrEMBLrel. 01, La
01-JUN-2001 (TrEMBLrel. 17, La
B-CASEIN (FRAGMENT).
Balaenoptera physalus (finback whale) (Common rorqual) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticet. Balaenopteridae; Balaenoptera. NCBI_TaxID=9770;
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neotele Actinopterygii; Neopterygii; Percomorpha; Atherinomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                          EMBL; AL390114; CAC02622.1;
                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2000)
                                                                                                                                                                                                                                                                                                                                          Murphy L., Quail M.,
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Mol. Biol. 2001. 0.0(0).

EMBL: U53900; AABO8405.1; -.

InterPro: IPR001588; Casein.

Pfam: PF00363; caseins; 1.

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SEQUENCE 141 AA; 15822 MW; ...
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01-MAR-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comhair S.A.A., Thomassen M.J., Erzurum S.C.;
"Differential induction of nitric oxide synthase 2 and extracellular gluthatione peroxidase in airways of healthy individuals exposed to 100% O2 or cigarette smoke.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF217787; AAF43005.1; -...
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EXTRACELLULAR GLUTATHIONE PEROXIDASE.
                                                              Trypanosoma brucci.
Eukaryota; Euglenozoa;
NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000889; Glut_peroxidase Pfam; PF00255; GSHPx; 1. PR1NTS; PR01011; GLUTPROXDASE.
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhin1; Hominidae; Homo.
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  SEQUENCE FROM Wickstead B.,
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Similarity 100.0%;
4; Conservative
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nilarity 100.0%;
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF207634; AAK21842.1; -.
Chloroplast.
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InterPro; IPR001812; Trypan_glycop.
Pfam; PF00913; Trypan_glycop; 1.
SEQUENCE 485 AA; 52687 MW; 9D5C
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01-FEB-1997 (TrEMBLrel. 02,
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INSIDE INTRON 5 (FRAGMENT).
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SEQUENCE FROM N.A.
MEDLINE-81069885; PubMed-6254986;
Bonitz S.G., Coruzzi G., Thalenfeld
"Assembly of the mitochondrial membr
                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharon Saccharomycetales; Saccharomycetaceae;
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Sytsma K.J.;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NADH DEHYDROGENASE F (FRAGMENT).
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Pterygota; Neo
Acridomorpha;
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Q15898;
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NON_TER
SEQUENCE
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01-NOV-1996 (TremBLrel.
01-NOV-1998 (TremBLrel.
CYTOCHROME B (FRAGMENT).
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mxcCracken A., Ohlenbusch I., Gellissen G.;
mxtructure of the cloned Locusta migratoria mitochondrial genome:
restriction mapping and sequence of its ND-1 (URF-1) gene.";
Curr. Genet. 11:625-630(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-AUG-1998 (TrEMBLrel. 07, CCLONE XP6A11B) (FRAGMENT).
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EMBL; V00694; CAA24066.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide sequence of the cytochrme oxidase.";
                                                                            SEQUENCE FROM N.A. MEDLINE=88223478; PubMed=2836084;
                                                                                                                                                                                                                Mitochondrion.
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Lee C.C., Yazdan
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Mammalia; Eutheria; Primates;
                                                                                                                                    NCBI_TaxID=7004;
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                                                                                                                                                      Metazoa; Arthropoda; Tracheata; Hexapoda;
Neoptera; Orthopteroidea; Orthoptera; Cae.
ha; Acridoidea; Acrididae; Locusta.
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Q62721;
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01-MAY-2000
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                                                  STRAIN-FISHER;

MEDLINE-95331633; PubMed-7607556;

Altus M.S., Wood C.M., Stewart D.A., Ro
Henderson T., Owens G.A., Danner D.B.,

McClung J.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                 Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core et
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spin
                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                   of the photosystem I reaction center.";
Eur. J. Biochem. 205:1175-1185(1992).
SEQUENCE 8 AA; 1082 MW; 2145BB1324069044
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PHOTOSYSTEM I REACTION CENTER SUBUNIT IV, PSI-E.
                          prohibitin-encoding genes.
Gene 158:291-294(1995).
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                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                               Rattus norvegicus (Rat)
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"Purification and membrane topology of PSI-D
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MEDLINE-94061059; PubMed=7694728;

Spritz R.A., Holmes S.A., Berg S.Z., Nordlund J.J., Fuka

Spritz R.A., Holmes S.A., Berg S.Z., Nordlund J.J., Fuka

A recurrent deletion in the KIT (mast/stem cell growth

receptor) proto-oncogene is a frequent cause of human pi

Hum. Mol. Genet. 2:1409-1500(1993).
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MEDLINE-84182507; PubMed-6325171;

Truong A.T., Duez C., Belayew A.,

Martial J.A.;

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EMBO J. 3:429-437(1984).
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Mammalia; Eutheria;
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CYTOKERATIN
                                                                             Blessing M., Jorcano J.L., Franke W.W.;
"Enhancer elements directing cell-type-specific cytokeratin genes and changes of the epithelial transfections of hybrid cytokeratin genes.";
EMBO J. 8:117-126(1989).
                                                                                                                                                                                                                                                                                                                                              Q28093 PRELIMINARY; PRT; 9 AA. Q28093; Q28093; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) CYTOKERATIN IV GENE UPSTREAM REGION (FRAGMENT).
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                                          Intermediate filament.
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    819A22D1B5B32B45 CRC64
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Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; C Manmalia; Eutheria; Rodentia; S
                                                                                                                             Splicing.";
J. Biol. Chem. 275:2589-2597(2000).
FMRI: AF199609; AAF31396.1; -.
                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-20112823; PubMed-10644718;

MEDCANDER-20112823; PubMed-10644718;

Munoz-Sanjuan I., Smallwood P.M., Nathans J.;

"Isoform Diversity among Fibroblast Growth Fa
Is Generated by Alternative Promoter Usage an
                                                                                                                                                                                                                                                                                                                                              FHF-2.
Gallus gallus (Chicken).
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 2 ISOFORM 1U
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
EMBL; AJ007030; CAA07429.1; -.
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01-MAY-2000
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Neognathae; Galliformes; Phasianidae; Phasiani
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Q9UC46;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Q1-MAY-0000 (TrEMBLrel. 13, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
NADH DEHYDROGENASE SUBUNIT 3 (FRAGMENT).
                                                                                                                                                                                                                                                                     MEDLINE=96326114; PubMed=8703476; Cooper J.A.Jr., Culbreth R.R.; Cooper J.A.Jr., Culbreth R.R.; "Characterization of a neutrophil inhibitor peptide harvested human bronchial lavage: homology to influenza A nucleoprotein. Am. J. Respir. Cell Mol. Biol. 15:207-215(1996). SEQUENCE 11 AA; 1262 MW; 951A1C3279C9DB45 CRC64;
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Mammalia; Eutheria;
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submitted (APR-1999) to the
EMBL; AF142479; AAD37355.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsukamoto N., Asakura N., Takumi S., Mori N., Nakamura C.; "The presence of paternal sub-genomic mitochondrial DNA copies in nucleus-cytoplasm hybrids of tetraploid wheat with the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of the cytoplasm of 
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O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-NOV-1998 (TrEMBLrel. 08, Last annotation update)
O1-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B LOCUS 4 (FRAGMENT).
Oreochromis niloticus (Nile tilapla) (Tilapla nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
C1childae; Oreochromis.
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Genetics 149:1527-1547(1998).
EMBL; AF049992; AAC41331.1; -
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B LOCUS 1 (FRAGMENT).

Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

Cukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Clichidae; Oreochromis.
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MEDLINE-98315113; PubMed-9649539;
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MEDLIND-98315113; PubMed-9649539;

MEDLIND-98315110 E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,

Sueltmann H., Figueroa F., Klein J.;

"Linkage relationships and haplotype polymorphism among cichlid Mhc class II B loci.";

Genetics 149:1527-1547(1998).

""". *F04995; AAC41334.1; -.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II BLOCUS 4 (FRAGMENT).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Oreochromis.
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Copyright (c) 1993 - 2000 Comp
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                                                                    Fibroblast growth
Fibroblast growth
Peptide #2273 enco
Peptide #2287 enco
Peptide #2259 enco
Modified murine ep
                                                                                                                                                                         Description
                           Human secreted pro
Human 5' EST relat
Human colon cancer
Arabidopsis
Arabidopsis
 thalia
thalia
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| aci | AAR1250 | 12 | 4 | 5 | N | 50 |
|--------------------|-----------|----|-----|----------|---|----|
| Enkephalin analogu | AAR12507 | 12 | 4 | | N | 49 |
| a, | AAR0702 | 11 | 4 | 5 | 2 | 48 |
| - | AAR04767 | 11 | 4 | | N | 47 |
| ecif | AAP81591 | 9 | 4 | 5 | 2 | 46 |
| ō, | AAP61359 | 7 | 4 | 5 | 2 | 45 |
| ō, | AAP50545 | g | 4 | | 2 | 44 |
| Sequence of enkeph | AAP40339 | σ | 4 | 5 | N | 43 |
| and | 20 | ω | 4 | 5 | N | 42 |
| | AAP20208 | ω | 4 | 5 | 2 | 41 |
| | AAP10625 | N | 4 | 5 | 2 | 40 |
| ۳. | AAP10620 | N | 4 | <u>ب</u> | N | 39 |
| ര | AAP10401 | N | 4 | بر د | 2 | 38 |
| ~ | AAP10433 | Ŋ | 4 | 5 | 2 | |
| N-adamantane tetra | AAP10599 | N | 4 | ū | N | |
| Generic analgesic | AAP10386 | N | 4 | | ۵ | |
| Enkephalin-like an | AAP10375 | N | 4 | 5 | 2 | |
| Enkephalin-like an | AAP10373 | Ν | 4 | 5 | 2 | |
| Enkephalin-like an | AAP10372 | N | 4 | 25.0 | N | 32 |
| enke | AAP10370 | | 4 | 5 | 2 | 31 |
| Sequence of trypto | AAP10154 | | 4 | 5 | 2 | 30 |
| ACE inhibitor SP3. | AAR42556 | | ω | 5 | 2 | 29 |
| Thermoanaerobacter | AAW17590 | | 685 | 7. | ω | 28 |
| Thermoanaerobacter | AAW17586 | ш | 685 | 7. | ω | 27 |
| Thermoanaerobacter | AAW17582 | | 685 | 7. | ω | 26 |
| Thermoanaerobacter | | | 684 | .7 | ω | 25 |
| Thermoanaerobacter | | | 684 | 7 | ω | 24 |
| ч | | | 684 | 7. | ω | 23 |
| heria | | | 533 | 7. | ω | 22 |
| | | | 329 | .7 | ω | 21 |
| Amino acid sequenc | | | 280 | 7. | w | 20 |
| ycin-dep | AAW084 | | 230 | 7. | ω | 19 |
| | | | 226 | .7 | w | |
| | | | 226 | 7. | w | 17 |
| _ | AAG281 | | 164 | .7 | w | |
| colon car | AAG757 | | 129 | .7 | ω | |
| secreteo | AAG0223 | 21 | 105 | 37.5 | ω | 14 |
| n lambda lig | AAW5849 | | 104 | 7. | ω | 13 |
| Human lambda light | AAR38596 | | 104 | 7. | ω | 12 |
| | , , , , , | | | 1 | J | |

ALIGNMENTS

RESULT AAW74457

ب

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Agonist identification; orphan receptor; constitutively active OR; Graves' disease; thyroid adenoma; hypertension; cardiomyopathy; schizophrenia; Kaposi's sarcoma; fibroblast growth factor receptor; adenylate cyclase constitutive activator; thyrotropin receptor; thyrotropin stimulating hormone; beta-adrenergic receptor.
 14-APR-1997;
                       14-APR-1998;
                                                                                                                                                                                                                                                                 12-MAY-1999
                                                                                                                                                                                                                                                                                          AAW74457;
                                                                                                                                                                                                                                                                                                                 AAW74457 standard; peptide;
                                              22-OCT-1998
                                                                     WO9846995-A1
                                                                                                         Misc-difference
                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                         Fibroblast growth factor 3 receptor mutational cassette
                                                                                                                                                                                                                                                                  (first entry)
97US-0839449
                       98WO-US07496
                                                                                                         Location/Qualifiers
                                                                                            /label= Glu, Asp, Gln, His, Lys
                                                                                                                                                                                                                                                                                                                  24
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RESULT
AAY90893
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                    WO200021987-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease, thyroid adenoma, hypertension, cardiomyopathy, schizophrenia, major depression, Kaposi's sarcoma and many others tabulated). It is based on identification of agents that reduce receptor activation, rather than compounds that antagonise the normal ligand. Once identified, (inverse) agonists can be used to study OR function. The method does not require knowledge of the endogenous receptor ligand or receptor function, and identifies directly compounds that inhibit the activated receptor, i.e. able to block both ligand-dependent and -independent activation, rather than only the ligand-dependent process, as is the case with compounds identified by ligand-dependent assays. It should accelerate drug discovery at a wide range of OR and since activated receptors have a greater response to the agents, potential drugs are more likely to have a greater response to the agents, potential drugs are more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is a fragment of a fibroblast growth factor 3 receptor mutational cassette. The invention relates to a method for the identification of candidate compounds as agonists, including inverse or partial, of an orphan receptor (OR), which comprises: (i) applying test compound to constitutively active OR; and (ii) measuring its effect on OR. The method is particularly used to identify inverse agonists of
                                                                                                                                                                                              orphan receptor; antithyroid; antidiabetic; neu cytostatic; G protein-coupled receptor agonist.
                                                                                                                                                                                                                                                                     Fibroblast growth factor 3 receptor mutational cassette #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR. The method is particularly used to identify inverse agonists of G protein-coupled OR, i.e. potential therapeutic agents for treating conditions in which constitutively active OR are implicated (e.g. Graves'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying agonists of orphan receptors from their effect on the constitutively active receptor - particularly therapeutically active inverse agonists at 6 protein coupled receptors, without requiring knowledge of endogenous ligand or receptor function
                20-APR-2000.
                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                           30-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 47; 114pp; English.
                                                                                                                                                                                                                                    Identification; modulator; cell surface membrane
                                                                                                                                                                                                                                                                                                                                              AAY90893;
                                                                                                                                                                                                                                                                                                                                                                            AAY90893 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-105468/09
                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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(CHAL/) CHALMERS D T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     have a greater
be detected.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.5%; Score 3; lilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                        Location/Qualifiers
                                                                                      /label= Glu, Asp, Gln,
                                                                                                                                                                                                                                                                                                                                                                                24
                                                                                                                                                                                                                 antidiabetic; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 3.5e+02;
0;
                                                                                    His,
                                                                                      Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 24;
                                                                                                                                                                                                                                  receptor; treatment;
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                                                                                                                                                                                                                 antidepressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inverse or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local :
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compound having inverse agonist activity, partial agonist activity or agonist activity to a constitutively active orphan receptor (ORR). The method comprises determining the efficacy of the compound by contacting it with the ORR. A compound identified by the above method having inverse agonist activity to ORR is useful for the treatment of diseases characterised by constitutive activation of the receptor e.g. Graves' disease, male precocious puberty, Jansen's disease, retinitis pigmentosa, hypoparathyroidism, neuropsychiatric diseases, schizophrenia, major depression, and cancerous growth in Kaposi's sarcoma. The method can identify (I) directly without prior knowledge or use of receptor ligands and is useful for accelerating drug discovery at a broad range of ORR. The present sequence represents a fibroblast growth factor 3 receptor mutational cassette, which is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                  AAM15839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying compounds with inverse agonist activity to orphan receptors useful for treating e.g. Graves' disease, and schizophrenia, involves contacting candidate compounds with constitutively activated receptors
                                                         30-JUN-2000;
                                                                     26-MAY-2000;
                                                                                      04-FEB-2000;
                                                                                                                  30-JAN-2001; 2001WO-US00670
                                                                                                                                           09-AUG-2001.
                                                                                                                                                                         WO200157278-A2
                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                 cervical
                                                                                                                                                                                                                                                Probe; human;
                                                                                                                                                                                                                                                                         Peptide #2273 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                                                                                     12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                              AAM15839 standard; Protein; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 47; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-317935/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Behan DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AREN-) ARENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention.
                                                                                                                                                                                                                                 cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 AA;
             2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention describes
                                                                                      2000US-0180312
                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                             microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0170496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US23935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.5%; 500
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 3;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a method for directly identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; L
). 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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2000GB-0024263

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                         04 FEH-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0632366.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0236359.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encode by one such probe. The SENPs are derived from human HeLa cells. The SEN can be used to produce a single exon microarray, which can be used for
 analyzing
          Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                        WO200157272-A2
                                                                                                                                                                                                                                                                                                       genetic disorder
                                                                                                                                                                                                                                                                                                                   Probe; microarray;
                                                                                                                                                                                                                                                                                                                                        Peptide #2387 encoded by probe for measuring placental gene
                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                 AAM28350 standard; Protein; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS
                                                                                  (MOLE-)
                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                           SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-488901/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful for thing gene expression in human cervical epithelial cells
                                                                                   MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
 gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
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                                                           Hanzel
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                                                           Ŗ,
                                                                                                                                                                                                                                                                                                                   human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.5%; Score 3; DB 22; L
100.0%; Pred. No. 4.4e+02;
Live 0; Mismatches 0;
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                                                           Chen
in human placenta
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                                                           Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 34;
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                                                                                                                                                                                                                                                                                                                                            expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100
Matches 4; Conservative
The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                       WPI; 2001-476286/51.
                                                                                                                                                                                                                                                                   Penn
                                                                                                                                                                                                                                                                                                                        04-OCT-2000,
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; human; inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM03577 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27;
                                                                                                                                                                                                                                                                                            (MOLE-)
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numan genetic disorders
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                                                                                                                                                                                            l single exon nucleic human breast -
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                                                                                                                                                                                                                                                                   SG,
                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                            MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                 SEQ ID No 12317; 322pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 AA;
                                                                                                                                                                                                                                                                                                                     2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breast disease; breast cancer; developedisease; proliferative breast disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded by
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100.0%; Pr
                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe
                                                                                                                                                                                                            acid
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0; Mismatches
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                                                                                                                                                                                                          probe used
                                                                                                                                                                                                                                                                 Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for measuring breast gene expression
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                                                                                                                                                                                                          measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        development disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-carcinoma tumour.
                                                                                                                                                                                                          gene expression
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encoded by one
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RESULT
AAG00560
ID AAGC
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AAR08007
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                                                                                              Matches
                                                                                                       Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                  The human rEGF is used to treat oversecretion of gastric acid or epithelial wound. EGF is modified to increase its chemical stability. Its storage life is improved without diminishing its biological activity. The proteins may be prepared by traditional chemical or recombinant means.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published not sammanon
                                                                                                                                                                                                                                                                    Human epidermal growth factor - is substituted at position 11 greater stability and improved storage life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified murine epidermal growth factor; st epithelial wounds; gastric acid secrection.
AAG00560 standard; Protein; 59 AA
                                                                                                                                                                                                                                               Claim 9; Page 25; 32pp; English.
                                                                                                                                                                                                                                                                                                     WPI; 1990-361427/48.
                                                                                                                                                                                                                                                                                                                                                                     12-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                         09-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                   W09013570-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified murine epidermal growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR08007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR08007 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                           Nascimento CG, Medina-Selby A;
                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-1991
                                                                                                                                                                                                                                                                                                                                               (CHIR-) CHIRON CORP.
                                                  5 syxg 8
||||
9 syxg 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 syxg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 syxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                               4;
                                                                                                                                                                       or recombinant AAR08004.
                                                                                                                                                    53 AA;
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                                                                                             37.5%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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11..11
/label= E, N, Q, A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 AA
                                                                                               0;
                                                                                                        Score 3;
Pred. No.
                                                                                               Mismatches
                                                                                                        DB 11; Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stability; storage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 34;
                                                                                                                 Length 53;
                                                                                               Indels
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                                                                                               Gaps
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RESULT
AAY65150
ID AAY6
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Best Local Similarity
Thehes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream requires commonce and to derive are desired to obtain upstream
                     Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
regulation;
                                                                                                                                   Human
                                                                                                                                                                                    01-FEB-2000
                                                                                                                                                                                                                                        AAY65150;
                                                                                                                                                                                                                                                                                            AAY65150 standard; Protein; 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; SEQ ID 4641; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-500381/45.
N-PSDB; AAC00566.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulatory sequences and to design expression and secretion vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                          48 kxxsy 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 kxxsy 6
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                                                                                                                                EST related polypeptide
  location; develor
n; identification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 3; I
100.0%; Pred. No.
tive 0; Mismatch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                   SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; L, 6.2e+02;
                                                                                                                                      NO:1311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Best Local Similarity
Thehes 5; Conserv
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                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences; corresponding to human secreted proteins. AAY64651 to AAY65438 represent the EST-related proteins corresponding to AAZ42265 to AAZ43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the clocation, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in clasmostic procedures to identify yndividuals, or in clasmostic procedures to identify yndividuals, or in clasmostic procedures to identify shadividuals having genetic diseases resulting from abnormal gene expression. The products may also be used in gene therapy protecols. The nucleic acids encoding signal peptides can be insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have called, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42264 and AAY64644 to AAY64650 represent
WO200122920-A2
                               Homo sapiens
                                                                                                         Human colon cancer antigen protein SEQ ID NO:8542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                              colorectal carcinoma
                                                                           Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                          03-SEP-2001
                                                                                                                                                                                                    AAG77776 standard; Protein; 72 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-1998;
28-APR-1998;
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48 kxxsy 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                        (first entry)
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98US-0069047.
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                                                                                                                                                                                                                                                                                                                                                Score 3; DB 2; Pred. No. 6.2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                DB 21; L
b. 6.2e+02;
                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                               Length 59
                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for
                                                          EP1033405-A2
                                                                                      Arabidopsis thaliana
                                                                                                                 hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                                                                                                                               Protein identification; signal transduction pathway; metabolic
                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID
                                                                                                                                                                                                             17-OCT-2000
                                                                                                                                                                                                                                         AAG28199;
                                                                                                                                                                                                                                                                       AAG28199 standard; Protein; 90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 9791-9792; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 4277 human useful for preventing, diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                             5 syxg
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99US-0163280.
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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and/or treating colorectal cancers -
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D. 7e+02;
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promoter;
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25-FEB-2000; 2000EP-0301439

06-SEP-2000

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| 990S-0144334 990S-0144335 990S-0144335 990S-0144834 990S-0145086 990S-0145086 990S-0145087 990S-0145087 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0146388 990S-0147303 990S-0147303 990S-0147303 990S-0147303 990S-0148171 990S-0148171 990S-014923 990S-014923 990S-014923 990S-014923 990S-0151066 990S-0151066 990S-0151066 990S-0151303 990S-0151333 990S-0153758 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-015479 990S-0155486 | 0142 |

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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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12-OCT-1999
13-OCT-1999
13-OCT-1999
                                                                                                                                                                Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 33327.
                                                                                                                                                                                                                                17-OCT-2000 (first
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                                                                                                                                           Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                 5 syxg
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38 syxg
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                                                                                                                                                                                                                                                                                                                                                                             n 37.5%;
Similarity 100.0%
4; Conservative
                                                                                                                                                                                                                                                                           standard; Protein;
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99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
99US-0126785.
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promoter;
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AAR38596
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                             Antibody; affinity;
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Misc-difference
                                                                                                                       Misc-difference
                                                                                                                                                               Misc-difference
                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                   Human lambda light chain subgroup 4 (hL4).
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR38596 standard; peptide; 104 AA
               14-DEC-1992;
                                        24-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                28-OCT-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            AAR38596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 syxg
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                                                                                                                                                                                                                                                                                    sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                             variable domain; light; L; heavy; H; consensus;
antigen; immunogenicity; humanisation; framework.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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99US-0160767
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                                                                                                                                                                                                                "residue conserved in less
known sequences of hL4"
                                                                                           "residues conserved in less
known sequences of hL4"
                                                                                                                                    "residue conserved in less
known sequences of hL4"
                                                                                                                                                                          "residue conserved in less
known sequences of hL4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 3; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; L
. 8.4e+02;
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                                                                                                                                                    than
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02-AUG-1999
03-AUG-1999
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The consensus amino acid sequences for the subgroups of light chains (hK1 - AAR38590, hK3 - NGK, hK2 - GST, hL1 - AAR38591, hL2 - AAR38592, hL3 - AAR38593, hL6 - AAR38594, hK4 - AAR38595, hL4 - AAR38596, and hL5 - AAR38597) and heavy chains (hH3 - AAR38598, hH1 - AAR38599 and hH2 - AAR38697) and heavy chains (hH3 - AAR38598, hH1 - AAR38599 and hH2 - AAR38600) of human variable domains may be used to propare, for example, a modified mouse antibody variable domain that retains the affinity of the natural domain for antigen while exhibiting reduced immunogenicity in humans.

Unlike other methods of humanisation, which advocate the replacement of entire antibody framework regions with those of human antibodles, this method involves only the introduction of human residues into those positions not critical for antigen binding. This ensures that the binding properties of the modified antibody
             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-1991;
                                      Misc-difference
                                                                Misc-difference
                                                                                          Misc-difference
                                                                                                                    Misc-difference
                                                                                                                                              Misc-difference
                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                     Human lambda light chain subgroup 2 consensus sequence hL2
                                                                                                                                                                                                                                                                                                                                18-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                  AAW58496 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are not diminished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 96; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        retain binding affinity, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies prepn. used for treatment of auto-immune diseases replacement of critical residues to reduce immunogenicity but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-213827/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fishwild DM, Kohn FR,
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                                                                                                                                                                                                                                                    autoimmune
                                                                                                                                                                                                                                                                   depletion;
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                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 syxg 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                               human; mouse; CD5; anti-CD5 antibody; immunoglobulin; cytotoxic; immunoconjugate; fusion protein; psoriasis disease; rheumatoid arthritis; type I diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                               (first entry)
                                   /note
91
                                                                                                                   /note: "not specified"
87
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                                                                                          /note: "not specified"
89
                                                                                                                                             /note "not specified"
32
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 /note:
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14-DEC-1992;
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The method comprises administering a cytotoxic protein containing a modified immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig molecule or an immunoconjugate or fusion protein containing an anti-CD5 Ig molecule, and where the modified Ig variable domain comprises at least one of (a) a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region (see AAW58478 or a modified light chain variable region chain vari
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92WO-US10906.
95US-0472788.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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100.0%; Pr
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Pred. No. 8.9e+02;
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EP1033401-A2

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a polypeptide encoded by one of a large number of 5′ ESTs derived from mRNAs encoding secreted proteins. The 5′ ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3′ untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5′ ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5′ UTR is rarely included. 5′ ESTs are derived from mRNAs with intact 5′ ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5′ ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                           Ruben SM,
WPI; 2001-235357/24
N-PSDB; AAH35138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                    05-APR-2001.
                                                                                                                                                                                                WO200122920-A2
                                                                                                                                                                                                                                                                                           Human colon cancer antigen
                                                                                                                                                                                                                                                                                                                        03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                             AAG75733 standard; Protein; 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; SEQ ID 6315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                         28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                      colorectal carcinoma
                                                                                                                                                                                                                                                                Human; colon cancer; colon
                                                                                                                                                                                                                                                                                                                                                   AAG75733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
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                                           Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105
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                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                99US-0157137
99US-0163280
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                                           Birse CE,
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                                                                                                                                                                                                                                                                  cancer antigen;
                                                                                                                                                                                                                                                                                           protein SEQ ID NO:6497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score 3; DB;
; Pred. No. 8.
0; Mismatches
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                                           Rosen CA;
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No. 8.9e+02;
0;
                                                                                                                                                                                                                                                                diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 105;
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                                                                                                                                                                                                                                                                   detection;
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RESULT 16
AAG28197
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           25-FEB-1999

05-MAR-1999

09-WAR-1999

23-MAR-1999

23-MAR-1999

21-APR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

16-APR-1999

11-APR-1999

21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as collon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention.

N.B. Pages 66 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                            06-SEP-2000
                                                                                                                                                                                                                                                                                            EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 33326
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG28197 standard; Protein; 164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 4277~{\rm human} colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                             25-FEB-2000;
                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                         termination sequence
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                                                                                                                                                                                                                             2000EP-0301439
99US-0121825

99US-0123548

99US-0125788

99US-0125788

99US-0126785

99US-0127462

99US-0127462

99US-0128714

99US-0128714

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99US-0130077

99US-01300449

99US-01300449
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100.0%; Pr
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Pred. No.
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promoter;
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| 30-APR 1999 30-APR 1999 30-APR 1999 30-APR 1999 30-APR 1999 30-APR 1999 30-APR 1999 30-APR 1999 30-APR 1999 30-APR 1999 30-APR 1999 31-AAV | 3-APR-199 |
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| 9908-0145086 9908-0145086 9908-0145086 9908-0145086 9908-0145087 9908-0145087 9908-0145087 9908-014518 9908-0145224 9908-0145918 9908-0146386 9908-0146388 9908-0147204 9908-0147204 9908-0147303 9908-0147303 9908-0147303 9908-0147303 9908-0147303 9908-0147303 9908-0147303 9908-0147303 9908-0147303 9908-0147303 9908-0147303 9908-0148341 9908-0149368 9908-0150866 9908-0150866 9908-0150866 9908-0150866 9908-0151086 9908-0151086 9908-01554886 9908-01554886 9908-01554886 9908-01554886 9908-01554886 9908-01554886 9908-01554886 9908-0158373 9908-0158383 9908-0158333 9908-0159333 | -014488 |
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RESULT 1
AAR72680
   Query Match
Best Local Similarity
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28-OCT-1999;
29-OCT-1999;
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25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
The deduced amino acid sequence of the human plasma glutathione
                               Disclosure; Fig 1; 33pp; French.
                                                             New immunogenic oligo:peptide of human plasma glutathione peroxidase - and derived antibodies that do not recognise other forms of the enzyme and are useful in immunoassays, e.g. to detect selenium deficiency
                                                                                                                                                                            Chaudiere J,
                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                              WPI; 1995-115435/15.
                                                                                                                                                                                                                                                          03-SEP-1993;
                                                                                                                                                                                                                                                                                      01-SEP-1994;
                                                                                                                                                                                                                                                                                                                        09-MAR-1995
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                                                                                                                                                                                                          (BIOX-) BIOXYTECH SA. (BIOX-) BIOXYTECH.
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26-OCT-1999;
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18-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutathione peroxidase; plasma; antibody; immunoassay; kidney;
ium deficiency; liver disease; graft rejection; hepatic cancer.
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99US-0161993
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99US-0161920.
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99US-0161360
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99US-0161406.
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99US-0160770
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99US-0159584.
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0161404
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                                                                                                                                                                                                                                                                                                                                                                                       /note= "unknown amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.5%;
                                                                                                                                                                              Malette P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 3; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21; L
D. 1.2e+03;
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RESULT :
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peroxidase as published (J. Biochem., 108, 1990,145-148). Immunogenic peptides (e.g. see AAR72679) were derived from hydrophobicity/flexibility profiles of the published sequence. Peptides containing this sequence can be conjugated to carrier proteins and used to produce antibodies. The antibodies can be used to detect plasma glutathione peroxidase in immunoassays e.g. for detection of selenium deficiency or in diagnosis of certain kidney or liver diseases e.g. graft
                                This sequence represents human plasma glutathione peroxidase H (pGPxH). The invention relates to this movel human glutathione peroxidase, nucleic acid encoding it, and to recombinant production of human pGPxH. The invention also encompasses applications for
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers Misc-difference 73
Sequence
                               peroxidase, nucleic of human pGPxH. The
                                                                                          Claim 2;
                                                                                                                  use
                                                                                                                                                    N-PSDB; AAA90423.
                                                                                                                                                               WPI; 2000-533631/49
                                                                                                                                                                                     Yu L,
                                                                                                                                                                                                                                   29-OCT-1998;
                                                                                                                                                                                                                                                          29-OCT-1998;
                                                                                                                                                                                                                                                                                 14-JUN-2000
                                                                                                                                                                                                                                                                                                       CN1256312-A
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       Plasma glutathione peroxidase H; pGPxH; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human plasma glutathione peroxidase H (pGPxH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB22828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB22828 standard; Protein; 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rejection
                                                                                                                                                                                                           (UYFU-) UNIV FUDAN.
                                                                                                                                                                                                                                                                                                                                                                                                              recombinant production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 syxg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 syxg 8
                                                                                                                         human glutathione peroxidase and its code sequence, preparation and
                     pGPxH.
                                                                                                                                                                                     Tu Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                          Page 20-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or certain hepatic cancers.
 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                     Fu 0;
 ΑA;
                                                                                                                                                                                                                                   98CN-0121973
                                                                                                                                                                                                                                                          98CN-0121973
                                                                                                                                                                                                                                                                                                                           /label= unknown
/note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.5%; >--
100.0%; Pr
                                                                                          26pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 3; DB 16; L
Pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                                                                              TGA"
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Query Match Best Local S Matches 4

Similarity 4; Conserv

Conservative

37.5%; >--100.0%; Pr

Score 3; I

DB 21; Lo

Length 226;

Mismatches

0

Indels

0;

Gaps

밁 Ş

5 syxg 8 ||||| |71 syxg 74

AAW08430

AAW08430 standard; Protein; 230 AA

Rapamycin-dependent activation of signal transduction fusion

10-OCT-1997 AAW08430;

(first entry)

RESULT 19

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The present sequence represents the representative construct fusion T6 CC which is involved in the rapamycin-dependent activation of signal CC transduction. This is involved in the construction of transcription CC factor fusion proteins, which in turn are involved in the production of canimal cells containing at least two recombinant DNAs. One DNA should CC encode a chimeric protein which is capable of binding to rapamycin, or a CC rapamycin analogue, and comprises at least one rapamycin binding domain CC (RBD) and at least one protein domain heterologous to it; the second CC recombinant DNA should encode a second chimeric protein which is capable CC first chimeric protein and comprises at least one FKBP:rapamycin binding CC (FRB) domain and at least one domain heterologous to it. Contacting CC those genetically engineered cells with rapamycin or analogues results in the formation of a complex (between the fusion proteins, and the CC activation of an intraccliular signal transduction pathway leading to CC e.g. gene expression or appoletic cell death, gene knock-out, blockade CC of a gene or inhibition of function of a gene product. They are used CC recombinant proteins and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-FEB-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion protein; rapamycin binding domain; RBD; FKBP; FK506-binding protein; FRB domain; genetic engineering; regulation; transcription; signal transduction; apoptosis; inhibition; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulating biological events
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Now rapamycin-responsive transfected cells - contg. recombinant DNA encoding fusion proteins which act as biological switches for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-065453/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clackson T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rapamycin; responsive transfected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ARIA-) ARIAD GENE THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                   Page 109; 149pp; English.
   230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gilman M2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0598776.
95US-0481941.
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                                   and viruses.
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Query Match Best Local Similarity

37.5%; 100.0%;

Score 3; Pred. No.

DB 18; I

Length 230

RESULT

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RESULT 2
AAB08728
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                                                  Matches
                                                              Query Match
Best Local :
                                                                                                                                    The present sequence represents a consensus B7RP1 (B7 related protein-1) polypeptide. The specification also describes a CRP1 (CD28 related protein-1) polypeptide. The polypeptides are involved in T-lymphocyte activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are predicted to be a type I transmembrane protein. The nucleic acids are useful for regulating T cell activation or proliferation in an animal. The polypeptides are useful for treating, preventing ameliorating or diagnosing a T-cell mediated disorder in an animal. They can also be used to identify test molecules that bind to the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T cell proliferation; T-cell mediated disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRP1; CD28 related protein-1; B7RP1; B7 related protein-1; T-lymphocyte activation; type I transmembrane protein; T cell activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB08728 standard; Protein;
                                                                                                                                                                                                                                                                 Disclosure; Page 161-162; 174pp; English.
                                                                                                                                                                                                                                                                                                     Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are in the treatment, prevention and diagnosis of T cell mediated
                                                                                                                                                                                                                                                                                                                                             WPI; 2000-543476/49
                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-1999;
08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-2000; 2000WO-US01871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-AUG-2000.
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                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
265 syxg 268
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                         5 syxg 8
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                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of a consensus B7RP1 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                280
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                               AA,
                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0244448
99US-0264527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..280
/note= "Xaa represent unspecified amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                               37.5%; Score 3; DB 100.0%; Pred. No. 1. Live 0; Mismatches
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                                                              DB 21; L
o. 1.7e+03;
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                                                                        Length 280;
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XX
AC AAR44893;
XX
DT 22-JUN-1994
XX
DE Diphtheria to
                                                                           RESULT 22
AAR44893
ID AAR448
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ID AAB(
                                                                                                                                                                   Š
                                                                                                                                            Db
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                              The present sequence represents a consensus B7RP1 (B7 related protein-1) polypeptide. The specification also describes a CRP1 (CD28 related protein-1) polypeptide. The polypeptides are involved in T-lymphocyte activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are predicted to be a type I transmembrane protein. The nucleic acids are useful for regulating T cell activation or proliferation in an animal. The polypeptides are useful for treating, preventing ameliorating or diagnosing a T-cell mediated disorder in an animal. They can also be used to identify test molecules that bind to the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
Diphtheria toxin (delta-147-148; H21X) mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRP1; CD28 related protein-1; B7RP1; B7 related protein-1; T-lymphocyte activation; type I transmembrane protein; T cell activation; T cell proliferation; T-cell mediated disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-1999;
08-MAR-1999;
                                                                             AAR44893 standard; Protein;
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 167-168; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoshinaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200046240-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a consensus B7RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB08730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the treatment, prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB08730 standard; Protein; 329
                                                                                                                                           312 syxg 315
                                                                                                                                                                   5 syxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-543476/49
                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SK;
                                                                                                                                                                                                                                                          329 AA;
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US01871
                          (first entry)
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99US-0264527.
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                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                       37.5%;
                                                                              533
                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                        Score 3; |
Pred. No.
                                                                              A
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                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins CRP-1 and B7RP1 are useful diagnosis of T cell mediated disorders
                                                                                                                                                                                                        DB 21; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide
                                                                                                                                                                                             0
                                                                                                                                                                                                                   Length 329;
                                                                                                                                                                                             Indels
                                                                                                                                                                                             0;
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RESULT
AAW17581
 XXX DXXX
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                                                                                                                                                                                                             QУ
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                  Oligonucleotide-directed mutagenesis of the wild-type diphtheria gene results in deletion of the codons for Val-147 and active site residue Glu-148. The resulting mutein is not toxic, making it useful in diphtheria vaccines. The risk of reversion to toxicity is much lower for the 147-148 double mutant than for the prior art 148 single mutein, while its immunogenicity is not impaired. The 147-148 mutein opt. has other amino acid residues substd. or deleted, e.g. wild-type His(21) in fragment A. The specification includes the wild-type DT amino acid sequence (see AAR44888) but does not include any mutant sequences; the wild-type sequence was modified according to the description in the claims to give AAR44893.
Cyclomaltodextrin glucanotransferase; CGTase; enzyme; Bacillus circulans;
                           Thermoanaerobacter CGTase variant beta-cyclodextrin #1.
                                                       01-JUL-1997
                                                                                                               AAW17581 standard;
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; ; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA encoding diphtheria toxin deletion mutants - with no toxicity and low risk of reversion, and derived toxoids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-007178/01.
N-PSDB; AAQ54341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collier RJ, Killeen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DT; protein exotoxin; NAD-dependent ADP-ribosyltransferase; diphtheria toxoid; deletion mutant; mutein; variant; double reversion mutation; site-directed mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transformed cells, useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9325210-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium diphtheriae.
                                                                                                                                                                                                 5 syxg
                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                    19 syxg
                                                                                                                                           23
                                                                                                                                                                                                                                          4:
                                                                                                                                                                                    22
                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                              533 AA;
                                                                                                                                                                                                                                          Conservative
                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0901712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93WO-US04606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                               protein;
                                                                                                                                                                                                                                         37.5%; Score 3; I
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "any amino acid other than wild-type His or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Diphtheria toxin mutant; Val(147) and Glu(148) have been deleted and His(21) is substd. by any other amino acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is substd. is absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mekalanos
                                                                                                               684 AA
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                     DB 15; LC.
NO. 2.5e+03;
0;
                                                                                                                                                                                                                                                                   Length 533;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant;
                                                                                                                                                                                                                                            0;
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| /label- P149W PR /152 /152 /153 /154 /155 /155 /155 /155 /155 /155 /155 | y, Asn, Ala, Gln" PF XX | - D148X | /Index 111/A /notes To Ala, Leu, Ile, Phe, Trp, Gly, Tyr, Arg, Asp, Thr, or absent" | Lys, Asp, Asn, or | la, Phe, Gln, Ser, Trp, Ile, Arg, Glu, | Elicontrol of tio, wig, ite, oil, of set to the bound of | "Toposible toposition of Dro Ale The Glo Or Cor" FT | /label∘ S145X FT /note∘ "Xº Ala, Glu, Trp, Leu" FT | "Xº Ala, Arg, Asn" | Modified-site 141 FT /labelo H140X FT | /labelo D135L FT | /HADGLO WIDIA FT /NOTEO "Xo Gly, Ala" FT | A. O+}, D+Q | /labelu H98X | "X- Gln, Lys, Arg, Trp, Phe, Asn, Ser, or absent" | E S94X | /label= G93X FT /label= G93X FT /note= "X= Glv, Aso, His, Thr or absent" | /label~ G92V FT 94 FT | "X- Ala, Val, Gly, Phe, Tyr, or absent" FT | Misc-difference 92 Misc-difference 92 FT FT FT FT FT FT FT FT FT F | /label T91X | /labelo S90X FT /noteo "Xo Gly, Ala, Ser" FT FT | absent" | | "Xº Pro, Asn, Lys, His" FT | Modified-site 88 FT /label- P88X FT | /label L87x /notee "Xe Ile, His" FT | "X- Gln, Leu, Ala, His, Arg" | ET ET | /notes "Xe Phe, Tyr" FT | | | אייסטראי דמשרווטרבי, מוסמפאוממממוב אומפרווי (מוסרבווי ביו |
|---|----------------------------|---------|---|------------------------------------|--|---|---|---|--------------------|---------------------------------------|------------------|--|---------------|---------------|---|---------------|--|--------------------------|--|---|---------------|--|---------------|----------------------|----------------------------|--|--|------------------------------|--|--|---------------|---------------|---|
| 16-NOV-1995; 21-APR-1995; 17-OCT-1995; | 22-APR-1996; | , | W09633267-A1. | | Modified-site | Woortten.Pite | i fi od | Modified-site | | Modified-site | MODIFIED-SICE | | Modified-site | Modified-site | ; ; | Modified-site | Modified-site | | Modified-site | Modified-site | 11 | Mod fied site | Modified-site | Modified-site | Modified-site | | Modified-site | Modified-site | | Modified-site | Modified-site | Modified-site | Modified-site |
| 95DK-0001281. 95DK-0000477. 95DK-0001173. | 96WO-DK00179. | | | /note= "X= unspecified amino acid" | x Aia, Fio, Giy, Aig, Lys | /100 R375X | /note= " | 374 /label= Y373X | | × | 3/1 /label= | /IBDEL= N326X /note= "X= Gln, Phe, Leu" | 328 | | | /note- " | 235 /label= H233X | | /note= ' | /note= 199 | /label= D196x | /label= F195X /note= "X= Leu, Ile, Trp, Tyr, Phe" | 2 | 195 /label= N193X | 194 /label= R192K | /label= S185X /note= "X= Pro, His, Arq, Glu, Asp" | | = F183X | /label= G180X /note= "X= Glv Ser Asn Asp" | / Tabel - Gly, Ser, Asn, Asp" /note= "X= Gly, Ser, Asn, Asp" 182 | | / 1 abol | |

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Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complexes with many small hydrophobic molecules. These CGTase mutants have a modified substrate binding and/or product selectivity, compared to this sequence. The mutants are created using primer mutagenesis to modify the gene encoding this sequence. These sequences have greater product selectivity and/or reduced product inhibition (better yields) than wild-type CGTase. These mutant sequences are used to manufacture the final CD types (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides, optionally in situ, e.g. during production of baked goods, to stabilise chemicals during their manufacture and in detergents. CD are known for their usefulness in foods, e.g. as a bread-improving agent, to encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals, pesticides or fungicides, to bind/remove lipophilic compounds such as cholesterol (e.g. in egg yolk or butter), i plastic laminates, films etc. and to make biodegradable plastics.
                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     have alter or linear
                                                                                                                                                       thermoanaerobacter; starch; cyclomaltodextrin; cyclodextrin; pesticide; transglycosylation; cyclic glucose oligomer; glucose oligosaccharide; cholesterol removal; food stabiliser; vitamin stabiliser; fungicide; plastic laminate; biodegradable plastic; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW17580-W17591, and AAW17606-W17652 represent mutant versions of the cyclomaltodextrin glucanotransferase (CGTase) of Thermoanaerobacter thermosulphurigenes sp. ATCC 53627. (see AAW06772 for wild type sequence). CGTase catalyses the conversion of starch and similar than the conversion of starch and similar than the conversion of starch and similar than the conversion of starch and similar than the conversion of starch and similar than the conversion of starch and similar than the conversion of starch and similar than the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conversion of the conver
                                                                                                                                                                                                               Cyclomaltodextrin glucanotransferase; CGTase; enzyme; Bacillus circulans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intramolecular transglycosylation reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a hydrophobic internal cavity that form inclusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 31;
Modified-site
                                                                                                                              Synthetic
                                                                                                                                                                                                                                             Thermoanaerobacter CGTase variant beta-cyclodextrin #2.
                                                                                                                                                                                                                                                                                                                               AAW17585 standard; protein; 684 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         substrates into cyclomaltodextrins (also known as cyclodextrins) via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andersen C,
                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nts of cyclo:malto:dextrin glucanotransferase (CGTase) - red substrate binding, useful for prodn. of cyclodextrin(s) oligosaccharide(s), opt. formed in situ in e.g. baked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    684
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                                                                                                                                                                                                                                                                        (first entry)
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                                           /note=
47
 /note=
87
                                                                                    Location/Qualifiers 21
                             /label=
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                                                        "X≖ Phe,
             "X= Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No.
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                                                        Tyr"
              Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
              Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . DB
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.9e+03;
             His,
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/note= "X= Pro,
89
/note=
194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
147
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                                         /note=
187
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146
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99
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95
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151
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102
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88
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136
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                                                        /label= F183X
/note= "X= Tr
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/note= "X= Ala,
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/note= "X= Gly,
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              = S185X
"X= Pro
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X= Gly,
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"X= Gln,
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"X= Gly,
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Thr, or
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"X= Gly,
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×=
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                                                                                                                                           "X= Ser,
                                                                                                                                            X=
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                                                                                                                                                                                                                                                                                                                                                                                                                                              "X= Pro, Ala, Phe,
Lys, Asp, Asn, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "X=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "X= Gly,
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              His,
                                                        Tyr,
                                                                                                                                                                                                                                              Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glu,
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                                                                                                                                          Asp"
                                                         Ala"
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16-NOV-1995;
21-APR-1995;
17-OCT-1995;
           AAW17580-W17591, and AAW17606-W17652 represent mutant versions of the cyclomaltodextrin glucanotransferase (CGTase) of Thermoanaerobacter thermosulphurigenes sp. ATCC 53627. (see AAW06772 for wild type sequence). CGTase catalyses the conversion of starch and similar substrates into cyclomaltodextrins (also known as cyclodextrins) via an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                         Claim
                                                                             New variants of cyclo:malto:dextrin glucanotransferase (CGTase) -
have altered substrate binding, useful for prodn. of cyclodextrin(s)
or linear oligosaccharide(s), opt. formed in situ in e.g. baked
                                                                                                                         Andersen C,
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     intramolecular transglycosylation reaction.
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                                                        Page -; 161pp; English.
                                                                                                                        Dijkhuizen L,
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95DK-0000477.
95DK-0001173.
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372
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complexes with many small hydrophobic molecules. These CGTase mutants have a modified substrate binding and/or product selectivity, compared to this sequence. The mutants are created using primer mutagenesis to modify the gene encoding this sequence. These sequences have greater product selectivity and/or reduced product inhibition (better yields) than wild-type CGTase. These mutant sequences are used to manufacture the 6 main CD types (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides, optionally in situ, e.g. during production of baked goods, to stabilise chemicals during their manufacture and in detergents. CD are known for their usefulness in foods, e.g. as a bread-improving agent, to encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals, pesticides or fungicides, to bind/remove lipophilic compounds such as cholesterol (e.g. in egg yolk or butter), in plastic laminates, films etc. and to make blodegradable plastics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclomaltodextrin glucanotransferase; CGTase; enzyme; Bacillus circulan thermoanaerobacter; starch; cyclomaltodextrin; cyclodextrin; pesticide; transglycosylation; cyclic glucose oligomer; glucose oligosaccharide; cholesterol removal; food stabiliser; vitamin stabiliser; fungicide; plastic laminate; biodegradable plastic; mutein.
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/note= "X= Phe,
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 than wild-type CGTase. These mutant sequences are used to manufacture 6 main CD types (comprising 6-11 glucose units), or linear 2-12 glucos oligosaccharides, optionally in situ, e.g. during production of baked goods, to stabilise chemicals during their manufacture and in
                                                                                                                    to this sequence. The mutants are created using primer mutagenesis to modify the gene encoding this sequence. These sequences have greater product selectivity and/or reduced product inhibition (better yields)
                                                                                                                                                                                                  AAW17580-W17591, and AAW17606-W17652 represent mutant versions of the cyclomaltodextrin glucanotransferase (CGTase) of Thermoanerobacter thermosulphurigenes sp. ATCC 53627. (see AAW06772 for wild type sequence). CGTase catalyses the conversion of starch and similar substrates into cyclomaltodextrins (also known as cyclodextrins) via an substrates into cyclomaltodextrins (also known as cyclodextrins)
                                         detergents. CD are known for their usefulness in foods, e.g. bread-improving agent, to encapsulate/stabilise/solubilise v dyes, pharmaceuticals, pesticides or fungicides, to bind/rem
 Sequence
                      plastic laminates,
                                                                                                                                                                    complexes with many small
                                                                                                                                                                              glucose oligomers with
                                                                                                                                                                                                                                                                   Claim 40; Page -; 161pp; English.
                                                                                                                                                                                                                                                                                                  New variants of cyclo:malto:dextrin glucanotransferase (CGTase) - have altered substrate binding, useful for prodn. of cyclodextrin(s) or linear oligosaccharide(s), opt. formed in situ in e.g. baked
                                                                                                                                                                                                                                                                                                                                               WPI; 1996-485774/48
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21-APR-1995;
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                                  lipophilic compounds such as cholestero.
                                                                                                                                                                             intramolecular transglycosylation reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a hydrophobic internal cavity that form inclusion
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                                                                                                                                                      lexes with many small hydrophobic molecules. These CGTase mutants a modified substrate binding and/or product selectivity, compared
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US-08-332-071B-16
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| US-09-202-621B-7 | US-09-193-365-14 | US-08-435-568A-19 | US-08-981-122-25 | US-09-112-656-14 | US-09-315-861-5 | US-09-222-373-50 | US-09-222-373-49 | US-08-997-263-1 | US-08-651-179B-3 | US-08-651-179B-2 | US-08-722-806A-7 | US-08-340-208B-1 | US-08-645-193B-27 | US-08-671-487A-8 | -659A-15 | US-08-488-659A-152 | US-08-488-659A-151 | US-08-488-659A-150 | US-08-685-589A-6 | US-08-441-871-65 | US-08-441-871-55 | US-08-441-871-1 |
| Sequence 7, Appli | Sequence 14, Appl | Sequence 19, Appl | Sequence 25, Appl | Sequence 14, Appl | Sequence 5, Appli | | Sequence 49, Appl | Sequence 1, Appli | Sequence 3, Appli | Sequence 2, Appli | Sequence 7, Appli | Sequence 1, Appli | Sequence 27, Appl | Sequence 8, Appli | • | Sequence 152, App | - | Sequence 150, App | Sequence 6, Appli | Sequence 65, Appl | Sequence 55, Appl | Sequence 1, Appli |

ALIGNMENTS

US-08-488-113B-153 Sequence 153, Application US/08488113B Patent No. 5744580GENERAL INFORMATION: SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/488,113B FILING DATE: 07-7UN-1995 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION UMBER: US 08/425,336 FILING DATE: 18-APR-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/988,430 FILING DATE: 09-DEC-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992 APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993 PRIOR APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy APPLICANT: Better, Marc D. APPLICANT: Carroll, Stephen F. APPLICANT: Studnika, Gary M. TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION: STREET: DVC CITY: Chicago CTTATE: Illinois CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: NUMBER OF SEQUENCES: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS REGISTRATION APPLICATION NUMBER: ADDRESSEE: 60661 MCNicholas, J RATION NUMBER: E: McAndrews, Held & Malloy, Ltd. Floppy disk UMBER: US 07/787,567 04-NOV-1991 169

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Best Local Similarity
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 104 amino acid
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APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                   APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07
FILING DATE: 09-DEC-1992
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CITY: Chicago
TMATE: Illinois
TMATE: TISA
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APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary
REGISTRATION NUMBER: 32,918
*, REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
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TELEFAX: 312/707-9155
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2.2e+02;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-107-669D-17
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                  Query Match
Best Local Similarity
Thes 4; Conserv
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US-08-107-669D-17
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Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 104 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/808,464 FILING DATE: 13-DEC-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 14-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/107,669D FILING DATE: 13-AUG-1993
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                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                         NAME: Michele A. Cimbala
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                                   104 amino acids
                                  Conservative
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                          37.5%; >cc
100.0%; Pr
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100.0%; Pred. No.
tive 0; Mismatch
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                                                Score 3;
Pred. No.
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                                  Mismatches
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                                                DB 1; Length 104; 2.2e+02;
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Best Local Similarity
Thes 4; Conserve
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US-08-472-788A-17
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GENERAL INFORMATION:
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APPLICATION NUMBER: 08/082,842
FILING DATE: 23-UN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
BEGIGTEPATTON NUMBER: 33-851
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APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
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TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
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1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 amino acids
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100.0%; Pr
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b; Pred. No. 2.2
0; Mismatches
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No. 2.2e+02;
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Matches 4; Conserv
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GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acid
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/US9
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/8
APPLICATION UNMBER: US 07/8
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 202/371-2540
FORMATION FOR SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PROPERTY OF SEC. TO THE PRO
                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: FILING DATE: 13-MAY CLASSIFICATION: 53(
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                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
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o. 5837491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: McAndrews, Held & Malloy, Ltd. 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 amino acids
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                     UMBER: US/08/646,360
13-MAY-1996
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100.0%; Pr
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                                                                                                                                        Version #1.25
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PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER:

DATE:

12-MAY-1994

PCT/US94/05348

FILING DATE: APPLICATION NUMBER:

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US 08/064,691

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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                             FILING DATE: 23-JUN-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/US
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
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APPLICATION NUMBER: |
                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Studnicka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION:
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FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/808,464 FILING DATE: 13-DEC-1991
                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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nes 4; Conserv
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STRANDEDNESS: dou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
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20005-3934
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                                                                                                                                                                                                                                                                                                         D.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 amino acids
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Conservative 0;
                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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Modified Antibody Variable Domains
89
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                                                                     PCT/US92/10906
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ER: 200-70.P4
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b. 2.2e+02;
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OPERATING SYSTEM: PC-DOS/MOOPERATING SYSTEM: PC-DOS/MOOPERATING SYSTEM: PC-DOS/MOOPERATING SYSTEM: PC-DOS/MOOPERATION OF SYSTEM SYSTEM OF SYSTEM SYSTEM OF SYSTEM SYSTEM OF SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SYSTEM SY
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
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REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
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REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
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APPLICATION NUMBER: US 08
FILING DATE: 12-MAY-1993
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                              FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/988,430 FILING DATE: 09-DEC-1992
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SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No.
tive 0; Mismatc
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-839-765-153
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Best Local 9
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                      APPLICATION NUMBER: (FILING DATE: 19-JUN-PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 09-DEC-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Immunoto:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Carroll, Stephen F. APPLICANT: Studnika, Gary M.
                                                                                                    FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                   NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TENGTH: 104 amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 SYXG 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09136389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 amino acids
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                                                                                                                                                                          NUMBER: US 07/901,707
19-JUN-1992
                                                                                                                         UMBER: US 07/787,567
04-NOV-1991
                                                                                                                                                                                                                                UMBER: US 07/988,430
09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.5%; Score 3; DB 4; Le 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/09/136,389
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Best Local Similarity
Watches 4; Conserv
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JS-08-428-188-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL
                                                                                                                                                                                                                                                                                                                                       CLASSIETT:: 02-MAY-17
                                                                                                                                                                                           TELEFAX: (202) 393-53 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9:
FILING DATE: 03-SEP-1993
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Holman, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                   MOLECULE MYPOTHETICAL: N
                                                               FEATURE:
                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                           FRAGMENT TYPE:
                                   NAME/KEY:
                                                                                                                                                                                                                                                            NAME: Holman, John (REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 SYXG 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
        OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                            TOPOLOGY:
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                                                                                                                                                                   LENGTH:
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                                                                                                                                                     amino acid
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400 Seventh St. N.W.
                                                                                                                                                                 226 amino acids
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Lemainque, Arnaud
Malette, Patricia
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                                     Modified-site 73
                                                                                                                            linear
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NO
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                                                                           N-terminal
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                                                                                                                                                                                                         393-5350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for the Specific Immunoassay of Human Plasma Glutathione Peroxidase, Kit for its Implementation, Oligopeptides and Antibodies Specific the Method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 3; DB 100.0%; Pred. No. 2. Live 0; Mismatches
         /note= "Amino acid at position is selenocysteine"
                                                                                                                                                                                                                                                                                                                FR 93 10504
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40. 2.2e+02;
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; MOLECULE TYPE:
US-08-895-590-5
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                                                                                      RESULT
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SeqNence 405, Application US/09461697
Patent NO. 6277974
GEMERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application Patent No. 6207410 GENERAL INFORMATION:
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                         Best
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zheng, Wei
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hall, Linda M.
APPLICANT: Ren, Dejian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 22314-3187
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                                                                                                                                      72 SYXG 75
                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                        TYPE:
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                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 SYXG 74
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                                                                                                                                                                                                                                                                                                                                                                 526 amino acids
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                                                                                                                                                                                                    37.5%; Score 3; DB 4; Let larity 100.0%; Pred. No. 6.5e+02; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                   Length 526;
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US-07-895-300A-8
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US-07-895-300A-8
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Edit of Invention: Compositions and Methods for Diagnosing
TITLE OF INVENTION: AND TREATHING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILLE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: 05-999
CURRENT APPLICATION NUMBER: 05-09/461,697
CURRENT FILLING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                          TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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TYPE: PRT
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                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Shire, Steven J.
APPLICANT: Sliwkowski, Mary B.
TITLE OF INVENTION: PURIFIED FORMS OF DNase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hensley, Max D.
REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: U.FILING DATE: 19920608
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                    TOPOLOGY:
                                                         LENGTH:
                                                                                                                                                                                                                                                                                FILING DATE
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                                      AMINO ACID
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                                                         4 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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s; Pred. No. 1.6
0; Mismatches
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hes 0;
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Query Match
Best Local Similarity ?
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US-08-079-445-3
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FILING DATE: 18-JUN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-HP 9648
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blondelle, Sylvie E.
APPLICANT: Pinilla, Clemencia
APPLICANT: Eichler, Jutta
APPLICANT: Eichler, Jutta
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: PEPTIDES HAVING ANTI-MICROBIAL,
TITLE OF INVENTION: HEMOLYTIC, ANTI-MELITTIN OR ANTI-ENZYMATIC ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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LENGTH: 4 amino acids
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                FEATURE:
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STATE: California
COUNTRY: United S'
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                                                                                                                       OTHER INFORMATION:
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                                                                                                                                                          LOCATION:
                                                                                                                                                                          NAME/KEY:
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4370 La Jolla Village Drive, Suite 700
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                     Conservative
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                                                                                                                                                                        Modified-site
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100.0%;
                                     25.0%; Score 2; DB 1; Le 100.0%; Pred. No. 1.6e+05;
                                                                                                                       /note ^{\circ} "C-terminal amino acid is amidated"
                                                                                                                                                                                                          /label- Xaa
/note- "Xaa
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/noten "XaaoKFmoc"
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; Pred. No. 1.6e+05;
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                     Indels
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RESULT 16
US-08-332-0718-16
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                                                            Sequence 16, Applicat Patent No. 5556836 GENERAL INFORMATION:
                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (505) 243-2542
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Compatibles
COMPUTER: Compatibles
OPERATING SYSTEM: PC-DOS or MS-DOS
SOFTWARE: WordPerfect 6.0a for Windows
CURRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
CORRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8:
FILING DATE: 03-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A Peacock
                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 87109-5802
COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (505) 242-9677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhomed Incorporated
STREET: 4261 Balloon Park
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    APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb MEDIUM TYPE: Storage COMPUTER: IBM PC/XT/AT, IBM PS/2 or COMPUTER: compatibles
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5. 5443816
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                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                              Application US/08332071B
ROEDERN, ERICH G.
KESSLER, HORST
KUTSCHER, BERNHARD
BERND, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                              4 amino acids
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                                                                                                                                                                                                                                                                                                                                                                  linear
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Buck A.
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100.0%; Pred. No. 1.
Live 0; Mismatches
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US-08-176-938-20
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                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
Schiller, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
STOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                    COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                    REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 01-NOV-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity hes 2; Conserv
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             CLASSIFICATION:
                                                                                                                                                                                            STATE:
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TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
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                                                                                                                                                                                           New York
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1155 Avenue of the Americas
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o. 1.6e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                  TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                       SOFTWARE: Patentin Release CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dooley, Colette T APPLICANT: Houghten, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 43, CONTY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
TOPOLOGY:
                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 yxg
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sterner Ph.D., Richard J. REGISTRATION NUMBER: 35,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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 amino acid
3Y: linear
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4370 La Jolla Village Drive, Suite 700
                                   4 amino acids
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                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                Floppy disk
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No. 5641861el Mu Opioid Receptor Ligands:
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/note= "phenylglycine"
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/note= "1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid"
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o. 1.6e+05;
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; OTHER INFORMATION: ; OTHER INFORMATION: US-08-487-006-150
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Best Local Similarity
Thes 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                     TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-TP 1706
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC compatible
COMPUTER: PC compatible
COMPUTER: PC compatible
COMPUTER: PC compatible
COMPUTER: PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,006
FILING DATE: 07-UN-1995
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dooley, Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: No. 5641861el Mu Opioid Receptor Ligands:
TITLE OF INVENTION: Agonists and Antagonists
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
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                               EATURE:
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NAME/KEY:
                                                                                                                                                                         TYPE: amd
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CITY: San Diego
STATE: California
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                                           NAME/KEY: Peptide LOCATION: 4 OTHER INFORMATION:
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                                                                                                           OTHER INFORMATION:
                                                                                                                          NAME/KEY: Peptide LOCATION: 2
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GY: linear
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100.0%; Pre
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                                             /note= "Xaa is Nap."
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Pred. No. 1.6e+05;
                                                                                                           "Xaa
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OTHER INFORMATION:
OTHER INFORMATION:
US-08-487-006-151
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OTHER INFORMATION:
US-08-487-006-152
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US-08-487-006-152
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Best Local Similarity
Matches 3; Conserv
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                                                          Matches
                                                                       Query Match
Best Local
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APPLICANT: Dooley, Colette T.
APPLICANT: Houghten, Richard
                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
NAME: Campbell, Cathryn A.
1,815
                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                       Local Similarity hes 3; Conserv
                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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California
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4370 La Jolla Village Drive, Suite 700
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                                                          Conservative
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                                                  25.0%; 5cc
100.0%; Pr
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100.0%; Pr
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the C-terminal."
                                                                                                                                                /note= "Amino acid is amidated
the C-terminal."
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                                                                       Score 2; Pred. No.
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                                                         Mismatches
                                                                       DB 1; Le
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US-08-170-360-17
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                                                           Patent No. 5656602

GENERAL INFORMATION:
APPLICANT: Tseng, Albert P. S.
APPLICANT: Inglis, Adam
TITLE OF INVENTION: PLA2 INHIB
NUMBER OF SEQUENCES: 17
                                                                                                                                                         Sequence 17,
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 535-89
INFORMATION FOR SEQ ID NO:
         CORRESPONDENCE ADDRESS:
*ADDRESSEE: Rothwell, Figg Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-TP 1706
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dooley, Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: No. 564,861el Mu Opioid Receptor Ligands:
TITLE OF INVENTION: Agonists and Antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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    STREET:
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LOCATION:
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OTHER INFORMATION:
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CLASSIFICATION:
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Washington
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                                                                                                                                                         Application US/08170360
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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                                                               PLA2 INHIBITORY COMPOUNDS
17
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                      /note= "Xaa is (D)Nle.
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                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                           DB 1;
1, ¢
                                                                                                                                                                                                                                                                                                              .6e+05
                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                         Length 4;
                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                              Gaps
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US-08-454-950-7
Sequence 7, Application US/08454950
Patent No. 5690905
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE: N
; FRAGMENT TYPE:
US-08-170-360-17
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202)783-603:
INFORMATION FOR SEQ ID NO:
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 I
MEDIUM TYPE: Storage
COMPUTER: IBM PC/XT/AT, IBM PS/2 or
COMPUTER: compatibles
OPERATING SYSTEM: PC-DOS or MS-DOS
SOFTWARE: Wordberfect 6.0a for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE N
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PCT/AU92/00333
FILING DATE: 06-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                             COUNTRY: U.S.A. ZIP: 87109-5802
                                                                                                                                                                                            CITY: Albuquerque STATE: NM
                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0
FILING DATE: 03-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: US/0
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ernst, Barbara G
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                         Zamora,
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                                                                                                                                                                                                                                          RhoMed Incorporated
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                                                                                                                                                                                                                                                                                                                        Buck A
                                                                                                                                                                                                                                                                                                                                         Paul O.
                                                                                                                                                                                                                                                                                          Pharmaceutical Preparation and Method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%; Score 2; I
100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                           Peptide-Metal Ion
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                US/08/454,950
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b. 1.6e+05;
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
FILING DATE: 20-FEB-1992
07/8

TELEFAX: (505) 243-254
NFORMATION FOR SEQ ID NO:

243-2542 NO: 7:

TELEPHONE: (505) 242-9677

APPLICATION NUMBER: 07/8: FILING DATE: 03-JAN-1992 ATTORNEY/AGENT INFORMATION: NAME: Deborah A. Peacock

07/840,077 -1992 07/816,477

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Best Local Similarity
Thes 2; Conserve
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US-08-434-761-3
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US-08-454-950-7
APPLICATION NUMBER: US 08/079,445
FILING DATE: 18-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-HP 9648
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9010
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08434761 Patent No. 5698673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: PEPTIDES HAVING ANTI-MICROBIAL,
TITLE OF INVENTION: HEMOLYTIC, ANTI-MELITTIN OR ANTI-ENZYMATIC ACTIVITY
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Blondelle, Sylvie i APPLICANT: Pinilla, Ciemencia APPLICANT: Eichlor, Jutta APPLICANT: Houghten, Richard /
                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4 amino ac
TYPE: amino acid
STRANDEDNESS: Sin
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CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Diego
STATE: Californ:
                                                                                                                                                                                                                                       APPLICATION NUMBER:
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2 WK 3
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                                                                                                                                                                                                                                                                                                                                                                                                    California
                                                                                                                                                                                                                                                                                                                                                                                                                                     4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 amino acids
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ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                   United States of America
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                                                                                                                                                                                                                                                                                                                                Floppy disk
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; Pred. No. 1.6e+05;
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Query Match

25.0%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Applic Patent No. 5700905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                 TELEFAX: (215)568-343
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: MODGCOCK, Washburn, Kurtz, Mackiewicz and No. 5700905ris STREET: One Liberty Place, 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (215)568-3100
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Malinoski, Lynn
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TOPOLOGY: 11 MOLECULE TYPE:
                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Spanevello, Rolando APPLICANT: Nutt, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One L__
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 4
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-POS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/338,890B
FILING DATE: NOV. 14, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 4 amino acids
                                                                                                                  TELEPHONE:
                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                           19103
                               amino acid
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                                                                                                 (215)568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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amidated"
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/note= "Xaa=any amino acid"
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                                                                                                                                                                   38,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ralph
                                                                                                                                                     UPN-2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Xaa=KFmoc"
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| | | | | | Search completed: January 14, 2002, 07:57:30 Job time: 375 sec | Sear Job |
|--|----|------|----|--------|---|----------------------|
| | 0; | Gaps | 0; | Indels | Best Local Similarity 100.0%; Prod. No. 1.6e+05; Matches 2; Conservative 0; Mismatches 0; 1 wk 2 1 2 WK 3 | Be Ma Qy Db |

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Listing first 50 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Word size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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1 wkxxayxg 8
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  January 14, 2002, 07:58:36;
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Copyright (c) 1993 - 2000 Comp
  DВ
E60274
S68326
PC2132
S32246
S33246
S33246
S68802
PT031
S66607
RHLMGS
C45474
S62880
P40309
148778
P10081
P70081
S78026
UCGM24
S62880
P70081
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major protein antigen MPT63 · Mycobacterium tuberculosis (fragment) C;Species: Mycobacterium tuberculosis (C;Species: Mycobacterium tuberculosis C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993 C;Accession: E60274 R;Nagai, S:; Wiker, H.G.; Harboe, M.; Kinomoto, M. Infect. Immun. 59, 372-382, 1991 Infect. Immun. 59, 372-382, 1991 A;Reference number: A60274; MUID:9109989
                                                                                             A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>
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A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides
A;Reference number: S68325; MUID:96132650
A;Accession: S68326
A;Molecule type: protein
A;Residues: 1-5 <TAY>
B;Accessiones:                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                               A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia A;Reference number: S33244; MUID:93265912
A;Accession: S33244
                                                                                                                                                                                                                                                                                                                                          R; Minakata, H.; Ikeda, T
FEBS Lett. 323, 104-108,
                                                                                                                                                                                                                                                                                                                                                                                                                               neuromodulatory peptide WWamide-1 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S33244
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A; Residues: 1-7 <MAU>
C; Keywords: amidated o
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A;Title: KSAYMRFamide: a novel FMRFamide-related heptapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FMRFamide-related heptapeptide - Panagrellus redivivus C;Species: Panagrellus redivivus C;Species: Panagrellus redivivus C;Date: 03-May-1994 #sequence_revision 15-Oct-1994 #text_change 11-Jul-1997 C;Accession: PC2132 C;Accession: PC2132 R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, R;Maule, A.G.; Shaw, C.; Bowman, J.W.; Halton, D.W.; Thompson, D.P.; Geary, R;Maule, A.G.; Shaw, C.; Bowman, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.W.; Halton, D.
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C;Date: 19-Mar-1997 #sequence_revision
C;Accession: S68326
                                                                                                                                   A; Molecule
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S33246
A; Experimental source:
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R:Yamada, M.; Wasserman, R.; Reichard, B.A.; $
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific A;Reference number: PT0222; MUID:91108337
A;Accession: PT0311.
                                                                                                               C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
C:Accession: PT0311
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: The inhibitor protein of phosphorylated nitrate reductase A; Reference number: S68802; MUID: 96244508 A; Accession: S68802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K. FEBS Lett. 332, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia A;Reference number: S33244; MUID:93265912
A;Accession: S33246
A; Molecule type: DNA
A; Residues: 1-8 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Spinacia oleracea (spinach)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Achatina
C; Date: 19-Mar-1997
C; Accession: S33246
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 1-8 < BAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Bachmann, M.; Huber, J.L.; Liao, P.C.; FEBS Lett. 387, 127-131, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nitrate reductase (NADH) inhibitor -
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fulica (giant African snail)
#sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
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                                                                               .; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, 1991
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2.2e+05;
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B lymphocyte

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thrombospondin 2 - bovine (fragment)
N;Alternate names: corticotropin-induced secreted protein (CISP); thrombospondin
C;Species: Bos prinigenius taurus (cattle)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 14-Aug-1998
                                                                      RESULT
C45474
                                                                                                                                                                                                                                                                                                                                                                                                                          gonadoliberin - sea lamprey
N;Alternate names: gonadotropin releasing hormone (GnRH)
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 18-Mar-1997
C;Accession: A01412
R;Sherwood, N.M.; Sower, S.A.; Marshak, D.R.; Fraser, B.A.; Brownstein, M.J.
J. Biol. Chem. 261, 4812-4819, 1986
A;Title: Primary structure of gonadotropin-releasing hormone from lamprey brain.
A;Reference number: A01412; MUID:86168192
A;Accession: A01412
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RHLMGS
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S66607
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C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental
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Best Local Similarity
Thinkhes 2; Conserv
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A; Rcsiducs: 1-10 <SHE>
C; Comment: This harmone was isolated from the brain
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Best Local :
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5. 2.2e+05;
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C;Accession: C45474
R;Pellerin, S.; Lafeuillade, B.; Scherrer, N.; Gr
J. Biol. Chem. 268, 4304-4310, 1993
A;Title: Corticotropin-induced secreted protein,
A;Reference number: A45474; MUID:93179438
A;Accession: C45474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: adrenocortical cells
A; Note: sequence extracted from NCBI backbone (NCBIP:125844)
C; Superfamily: thrombospondin 1; EGF homology; thrombospondi
                                                                                A; Status, Proceedin
A; Molecule type: protein
A; Residues: 1-10 <SOW>
A; Experimental source: brain
A; Experimental source: brain
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A49187
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R;Stratilova, E.; Dzurova, M.; Markovic, O.; Joernvall, H.
FEBS Lett. 382, 164-166, 1996
A;Title: An essential tyrosine residue of Aspergillus polygalacturonase.
A;Reference number: S62880; MUID:96196586
A;Accession: S62880
                                                                                                                                                                                         R;Sower, S.A.; Chiang, Y.C.; Lovas, S.; Conlon, J.M. Endocrinology 132, 1125-1131, 1993
A;Title: Primary structure and biological activity c A;Reference number: A49187; MUID:93178316
A;Accession: A49187
                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                     gonadotropin-releasing hormone III - sea lamprey
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C;Accession: A49187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-10 <STP>
C; Keywords: 91yoosidase; hydrolase
F;4/Active site: Tyr #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment) C; Species: Aspergillus sp.
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25.0%; but
100.0%; Pr
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b; Pred. No. 1.9
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o. 1.9e+03;
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R; Fautsch, M.P.; Thompson, M.A.; Holicky, E.L.; Schultz, P.J.; Hallett, J.B.; Wieben, I Genomics 14, 883-890, 1992
A; Title: Conservation of coding and transcriptional control sequences within the snRNP A; Reference number: A44368; MUID:93122798
A; Accession: 148778
A; Accession: 148778
                                                                                                                                      protein QA300023 - Arabidopsis thaliana (fragment) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 C;Accession: PT0081 R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y. submitted to JIPID, December 1995
                                                                                                                                                                                                                                                      RESULT
PT0081
                    A; Experimental source: Leaf C; Keywords: acetylated amino end
                                                       A; Molecule type: protein A; Residues: 1-11 <TSU>
                                                                                         A; Accession: PT0081
                                                                                                          A;Description: Two dimensional electrophoresis A;Reference number: PN0173
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
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J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain CRD3 region (clone 6-94) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 F;1/Modified site: acetylated
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A; Residues: 1-10 <RES>
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A; Residues: 1-10 <YAM>
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urotensin II - telostean fish C;Species: telostean fish C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 C;Accession: S42765 R;Bhaskaran, R.; Arunkumar, A.I.; Yu, C. Biochim. Biophys. Acta 1199, 115-122, 1994
                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: urotensin II
C;Keywords: neuropeptide; osmoregulation
F;6-11/Disulfide bonds: #status experime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  urotensin II - long-jawed mudsucker
C;Species: Gillichthys mirabilis (long-jawed mudsucker)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 15-Oct-1996
C;Accession: A01409
                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: the proposed sequence was confirmed by synthesis of a peptide with the same C;Comment: Urotensin II is found in the teleost caudal neurosecretory system and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Urotensin II: a somatostatin-lik A; Reference number: A01409; MUID:81054904 A; Accession: A01409
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A;Title: Urotensin II: a somatostatin-like peptide in the caudal neurosecretory sys
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245, 449-456, 1997
                                                                                                                                                                                                                                                               Conservative
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b. 2e+03;
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2.2e+03;
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                                                        #text_change 05-Dec-1997
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A:Molecule type: protein A:Residues: 1-12 <BHA> C:Superfamily: urotensin II C:Keywords: neuropeptide; os F:6-11/Product: urotensin I]
RESULT
S01122
                                                                                                             Query Match
Best Local Similarity
Conserve
                                                                                                                                                                                                                                                          A; Title: Properties of the soluble polypeptide of the proton-translocating transhydrogen A; Reference number: S69123; MUID:95255277
A; Accession: S69123
                                                                                                                                                                                                                                                                                                          proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment) C;Species: Rhodospirillum rubrum C;Date: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998 C;Accession: S69123 R;Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B. Eur. J. Blochem. 228, 719-726, 1995
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
S69123
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Thes 2; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:McMaster, D.; Lederis, K.
Peptides 4, 367-373, 1983
A;Title: Isolation and amino acid sequence of two
A;Reference number: JS0423; MUID:84041959
A;Accession: JS0423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             urotensin II-A peptide - white sucker
C;Species: Catostomus commersoni (white sucker)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-May-1997
C;Accession: JS0423
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JS0423
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A:Accession: S42765
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A;Molecule type: proto
A;Residues: 1-12 <DIG:
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plastocyanin 2 - Arabidopsis thaliana (fragment) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995 C;Accession: PA0037 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A. submitted to JIPID, July 1994
                                                                                                                                                                                                                                                                                                                                                                    RESULT
PA0037
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A;Residues: 1-12 <SCH>
C;Keywords: chloroplast; photosynthesis; photosystem
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C;Species: Spinacia oleracea (spinach)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C;Accession: S01122
R;Schroeder, W.P.; Henrysson, T.; Akerlund, H.E.
FEBS Lett. 235, 289-292, 1988
A;Title: Characterization of low molecular mass proteins of photosystem II
A;Reference number: S01120
                                                                                                                                        A;Accession: PA0037
A;Molecule type: protein
A;Residues: 1-12 <KAM>
A;Experimental source: stem
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A; Residues: 1-12 <KAM>
A; Experimental source: callus
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A;Description: Separation and characterization of Arabidopsis A;Reference number: PA0001
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RESULT 25
PNO160
PNO160
ribosomal protein S16 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994
C;Accession: PNO160
R;Fukaya, N; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich A;Reference number: PNO160
A;Accession: PNO160
A;Accession: PNO160
A;Residues: 1-12 <FUK>
C;Keywords: protein biosynthesis; ribosome
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Search completed: January 14, 2002, 07:58:36 Job time: 386 sec
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WWA3_ACHFU
UFF06_MOUSE
GON1_PETMA
GON3_PETMA
Q20B_COMTE
PSP3_PHYPA
UR2A_CATCO
UR2B_CYPCA
UR2B_CYPCA
UR2_GILMI
UR2_POLSP
UR2_SCYCA
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| RL41_METJA | TERT_APIME | MDH_PSEIN | MDH_BURCE | SYR_RAT | RLC1_HALMA | MCRG_METTE | LPP2_HUMAN | CAT4_FASHE | UC03_MAIZE | ALL2_CYDPO | AGI_EUPMA | YPFK_SALTY | TPIS_PINPS | GAST_MACMU | ATPI_PAVLU | UPAB_HUMAN |
| P54025 I | P56587 | P80538 | P80537 1 | P40329 | P12740 I | P22950 I | P56642 1 | P80528 | P80609 : | P82153 o | P33889 6 | Q9zfu5 : | P81666 J | P33714 r | P28529 I | P31935 I |
| methanococc | apis mellif | pseudomonas | burkholderi | rattus norv | haloarcula | methanosarc | homo sapien | fasciola he | zea mays (m | cydia pomon | euphorbia m | salmonella | pinus pinas | macaca mula | pavlova lut | homo sapien |

ALIGNMENTS

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RESULT VAOH_BO VAOH_BO VAOH_BO VAOH_BO VAOH_DO VAOH_DO TO SECOUS ROOTH TO SECOUS RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LUGUIN RA LU
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VAOH_BOVIN
VAOH_BOVIN
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VACUULA:
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
VACUULAR ATP SYNTHASE SUBUNIT H (EC 3.6.1.34) (V-ATPASE H SUBUNIT)
(VACUULAR PROTON PUMP H SUBUNIT) (V-ATPASE M9.2 SUBUNIT) (V-ATPASE

YOA MEMBRANE ACCESSORY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granules.";

J. Biol. Chem. 273:10939-10947(1998).

J. Biol. Chem. 273:10939-10947 (1998).

I. FUNCTION: VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.

OF INTRACELLULAR COMPOSED OF AT LEAST 10 SUBUNITS.

I. SUBUNIT: COMPOSED OF AT LEAST 10 SUBUNITS.

I. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

ADRENAL GLAND. NOT FOUND IN BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-19, AND SEQUENCE OF TISSUE-Adrenal medulla; MEDLINE-98225166; PubMed-9556572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification and characterization of a novel 9.2-kDa membrane sector-associated protein of vacuolar proton-ATPase from chromaf:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ludwig J., Kerscher S., Brandt U., Pfeiffer K., Schagger H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                 Hydrolase; Hydrogen ion transport; Transmembrane. TRANSMEM 7 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                        EMBL; Y15285; CAA75570.1;
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0 AA;
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9129
                             37.5%;
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Score 3; DB 1; Pred. No. 1.9 0; Mismatches
                                                                                                                                                                           POTENTIAL.
87B2CEB7D47E5427 CRC64;
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                                 DB 1; Le
b. 1.9e+02;
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Similarity 4; Conserv

Conservative

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ALL2_CARMA
P81805;
30-MAY-2000
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Leptinotarsa decemlineata (Colorado potato beetle).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insec Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae; Leptinotarsa.
                               P42985;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation updat
01-NOV-1995 (Rel. 32, Last annotation updat
                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                    TISSUE=Cerebral ganglion, and Thoracic MEDLINE=98121193; PubMed=9461295;
                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J., Proost P., Torrekens S., de Loof A.; "Isolation, identification and synthesis of novel oviductal m
 SEQUENCE
            Neuropeptide; Amidation; Multigene family.
MOD_RES 7 7 AMIDATION (PO
                                                                                                      Duve H.,
                                                                                                                                            SEQUENCE.
                                                                                                                                                                                                              Carcinus maenas (Common shore crab) (Green crab)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation, identification and synthesis of stimulating head peptide in the Colorado pot
                                                                                                                                                                 NCBI_TaxID=6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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2; Conserv
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 770 MW;
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AMIDATION (POTENTIAL) 672879CDCB5DDB70 CRC64;
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6B07632B5DD03000
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b. le+05;
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                                                                                                                    SEQUENCE, AND SYNTHESIS.

SEQUENCE, AND SYNTHESIS.

MEDLINE=94235053; PubMed-8179635;

MeDLINE=94235053; PubMed-8179635;

Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,

Geary T.G., Thim L.;

Geary T.G., Thim L.;

"KSAYNRFamide: a novel FMRFamide-related heptapeptide from the

"KSAYNRFamide: a novel FMRFamide-related heptapeptide from the

living nematode, Panagrellus redivivus, which is myoactive in t

parasitic nematode, Ascaris suum.";

parasitic nematode, Ascaris suum.";

parasitic nematode, Ascaris suum.";

parasitic nematode, Ascaris suum.";

parasitic nematode, Ascaris suum.";
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P81298;

30-MAY-2000 (Rel.

30-MAY-2000 (Rel.

30-MAY-2000 (Rel.
                                                                       Biochem. Biophys. Res. Commun. 20
-: FUNCTION: MYOACTIVE; INDUCES
MUSCLE TENSION INCREASE.
-!- SIMILARITY: BELONGS TO THE FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marks N.J., Sangster N.C., Maule A.G., Halton D
Thompson D.P., Shaw C.;
Submitted (MAY-1998) to the SWISS-PROT data ban
-!- FUNCTION: ACTIVE ON NEUROMUSCULATURE.
                                                                                                                                                                                                                                                                                                                                                               Panagrolaimoidea; Panagrolaimidae; NCBI_TaxID=6233;
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MOD_RES 7 7
SEQUENCE 7 AA; 902 MW
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Neuropeptide;
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NCBI_TaxID=6289;
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EPTIDE PF3 (KSAYMRF-AMIDE).
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69D4068B5DC5B350
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01-JUN-1994 (
01-JUN-1994 (
01-OCT-1994 |
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P42984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leptinotarsa decemilneata (Colorado potato beetle).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insec Eukaryota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae; Leptinotarsa.

NCBI_TaxID=7539;
                                                                                                                                                                                                                                                                                                                                                                                           Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S., Grauwels L., van Leuven F., de Loof A.; "Identification, characterization, and immunological localization a novel myotropic neuropeptide in the Colorado potato beetle, Leptinotarsa decemlineata."; Peptides 16:365-374(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
MYOTROPIC NEUROPEPTIDE 1 (LED-MNP-I)
"Minakata H., Ikeda T., Muncoka Y., Kobayashi M., Nomoto K.; "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated ganglia of the African glant snall, Achatina fulica."; FEBS Lett. 323:104-108(1993).
                                       TISSUE Ganglion;
MEDLINE-93265912; PubMed-8495720;
                                                                                             Achatina fulica (Giant African snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
Achatinacea; Achatinidae; Achatina.
                                                                                                                               WWAMIDE-2
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MOD_RES 7 7
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69D4068B5DC5B350 CRC64;
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WWA3_ACHFU
P35921;
01-JUN-1994
01-JUN-1994
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01-OCT-1994
         Neuropeptide;
MOD_RES
SEQUENCE 7 A
                                                                                                                                      _MOUSE __MOUSE STANDARD; PRT; 8 AA. P38644; P38644 (Rel. 30, Created) 01-OCT-1994 (Rel. 30, Last sequence update) 01-FEB-1995 (Rel. 31, Last annotation update) UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P50)
NON_TER
SEQUENCE
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MOD_RES 7 7 7
SEQUENCE 7 AA; 965 MW
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                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mollus
Achatinacea; Achatinidae;
                                                                                     SEQUENCE
                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                               Mus musculus (Mouse).
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7362D5B69B132310
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Sciurognathi; Muridae;
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Gastropoda;
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P30948;
01-JUL-1993
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MEDLINE-86168192; PubMed-3514603;
MEDLINE-86168192; PubMed-3514603;
Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A.,
Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A.,
"Primary structure of gonadotropin-releasing hormone f
brain.";
J. Biol. Chem. 261:4812-4819(1986).
-i- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINJ
FOLLICLE-STIMULATING HORMONES.
-i- SIMILARITY: BELONGS TO THE GNRH FAMILY.
                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GONADOLIBERIN III (GONADOTROPIN-RELEASING HORL
(LULLBERIN III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
Hormone;
MOD_RES
MOD_RES
SEQUENCE
MEDLINE=93178316; PubMed=8440174;
Sower S.A., Chiang Y.-C., Lovas S., Conlon
"Primary structure and biological activity
                                                                                                                                                                       Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Petromyzontijormes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR 1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
GONADOLIBERIN I (GONADOTROPIN-RELEASING HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PETMA
                                                                T\SSUE=Brain;
                                                                                         SEQUENCE.
                                                                                                                               Petromyzontiformes;
NCBI_TaxID=7757;
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cPro; IPR002012; GnRH.
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FE; PS00473; GNRH; 1
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larity 100.0%;
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1E4B36237B1735AB CRC64;
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DB 1;
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1.4e+02;
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                                                                                                                                                                         Hyperoartia;
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  gonadotropin-
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PSP3_PHYPA
ID PSP3_PHYPA
AC P80662;
DT 01-OCT-1996
DT 01-OCT-1996
DT 20-AUG-2001
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Best Local Similarity
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Q2OB_COMTE
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Best Local :
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NON_TER 10 10
SEQUENCE 10 AA; 1241 MW; (
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STRAIN=63;
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P80465;
P80465;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
QUINOLINE 2-OXIDOREDUCTASE, BETA CHAIN (Ed. 1.3.99.17) (FRAGMENT).
Comamonas testosteroni (Pseudomonas testosteroni).
Bocteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
NCBI_TaxID=285;
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MOD_RES
MOD_RES
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-!- CATALYTIC ACTIVITY: QUINOLINE + ACCEPTOR + H(2)O = ISOQUINOLIN-
-!- CATALYTIC ACTIVITY: QUINOLINE + ACCEPTOR + H(2)O = ISOQUINOLIN-
-!- COPACTOR: FAD, MOLYBERNIM AND IRON-SULFUR.
-!- COPACTOR: FAD, MOLYBERNIM AND IRON-SULFUR.
-!- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND
-!- CATALYTIC DEGRADATION OF QUINOLINE AND
-!- CATALYTIC DEGRADATION OF QUINOLINE AND
                                                                                                                                                                                                                                                                                                                                                                        Schach S., Tshisuaka B., Fetzner S., Lingens F.; "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline dioxygenase from Comamonas testosteroni 63. The first two e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUr. J. Biochem. 232:330-344(1222).
-!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO
                                                                                                                                                                                                                                                                                                                                                  quinoline and 3-methylquinoline degradation.";
Eur. J. Biochem. 232:536-544(1995).
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96035889; PubMed=7556204;
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                                                                                                                                                                                                                                               TWO GAMMA CHAINS (PROBABLE)
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9 AA;
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                                               STANDARD;
34, Created)
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284B36237AA1F5A3
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Best Local Similarity
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
UROTENSIN IIA (U-IIA) (UIIA).
Catostomus commersoni (White sucker).
Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Catostomidae; Catostomus.
NCBI_TaxID-7971;
                                                                                                                                                                                                                                                                                                                                                                     UR2A_CA
P04558;
                                                                                                                                                                "Isolation and amino acid sequence of two urotensin II peptides from Catostcomus commersoni urophyses.";
Peptides 4:367-373(1983).
-I- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CORTICOTROPIN-RELEASING FACTOR.
                                                                                                              InterPro; IPR001483; Urotensin_II.
Pfam; PF02083; Urotensin_II; 1.
PROSITE; PS00984; UROTENSIN_II; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multigene family.
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                                                                                                                                               PIR; JS0423; JS0423.
                                                                                                                                                                                                                                McMaster D.,
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AA;
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1336 MW;
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Pred. No.
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Pred. No. 9.8e+02
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PROSITE;
Hormone.
DISULFID
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SEQUENCE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Catostomidae; Catostomus.

NCBI_TaxID-7971;
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"Isolation and amino acid sequence of two urotensin II peptides from Catostomus commersoni urophyses.";
Peptides 4:367-373(1983).
-I- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORN
                                                                                                     Munekata E., Ohtaki T., Ichikawa T., McMaster D., Lederis K.;
(In) Rich D.H., Gross E. (eds.);
Proceedings of the 7th american peptide symposium, pp.69-72,
Pierce Chemical Co., Rockford II. (1981).
-!- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyprinus carpio (Common carp).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.

NCBI_TaxID=7962;
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SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION A
CORTICOTROPIN-RELEASING FACTOR.
1-1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
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InterPro; IPR001483; Urotensin_II.
Pfam; PF02083; Urotensin_II; 1.
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Best Local Similarity
Watches 2; Conserv
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Best Local
                                                                                                              UR2_POLSP STANDARD; PRT; 12 AA.
P81022;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UROTENSIN II (UTI).
Polyodon spathula (North American paddlefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bolyodon; Chondrostei; Acipenseriformes; Polyodontidae;
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SEQUENCE
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21-JUL-1986
SEQUENCE FROM N.A. TISSUE-Spinal cord;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-81054904; PubMed=6107911;
Pearson D., Shively J.E., Clark B.R., Geschwind I.I., Barkley M.,
Nishioka R., Bern H.A.;
"Urotensin II: a somatostatin-like peptide in the caudal
neurosecretory system of fishes.";
Proc. Natl. Acad. Sci. U.S.A. 77:5021-5024(1980).
-i- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CORTICOTROPIN-RELEASING FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
UROTENSIN II (U-II) (UII).
Gillichthys mirabilis (Long-jawed mudsucker).
Eukaryota; Metazoa; Chordata; Cranitati; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidei;
Gobiidae; Gillichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001483; Urotensin_II.
Pfam; PF02083; Urotensin_II; 1.
PROSITE; PS00984; UROTENSIN_II; 1.
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                                                                        NEBI_TaxID=7913;
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ilarity 100.0%;
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1364 MW;
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Pred. No.
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73960A9FB879CEBB CRC64;
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RESULT 20 PSBP_PINPS ID PSBP_P AC P81668

PSBP_PINPS P81668;

STANDARD;

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Best Local
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DISULFID
SEQUENCE
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Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
Scyliorhinus canicula (Craniata; Vertebrata; Chondrichthyes; Elasmobranchi; Galeomorphii; Galeoidea; Carcharhiniformes; Scyliorhinidae; Scyliorhinus.
NCBI_TaxID=7830;
                                                                                                                                                     MUSCLE STIMULATION.

-:- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
InterPro; IPR001483; Urotensin_II.
pfam; pF02083; Urotensin_II; 1.
proSITE; pS00984; UROTENSIN_II; 1.
                                                                                                                                                                                                                    MEDLINE=92319231; PubMed=1620290; Conlon J.M., O'Harte F., Smith D.D., Balment R.J., Hazon N.; Conlon J.M., O'Harte F., Smith D.D., Balment R.J., Hazon N.; Purification and characterization of urotensin II and parva from an elasmobranch fish, Scyliorhinus canicula (common dog neuroendocrinology 55:230-235(1992).
-i- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS. CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96051494; PubMed=8536944; Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.; Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.; "Urotensin II from the river lamprey (Lampetra fluviatilis), the lamprey (Petromyzon marinus), and the paddlefish (Polyodon
                                                                                                                                                                                                                                                                                                           TISSUE=Spinal cord;
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PF02083; Urotensin_II; 1.
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Pred. No.
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5. 9.8e+02;
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SMOOTH
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                                                                                                        MEDLINE-93300795; PubMed-8314774;

Smith R.L., Banks J.L., Snavely M.D., Maguire M.E.;

Smith R.L., Banks J.L., Snavely M.D., Maguire M.E.;

"Sequence and topology of the Cora magnesium transport systems of salmoncila typhimurium and Escherichia coli. Identification of a new class of transport protein,";

J. Biol. Chem. 268:14071-14080(1993).

J. BIOCTION: HAS BOTH ATPASE AND HELICASE ACTIVITIES. UNWINDS DNA DUPLEXES WITH 3' TO 5' POLARITY WITH RESPECT TO THE BOUND STRAND AND INITIATES UNWINDING MOST EFFECTIVELY WHEN A SINGLE-STRANDED REGION IS PRESENT. INVOLVED IN THE POSTINCISION EVENTS OF NUCLEOTIDE EXCISION REPAIR AND METHYL-DIRECTED MISMATCH REPAIR.

-1- SIMILARITY: BELONGS TO THE UVRD SUBFAMILY OF HELICASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UVRD_SALTY
Q05311;
Q1-OCT-1994
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999
15-JUL-1999
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF PHOTOSYSTEM II.
-I- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; ASSOCIATED
-I- MITH THE PHOTOSYSTEM II COMPLEX (BY SIMILARITY).
-I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
(SPOT N179) IS: 5.9, ITS MW IS: 22 KDA.
-I- SIMILARITY: BELONGS TO THE PSBP FAMILY.
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Eukaryota; Viridiplantae; Streptophyta; Emi
Spermatophyta; Coniferopsida; Coniferales;
NCBI_TaxID-71647;
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01-OCT-1996
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Electrophoresis 20:1098-1108(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99274088; PubMed-10344291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-2001 (Rel. 40, Last annotation update) OXYGEN-EVOLVING ENHANCER PROTEIN 2 (OEE2) (23 EVOLVING SYSTEM OF PHOTOSYSTEM II) (FRAGMENT).
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(Rel. 30, Last sequence update)
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II (EC 3.6.1.-) (FRAGMENT).
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es; Pinaceae;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TESTIS ECDYSIOTROPIN PEPTIDE C (TE).
Lymantria dispar (Gypsy moth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Naturally occurring analogs of Lymantria testis ecdysiotropin, gonadotropin isolated from brains of Lymantria dispar pupae."; Arch. Insect Biochem. Physiol. 36:37-50(1997).
-!- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES OF LARVAE AND PUPAE.
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Pterygota; Neoptera;
Pterygota; Vespidae;
Vespoidea; Vespidae;
NCBI_TaxID=31921;
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Loeb M.J., Wagner R.M., Woods C.W.,
Bell R.A.;
                            TISSUE-Venom;
Toki T., Yasu
                                                                                                                                                                                                                                                                                                              MASTOPARAN.
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                                                                                                                                                                                                                                                                             Parapolybia indica
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"A new mast cell degranulating peptide, poliste
venom of Polistes jadwigae.";
Biomed. Res. 1:185-187(1980).
-!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE.
THAT COUPLE TO PHOSPHOLIPASE C.
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                                                                   Pterygota; Neoptera;
Vespoidea; Vespidae;
NCBI_TaxID=7448;
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MOD_RES 14 14 AMIDATION.

SEQUENCE 14 AA; 1619 MW; CA376CD3BA6D80DD CRC64;
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Eisei Dobutsu 39:105-111(1988).
-i- FUNCTION: MAST CELL DEGRANULATING PEPTIDE.
-i- THAT COUPLE TO PHOSPHOLIPASE C.
 MEDLINE=80155338; PubMed=540363; Hirai Y, Kuwada M., Yasuhara T.,
                              TISSUE=Venom;
                                                                                                           Vespa xanthoptera (Japanese hornet).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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"G protein-bound conformation of mastoparan-X: heteronuclear
multidimensional transferred nuclear overhauser effect analys
peptide uniformly enriched with 13C and 15N.";
Biochemistry 37:4782-4790(1998).

-i- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PR
THAT COUPLE TO PHOSPHOLIPASE C.
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92304942; PubMed-1610813; Wakamatsu K., Okada A., Miyazawa T., Ohya M., "Membrane-bound conformation of mastoparan-X,
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PDB; 1A13; 16-FEB-99.
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MEDLINE-98077503; PubMed-9414319;
Armes N., Gilley J., Fried M.;
"The comparative genomic structure and homologs in the puffer fish Fugu rubrip CpG-rich islands.";
Genome Res. 7:1138-1152(1997).
                                                                                                                                                                                                                                                                                             O57591 PRELIMINARY; PRT; 34 AA. O57591; O1-JUN-1998 (TrEMBLrel. 06, Created) O1-JUN-1998 (TrEMBLrel. 06, Last sequence up O1-JUN-2001 (TrEMBLrel. 17, Last annotation ARGININOSUCCINATE SYNTHETASE (FRAGMENT).
                            Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases EMBL; Y15170; CAA75440.1; -. Interpro; IPR001518; Arginosuc_synth. PF007544; Arginosuc_synth; 1.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
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Q9EW42;
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLREL. 16, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE HYPOTHETICAL 77.1 KD PROTEIN (FRAGMENT).
LM12.160.
                                                                                                                                                                                                                                                                      Overweg K., Bogaert D., Sluijter M., de Groot "Molecular characterization of Streptococcus resistance in the Netherlands.";
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=950473;
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                                                                                                                                                                                                       EMBL;
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Eukaryota; Euglenozoa;
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11265 MW;
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Pred. No.
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   Length 163;
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Matches 4
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InterPro; IPR001750; Oxidored_q1.
InterPro; IPR002128; Oxidored_q1_C.
InterPro; IPR001516; Oxidored_q1_N.
Pfam; PF00361; oxidored_q1_C; 1.
Pfam; PF01010; oxidored_q1_C; 1.
Pfam; PF00662; oxidored_q1_N; 1.
Chloroplast; NAD; Oxidoreductase; Pla
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Q24837;
Q1-NOV-1996 (TrEMBLrel. C
01-NOV-1996 (TrEMBLrel. C
01-NOV-1998 (TrEMBLrel. C
OFR 1.5 (FRAGMENT).
                                                                                                                                                                                                                                                                         Q9MS52;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MADH DEHYDROGENASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X7
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MEDLINE-94099892; PubMed-8274224;

Bruchhaus I., Leippe M., Lioutas C., Tannich E.;

"Unusual gene organization in the protozoan parasite Entamoeba histolytica.";

DNA Cell Biol. 12:925-933(1993).
                                                                                                         "The phylogenetic relationships of Lembocarpus and Goyazia (Gesneriaceae) based on ndhf sequences.";
Ann. Mo. Bot. Gard. 0:0-0(2000).
-i- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PL-1- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX
                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Gesneriaceae; Goyazia.
                                                                                    EMBL; AF257485; AAF75262.1;
                                                                                                                                                                                                                                                     Goyazia rupicola.
Chloroplast.
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                                                                                                                                                                      Smith J.F.;
                                                                                                                                                                                SEQUENCE FROM N.A.
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Submitted (JUN-1999) to the EMBL; AF162771; AAD46628.1; NON TER 8
                                                          ROY D., Coulombe M., Perron K., Roy P.H.; "Characterization of a novel 6'-N-aminoglycoside gene aac(6')-IIc from the integron of a Chinese Fclinical isolate.";
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MEDLINE-81069885; PubMed-6254986;
Bonitz S.G., Coruzzi G., Thalenfeld B.,
"Assembly of the mitochondrial membrane
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"Proteomics of the chloroplast: systematic targeting analysis of lumenal and periphera Plant Cell 12:319-341(2000).
MEDLINE-95331633; PubMed-7607556; Altus M.S., Wood C.M., Stewart D.A., Rohenderson T., Owens G.A., Danner D.B., McClung J.K.;
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Eukaryota; Viridiplantiae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
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Mammalia; Eutheria;
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Fukarvota; Metazoa; Chordata;
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01-WINDWN PROTEIN FROM 2D-PAGE OF THYLAKOID (SPOT105)
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                                     Homo sapiens (Human).
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Gene 158:291-294 (1995).
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Eur. J. Biochem. 210:53-58(1992).
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MEDLINE-94061059; PubMed-7694728;

Spritz R.A., Holmes S.A., Berg S.Z., Nordlund J.J., Fukal n.,

"A recurrent deletion in the KIT (mast/stem cell growth factor receptor) proto-oncogene is a frequent cause of human piebaldism.

Hum. Mol. Genet. 2:1499-1500(1993).
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Q9TVF1;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MUCIN-LIKE PROTEIN (FRAGMENT).
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SEQUENCE
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MEDLINE-9825151; PubMed=9556557; 
MEDLINE-9825151; PubMed=9556557; 
Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., F
"The Trypanosoma cruzi mucin family is transcribed 
genes having hypervariable regions."; 
J. Biol. Chem. 273:10843-10850(1998). 
EMBL; AF036447; AAC14246.1; -. 
NON_TER 1 1
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Eukaryota; Euglenozoa;
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation updat
NADH DEHYDROGENASE SUBUNIT 6 (FRAGMENT).
STRAIN=VUL-
Haring E.,
                                              SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=115228;
                                                                                                                  Accipitrinae;
                                                                                                                                     Archosauria; Aves;
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                    Mitochondrion
                                                                                                                                                                                                       Buteo buteo vulpinus (western steppe-buzzard).
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                                                                                                                  Buteo.
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    Pinsker W.,
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                                                          Mitochondrion.

EuKaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooidea
Triticeae; Acgilops.

NCBI_TaxID=37682;
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01-NOV-1999 (TTEMBLTEL. 12, L
01-MAR-2001 (TTEMBLTEL. 16, L
NADH DEHYDROGENASE SUBUNIT 3
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J. Zool. Syst. Evol. Res. 37:185-194(1999).
EMBL; AF202212; AAF61894.1; -.
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J. Zool. Syst. Evol. Res. 37:185-194(1999).
EMBL; AF202197; AAF61879.1; -.
Mitochondrion.
          SEQUENCE FROM N.A. STRAIN-KU29;
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01-OCT-2000
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EMBL; U41726; AAB60580.1; -.
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                Submitted (DEC-1995) to the EMBL/GenBank/DDBJ EMBL; U41727; AAB60581.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Camerison between the viral transforming gene (src) of recovered avian sarcoma virus and its cellular homolog.";
Mol. Cell. Biol. 1:1024-1037(1981).
EMBL; U41729; AAA84421.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-SCHMIDT-RUPPIN SUBGROUP A (NY);
Hara H., Kaji A.;
                                                                                                                                                                                                       Williams K.P., Bartel D.P.;
"Phylogenetic analysis of tmRNA secondary RNA 2:1306-1310(1996).
EMBL; U68081; AAB48023.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desulfovibrio desulfuricans.
Bacteria; Proteobacteria; delta subdivision; Desulfovibrio NCBI_TaxID=876;
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MEDLINE=82271824; PubMed=6287213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rous sarcoma virus.
Viruses; Retroviridae;
Viruses; Retroviridae;
NCBI_TaxID=11886;
                                                                                                                                                   SEQUENCE
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MEDLINE=97128184; PubMed=8972778;
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о. 3.6e+03;
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O68237;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-AUG-1998 (TrEMBLrel. 07, Last annotation update)
PLASMID CP32-4, POSSIBLE PARTITION PROTEINS, COMPLETE
PLASMID CP32-4, POSSIBLE PARTITION PROTEINS, COMPLETE
OF A PROTEINS (Lyme disease spirochete).
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Q99292;
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NON_TER
SEQUENCE
                            Drosophila heteroneura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muso
Ephydroidea; Drosophilidae; Drosophila.
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EMBL; AF022481; AAC35449.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91184004; PubMed=2081457;
MacDonald P.M.;
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NCBI_TaxID=32382;
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         8CE802305DD9D6C1 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 09, Last annotation update)
01-JAN-1999 (TrEMBLrel. 09, Lost annotation update)
2-HYDROXYACID DEHYDROGENASE HONOLOGUE (FRAGMENT).
Synechocystis sp. (strain PCC 6803).
Bacteria: Cynnobacteria; Chroococcales; Synechocyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92250478; PubMed-1533622;
Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H
"A calcyclin-associated protein is a newly identified member
Ca2+/phospholipid-binding proteins, annexin family.";
J. Biol. Chem. 267:8919-8924(1992).
SEQUENCE 11 AA; 1310 MW; 55580B0F5DDAA9C7 CRC64;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-PCC6803;
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Gryctolagus cuniculus (Rabbit).

Gryctolagus cuniculus (Rabbit).

Gryctolagus cuniculus (Rabbit).

Gryctolagus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Capto-captopholipid-Binding Protein
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                                                                                             SEQUENCE FROM N.A. White G.R.M., Varley J.M., H Submitted (MAY-1999) to the EMBL; AJ244500; CAB60202.1;
                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-99153747; PubMed-10030676;

MEDLINE-99153747; PubMed-10030676;

White G.R.M., Variey J.M., Heighway J.;

"Isolation and characterisation of a human homologue of the latrophilin gene from a region of 1p31.1 implicated in breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem, J. 315:119-126(1996).
-:- SUBUNIT: MONOMER.
-:- SINDERTIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96207571;
Larcher G., Cimon
Bouchara J.-P.;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ALKALINE EXTRACELLULAR PROTEASE (EC 3.4.21.-) (AEP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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-!- SIMILARITY: BELONGS TO PEPTIDASE
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                                                                                                                                             Oncogene 17:3513-3519(1998).
                                                                                                                                                                                                                          NCBI_TaxID=9606;
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B., Symoens F.,
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Search completed: January 14, 2002, 08:07:31 Job time: 761 sec DЪ

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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//SIDSZ/9cgdata/geneseq/geneseqp/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

| 3 37.5 13 3 37.5 110 3 37.5 110 3 37.5 110 3 37.5 1121 3 37.5 185 3 37.5 275 3 37.5 275 3 37.5 275 3 37.5 275 3 37.5 275 | Query Score Match Length DB |
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| Kyotorphin analogu | | 3 | Tetrapeptide chole | 5 amino acid resid | | ogue | | deri | Enkephalin analogu | Cyclic enkephalin | Organ specific neo | componen | of. | 0f | of en | and | 5 | Ċ | Analgesic tetrapep | peptide. | Analgesic tetrapep | ntane te | Generic analgesic | like | | phal | eric enkephali | inhibitor | illus CGTase | illus CGTase | illus CGTase | illus CGTase | illus | Bacillus CGTase va | Mutated alpha-amyl | Neisseria meningit | ¥ | Consensus sequence | Consensus sequence |

ALIGNMENTS

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27-JUN-1998;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel sphingolipid desaturase that selectively introduces a double bond into the sphingobase of the ceramid residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base deficiency, to compensate for a delta-8-unsaturated long-chain base deficiency, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antidiabetic; cytostatic; auditory; cholecystokinin-8; CCK-8; neuropathy; peripheral nervous system; diabetes mellitus; cancer treatment; cytostatica; hearing impairment; visual handicap; alcohol-induced neuropathy; dystrophy.
                            03-MAY-2000; 2000WO-SE00870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholecystokinin peptide fragment analogue #10.
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                                                                                       09-NOV-2000.
                                                                                                                                                   WO200066150-A1
                                                                                                                                                                                                                                          Modified-site
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100.0%; Pr
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RESULT
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11-APR-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to peptides showing cholecystokinin (CCK)-8 activity, which can be used to treat neuropathies in the peripheral nervous system (PNS). The present sequence is one such peptide. The peptides of the present invention may be used to treat neuropathies in the PNS associated with diabetes mellitus, cancer treatment such as cytostatica, hearing impairment and/or visual handicap, alcohol-induced
                                                                                                                                                         05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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                                                                                                                                  23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                               25-FEB-1999;
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                                                                                                                                                                                                                                               EP1033405-A2
                                                                                                                                                                                                                                                                      Zea mays subsp. mays
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                                                                                                                                                                                                                                                                                                                                                                                                        AAG22631 standard; Protein;
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99US-0126264

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99US-0128234

99US-0128714

99US-0128077

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RESULT
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25-OCT-1999;
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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
The present sequence represents a Staphylococcus aureus protein, that,
                 Claim 6; Page 270; 989pp; English.
                                                                          WPI; 1997-424969/39.
N-PSDB; AAT83748.
                                                                                                                                                                                                                             /note=
Misc-difference 18
                                                                                                                                                                                                                                                                                                              Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                              Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 to isolate antimicrobial compounds, and in vaccines against S
                                                                                                               Black
                                                                                                                                                                                                           WO9730070-A1.
                                                                                                                                                                                                                                                                                   Staphylococcus aureus
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                                     aureus infection
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                                                                                                                                                                     19-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                   Amino
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                                                                                                                                                                                                                                                                                                                                                                                         AAW27779;
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29-OCT-1999;
                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                       COXIC
                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                                                                                  acid sequence of pseudouridylate synthase
                                                                                                                                                                                                                                                                                                      shock syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                               Burnham MK,
                                                                                                      Reichard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0161405
99US-0161359
99US-0161350
99US-0161360
99US-0161361
99US-0161920
99US-0161992
99US-0161993
99US-0162142
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                                                                                                                                                    96US-0011888
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99US-0160770
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99US-0161404.
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99US-0160815
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                                                                                                                                                                                                                                               "not specified"
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                                                                                                    Hodgson JE, Kr
Rosenberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 3; ; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                    Knowles DJC,
, Ward JM;
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RESULT 5
AAG22630
ID AAG22630 standard; Protein; 121 AA.
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Best Local S
Matches 4
                                     30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   based on homology with an Escherichia coli protein, is believed to be pseudouridylate synthase I (pseudouridine synthase I, uracil hydrolyase. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, short staphylococcal food poisoning, scaled skin syndrome, and toxic
 11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                  23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                               28-APR-1999
                                                                                                                                             23-APR-1999
                                                                                                                                                        21-APR-1999,
23-APR-1999,
                                                                                                                                                                                                           08-APR-1999,
                                                                                                                                                                                                                       06-APR-1999;
                                                                                                                                                                                                                                                                                   05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                              25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                      25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays subsp. mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                       termination sequence; corn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays protein fragment SEQ
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                                                                                                                                                                                 19-APR-1999;
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nes 4; Conserv
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99US-0130891

99US-0131449

99US-0132048

99US-0132407

99US-0132484

99US-0132486

99US-0132487

99US-0132487

99US-0132487

99US-0134218

99US-0134218
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99US-0130077.
99US-0130449.
99US-0130510.
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99US-0128234
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99US-0126264
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99US-0123548.
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| 200000000000000000000000000000000000000 | | 900S-0139454 990S-0139454 990S-0139455 990S-0139457 990S-0139459 990S-0139460 990S-0139460 990S-0139463 990S-0139463 990S-0139763 990S-0139763 990S-0139763 990S-0139763 990S-014083 990S-014083 990S-014083 990S-014083 990S-014083 990S-014083 990S-014083 990S-014083 990S-014083 990S-014083 990S-014083 990S-014083 990S-014083 990S-014083 | |
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| 9US-015958 9US-015074 9US-016076 9US-016077 9US-016077 9US-016081 9US-016088 9US-016098 9US-016098 | 905-015513 905-015548 905-015565 905-015659 905-015659 905-015775 905-015786 905-015823 905-015823 905-015923 905-015923 905-015923 | 99US-0148684 99US-0149176 99US-0149723 99US-0149723 99US-0149723 99US-0149930 99US-0150566 99US-0150566 99US-0151065 99US-0151065 99US-0151080 99US-0151303 99US-01514383 99US-01514383 99US-01514383 99US-0153758 99US-0153758 | 9US-014591 9US-014591 9US-014591 9US-014638 9US-014638 9US-014638 9US-014730 9US-014720 9US-014770 9US-014771 9US-014771 9US-014771 |
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RESULT
AAW20262
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25-OCT-1999
26-OCT-1999
26-OCT-1999
26-OCT-1999
28-OCT-1999
28-OCT-1999
28-OCT-1999
29-OCT-1999
                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori
                           WPI; 1997-052306/05.
N-PSDB; AAT67760.
                                                                                      01-APR-1996;
07-JUN-1995;
                                                    Berglindh OT,
                                                                                                               06-JUN-1996;
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                                                                                                                                                 WO9640893-A1
                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                                            Key
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAW20262;
                                                                    (ASTR ) ASTRA
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                                                                                                                                                                                                                                                                                                                                           pylori
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                     AB.
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990S-0161359
990S-0161350
990S-0161360
990S-0161361
990S-0161920
990S-0161992
990S-0161993
990S-0162142
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157
                                                    Smith
                                                                                     96US-0630405
95US-0487032
                                                                                                               96WO-US09122
                                                                                                                                                                                   /note=
158
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                                                                                                                                                                                                                             'label= unknown
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                                                    Mellgaerd BL;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is a H. pylori secreted or periplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                      /note= "encoded by RAA" Misc-difference 142
                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise;
Smith DH;
                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                           /note=
Misc-difference 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW24622 standard; Protein; 185 AA
                         (ASTR ) ASTRA AB
                                                    17-NOV-1995;
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                                                                                                                                  WO9719098-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection, and to detect Helicobacter
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                                                    95US-0561469
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157
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100.0%; Pr
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0; Mismatches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               also useful for generating vaccines for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in a sample. Annisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pMPX vectors to construct a series of shotgun subclone libraries. The purified DNA samples were then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is a H. pylori secreted or periplasmic protein. Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are
WPI; 1991-021675/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori nucleic acid sequences used for diagnostics and therapeutics
                           Bryan PN,
                                                                                                14-DEC-1987;
                                                                                                                             14-DEC-1987;
                                                                                                                                                                                    US4980288-A
                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                       Mutant; subtilisin; detergent; serine
                                                                                                                                                                                                                                                                                                    Mutant subtilisin polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                  12-FEB-1986;
                                                                                                                                                         25-DEC-1990
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                                                    (GENE-) GENEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The ORF/protcin reference number for this sequence was obtained the related specification, WO9640893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Page 153; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143
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                           Rollence MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                       CORP.
                                                                                 87US-0143949
86US-0828545
                                                                                                                             87US-0143949
                                                                                                                                                                                                                               Location/Qualifiers 218..218
                                                                                                                                                                                                                 /label~ S, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.5%;
                         Pantoliano MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                         protease
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). 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and related proteins
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X444X4X0000000000XX
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Best Local S
Matches 4
the proteins are collectively known as colon cancer antigens. The color cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the specification (Ser/Asp-Asn218).

The mutant subtilisin does not lose activity as rapidly when stored in soln. with detergents or when subjected to high heat during use in cleaning. It is used for the removal of proteinaceous stains or fabric. Other stabilising mutants may be introduced into the fabric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NB: to construct sequences AAR10204-13, the B. subtilis wild-type sequence was retrieved from the GENESEQ database (AAP90095; J0113 and amino acid residues altered according to the mutations described and amino acid residues altered according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutations described according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to the mutation according to 
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03-NOV-1999;
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                                                                                                                                                                                                                 Claim 11; Page 7294-7295; 9803pp; English.
                                                                                                                                                                                                                                                                    Nucleic acids encoding 4277 human useful for preventing, diagnosing
                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detergent compsns
                                                                                                                             cancer-associated nucleic acid molecules (N) and proteins (P),
                                                                                                                                                            AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2000; 2000WO-US26524
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                                                                                                                                                                                                                                                                                                                                                                              2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 37.5%; Si Similarity 100.0%; | 4; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                     AAH34418
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0157137.
99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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by muta-genesis of subtilisin gene used in liq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteases
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b; Pred. No. 1.2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                 colon cancer-associated polypeptides,
and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; L
D. 1.2e+03;
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described
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                                                                                                 The colon
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RESULT
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Best Local
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N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
                                                          AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AATThe prostate cancer antigens can have neuroprotective, cytostatic,
                                                                                                                                                                        Prostate cancer associated gene sequences, referred to cancer antigens, useful for treatment, prevention, and
                                                                                                                           Claim 11; Page 1743-1744; 2338pp; English.
                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                                                12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate cancer antigen
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                                                                                                                                                                                                                                                                                                                   ( HUMA - )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infectious
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ROSEN C A.
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                                                                                                                                                         such as prostate cancer
                                                                                                                                                                                                                                                                    Ruben SM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑA;
                                                                                                                                                                                                                                                                                                                                                99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein sequence SEQ ID NO:1322.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Le
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                          as prostate
diagnosis o
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                                                                               to AAB57302
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RESULT 1
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Best Local
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                                                                                         This sequence is derived from the nucleotide sequence encoding the light chain variable region. The "x" residues represent nonsense codons. The coding sequence has been translated in all 3 reading frames (see also AAR12130 and AAR12131). The L'V region is duplicated in so-called "aberrant" light chains (see AAQ11878), conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAP16506 to AAF16514 to
                                                                                                                                                                                                                                                                                                                             Oligomeric immunoglobulin(s) with high avidity for antigen(s) formed by duplicating esp. variable region of light chain of :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders, wounds, and injectious uiseases. Amazone of the present AAB57303 represent sequences used in the exemplification of the present
Sequence
                                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ11879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shuford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR12129 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                 See also AAQ11880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-may-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                                            increased avidity on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .mmunoglobulin G; light chain; variable region; duplication;
vassive immunity; group B streptococci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 ayxg 266
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||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                   1991-163947/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WW,
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  401
                                                                                                                                                                                                                                                      Fig 17; 104pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284
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  AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-0432700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90WO-US06426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĽJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.5%;
100.0%;
                                                                            antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raff
                                                                                                                                                                                                                                                      English.
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Pred. No.
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                                                                            comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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5. 1.2e+03;
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                                                           The present sequence represents a consensus sequence of glial cell-line derived neurotrophic factor receptor (GDNFR) protein and GDNFR-related (GRR) proteins GRR and GRR3. The proteins have similar functions. GDNFR proteins are functionally characterised by the ability to bind glial cell line-derived neurotrophic factor (GDNF) and/or neurturin specifically, and to act as part of a molecular complex which mediates or enhances the signal transduction affects of GDNF and/or neurturin. The proteins can be used for treating improperly functioning dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic lateral sclerosis. They can also be used for treating neurological disorders associated with diabetes, glaucoma or other diseases and conditions involving retinal ganglion cell degeneration of sensory neuropathy caused by injury to, insults to, or degeneration of sensory neurons, pathological conditions, or disease or injury-related neuropathy caused by a conditions or disease or injury-related neuropathy caused for description derived for description of the conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNFR; glial cell line-derived neurotrophic factor; GDNF; neurturn; signal transduction; dopaminorgic nerve cell; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; neurological disorder; diabetes; glaucoma; sensory neuron; retinal ganglion cell degeneration; sensory neuropathy;
Sequence
                                                                                                                                                                                                                                                                                                                                     Claim 51; Fig 26; 318pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         used to develop products for treating e.g. improperly functioning dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated glial cell line-derived neurotrophic factor receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPT; 1999-080806/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glial cell-line derived neurotrophic factor receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus sequence of GDNFR and GRR2 and GRR3 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW84298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW84298 standard; Protein; 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            retinopathy; gene therapy; GDNFR-related protein; GRR2; GRR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                          amyotrophic lateral sclerosis
                                 nopathies. The products can also be screening and gene therapy.
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489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97us-0866354
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1..489
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                                                  used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                The present sequence represents a consensus sequence of rat and human glial cell-line derived neurotrophic factor receptor (GDNFR) protein and GDNFR-related (GRR) proteins. The proteins have similar functions. GDNFR proteins are functionally characterised by the ability to bind glial cell line-derived neurotrophic factor (GDNF) and/or neurturin specifically, and to act as part of a molecular complex which mediates or enhances the signal transduction affects of GDNF and/or neurturin. The proteins can be used for treating improperly functioning dopaminergic nerve cells, parkinson's disease, Alzheimer's disease or amyotrophic lateral sclerosis. They can also be used for treating neurological disorders associated with diabetes, glaucoma or other diseases and conditions involving retinal ganglion cell degeneration, as the processis of the conditions of the conditions of the conditions of the conditions involving retinal ganglion cell degeneration, as the conditions of the conditions involving retinal ganglion cell degeneration.
                                                                                                                                                                                                                                                                                                                                                             New isolated glial cell line-derived neurotrophic factor receptors used to develop products for treating e.g. improperly functioning dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDNFR; glial cell line-derived neurotrophic factor; GDNF; neurturin; signal transduction; dopaminergic nerve cell; Parkinson's disease; Alzheimer's disease; amyotrophic lateral neurological disorder; diabetes; glaucoma; sensory neuron; retinal ganglion cell degeneration; sensory neuropathy;
 retinopathies. The drug screening and
                                  *sensory neuropathy caused by injury to, insults to, or degeneration of sensory neurons, pathological conditions, or disease or injury-related
                                                                                                                                                                                                                                                                                                           Claim 51; Fig 19; 318pp; English.
                                                                                                                                                                                                                                                                                                                                               or amyotrophic lateral sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-080806/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fox GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           retinopathy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus sequence of rat and human GDNFR and GRR proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S, Wen
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products can also be used gene therapy.
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100.0%; Pro
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Pred. No.
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                    for detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 489;
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Best Local Similarity
""" 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilication of the activities with a second and transcript of the activities.
utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                  Zhao
                                                                                                                                                                                                                                                                                                           Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                           Example
                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2000; 2000WO-US34263
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                                                                                                                                                                                                                  Novel
                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                                                                                    (HYSE-)
                                                                                                                                                                                                                                                                                                                                                               29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leukaemia
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QA,
                                                                                                                                                                                                                                                        2001-442253/47.
                                                                                                                                                                                                    nucleic acids and as central nervous
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                                                                                                                                                                                                                                                                                                                                    HYSEQ INC.
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                                                                                                                                                                                                                                                                               Liu C,
Wang 2,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
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                                                                                                                                                                          SEQ ID NO 5689; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                              2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                               Asundi V, Ch
Wehrman T, X
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 5689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%;
                                                                                                                                                                                                    polypeptides, useful for treating disorders
system injuries -
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Pred. No.
                                                                                                                                                                                                                                                                                             Chen R,
Xu C,
                                                                                                                                                                                                                                                                                  hen R, Ma Y, Xu C, Xue AJ, Drmanac RT;
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b. 1.8e+03;
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                                                                                                                                                                                                                                                                                             Qian XB,
Yang Y,
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Zhang J;
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RESULT 15
AAY38787
ID AAY387
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18-NOV-1997;
27-NOV-1997;
10-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        assays for receptor activity, arthritis and inflammation, leukaen C.N.S disorders. Note: The sequence data for this patent did not form part of the
                             their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY38787 standard; Protein; 513
Sequence
                                                                                                                    Claim 4; Page 331; 524pp; English.
                                                                                                                                         Proteins from Neisseria meningitidis and N. gono diagnosis, treatment and prevention of infection
                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                       WPI; 1999-327407/27
                                                                                                                                                                                                           Grandi G,
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06-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification.
                                                                                                                                                                                                                                (CHIR-) CHIRON
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                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis.
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                                                                         N. gonorrhoeae antigenic proteins. They are encoded by open ding frames (ORFs) AAZ11972-Z12358. The antigenic proteins,
                                                                                                 acid sequences AAY38499-Y38944 represent Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
  Neisseria infection; meningitis; septicaemia; gonorrh
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 513
                   as hybridisation probes and antisense reagents.
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97GB-0023516.
97GB-0024190.
97GB-0024386.
97GB-0025158.
97GB-0026147.
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Conservative

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Score 3; 1 Pred. No.

DB 20; Lo

Length 513;

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Mismatches

Indels

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RESULT 16
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470 ayxg 473
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e 51..51
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e 48..48
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/labelov, E
/notec="Wild-Type i
e 15..15
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/noteo"Wild-Type i
e 25..25
/labelon, K
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34..34
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22...22
/label-S, C, Y
/note="Wild-Type is Y"
60..60
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24...24
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21.21
/labelsP, S, T
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/note="Wild-Type
18..18
                                       /note-"Wild-Type
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                    /labelca, V, D
/notec.Wild-Type is
57..57
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/note="Wild-Type
Misc-difference 134..134
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/note="Wild-Type
Misc-difference 129.129
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/note="Wild-Type
Misc-difference 126..126
/1-1:
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/note="WT
Misc-difference 255..255
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/note="Wild-Type
Misc-difference 67.67"
/label=D, E
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Misc-difference 264..264
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/note="Wild-Type i
e 61..61
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e 331..331
                   /note="WT 336..336
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/note="WT
: 335..335
/label=C,
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277..277
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/note="WT
265..265
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261..261
/label=S,
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257..257
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    /note="W
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                                                       Introducing random point mutations into nucleic acids - by prepn of single stranded template, annealing a primer, misincorporation, completion of molecules and screening.
                                                                                WPI;
                                                                                                                    03-APR-1987;
                                                                                                                                             05-MAY-1988
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46 ayxg
            5 ayxg 8
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/note="WT
419..419
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343.343
/label=A,
/note="WT
347..347
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RESULT

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/label= D147X
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95
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102
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136
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                                                 /label= S146X
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                                                                                                /label= H140X
/note= "X= Ala,
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/note= "X= Gly,
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/note= "X= Pro,
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/note= "X= Ala,
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197
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198
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170
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/note "X Gly,
151
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199
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!52
                                                                                                'note⇒ "X= unspecified amino acid"
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Best Local
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21-APR-1995;
17-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of cyclo:malto:dextrin glucanotransferase (CGTase) - have altered substrate binding, useful for prodn. of cyclodextrin(s) or linear oligosaccharide(s), opt. formed in situ in e.g. baked
                                                                                                                           Cyclomaltodextrin glucanotransferase; CGTase; enzyme; Bacillus circulans; thermoanaerobacter; starch; cyclomaltodextrin; cyclodextrin; pesticide; transglycosylation; cyclic glucose oligomer; glucose oligosaccharide; cholesterol removal; food stabiliser; vitamin stabiliser; fungicide;
                    Modified-site
                                                                        Synthetic
                                                                                                          plastic laminate; biodegradable plastic; mutein.
                                                                                                                                                                                                                      Bacillus CGTase variant beta-cyclodextrin #3
                                                                                                                                                                                                                                                          30-JUN-1997
                                                                                                                                                                                                                                                                                               AAW17577;
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95DK-0000477.
95DK-0001173.
Location/Qualifiers
21
/label= F21Y
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Pred. No.
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87
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182
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147
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/label= D147X
 /label= T185X
/note= "X= Pro,
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146
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/note= "X= Gly,
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/note= "X= Gly, Ala"
                              note= "X= Trp,
                                        /label= F183X
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/note= "X= Asn,
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                                                           note= "X= Ser,
                                                                   'label= G180x
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'note= "X= Ala,
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= "X= Ser,
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= "X= Gly,
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= "X= Ala,
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"X= Pro,
                                                                                                                                     "X= Ala,
                                                                                                                                                                                                                                                                                                            "insertion of Pro,
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in, or
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  His, Arg, Glu,
                              TYĽ,
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absent"
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   AAW17568-W17579, and AAW17592-W17605 represent mutant versions of the cyclomaltodextrin glucanotransferase (CGTase) of Bacillus circulans strain 251 (see AAW06773 for wild type sequence). CGTase catalyses the conversion of starch and similar substrates into cyclomaltodextrins (also known as cyclodextrins) via an intramolecular transglycosylation reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a hydrophobic internal cavity that form inclusion complexes with many small hydrophobic molecules. These CGTase mutants have a modified substrate binding and/or product selectivity, compared to this sequence. The mutants are created using primer mutagenesis to modify the gene
                                                                                                                                      or linear
                                                                                                         Claim 40;
                                                                                                                                   New variants of cyclo:malto:dextrin glucanotransferase (CGTase) - have altered substrate binding, useful for prodn. of cyclodextrin(s) or linear oligosaccharide(s), opt. formed in situ in e.g. baked
                                                                                                                                                                           WPI; 1996-485774/48
                                                                                                                                                                                             Andersen C,
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21-APR-1995;
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                                                                                                                                                                                            Dijkhuizen L,
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95DK-0000477
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602
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372
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/label=
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377
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266
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373
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/note= "X= Gln,
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/note= "X= Ala,
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/note= "X= Leu,
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'note= "X= Ala,
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"X= Gly,
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AAW17573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              These mutant sequences are used to manufacture the 6 main CD types (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides, optionally in situ, e.g. during production of baked goods, to stabilise chemicals during their manufacture and in detergents. CD are known for their usefulness in foods, e.g. as a bread-improving agent, to encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals, pesticides or fungicides, to bind/remove lipophilic compounds such as cholesterol (e.g. in egg yolk or butter), in plastic laminates, films otc. and to make biodegradable plastics.
                                                                                                                                                                                                                                                                                                         thermoanaerobacter; starch; cyclomaltodextrin; cyclodextrin; pesticide; transglycosylation; cyclic glucose oligomer; glucose oligosaccharide; cholesterol removal; food stabiliser; vitamin stabiliser; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding this sequence. These sequences have greater product selectivity and/or reduced product inhibition (better yields) than wild-type CGTase.
                                                                                                                                                                                                                                                               Key
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                                                                                                                                                                                                                                                                                                 plastic laminate; biodegradable plastic; mutein.
                                                                                                                                                                                                                                                                                                                                    Cyclomaltodextrin glucanotransferase; CGTase; enzyme; Bacillus circulans;
                                                                                                                                                                                                                                                                                                                                                    Bacillus CGTase variant beta-cyclodextrin #2
                                                                                                                                                                                                                                                                                                                                                                       30-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                         AAW17573 standard;
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Local Similarity
Local Similarity
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                                                                                                              /label- S90x
/note- "x- Gly,
91
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/noten
                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                   /label~ R47X
/note~ "X~ Ala,
                                                                                            /label- G91X
/note- "X- Ala,
                                                                                                                                                /note: "X= Asp,
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                                                           label⇔ V92G
                                                                                                                                                                                                                                                                                                                                                                                                         protein; 688 AA.
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                                .⊸ N93X
, "X∽ Gly,
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Pred. No.
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       Arg,
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                                  or absent"
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         ser,
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        or absent"
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/note= "X= Ala,
146
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147
/note=
266
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136
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197
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182
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170
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151
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/note= "X= Pro, Ala, Phe,
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148
                                                           /note=
                                                                                                       199
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187
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/note= "X= Gly,
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/note= "X= Ala,
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                                                                                                              'note= "X= Ala,
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                                - н233х
"X- Gln,
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Thr, or
                                                           "X= Gln,
                                                                                     "X= Asp,
                                                                                                                                                                                                            "X= Pro,
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        Trp, Ala"
                                 Asn,
                                                                                                                                      Ile,
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                                  Ile"
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absent"
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Query Match
Best Local S
                                          Matches
                                                                                                                                               chemicals during their manufacture and in detergents. CD are known for their usefulness in foods, e.g. as a broad-improving agent, to encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals, pesticides or fungicides, to bind/remove lipophilic compounds such as cholesterol (e.g. in egg yolk or butter), in plastic laminates, films
                                                                                                                                                                                                                     The mutants are created using primer mutagenesis to modify the gene encoding this sequence. These sequences have greater product selectivity and/or reduced product inhibition (better yields) than wild-type CGTase. These mutant sequences are used to manufacture the 6 main CD types (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides, optionally in situ, e.g. during production of baked goods, to stabilise
                                                                                                                                                                                                                                                                                                                                                        AAW17568-W17579, and AAW17592-W17605 represent mutant versions of the cyclomaltodextrin glucanotransferase (CGTase) of Bacillus circulans strain 251 (see AAW06773 for wild type sequence). CGTase catalyses the conversion of starch and similar substrates into cyclomaltodextrins (also known as cyclodextrins) via an intranolecular transglycosylation
                                                                                                                                                                                                                                                                                                      reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a hydrophobic internal cavity that form inclusion complexes with many small hydrophobic molecules. These CGTase mutants have a modified substrate binding and/or product selectivity, compared to this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New variants of cyclo:malto:dextrin glucanotransferase (CGTase) - have altered substrate binding, useful for prodn. of cyclodextrin(s) or linear oligosaccharide(s), opt. formed in situ in e.g. baked
                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 34; Page -; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-NOV-1995;
21-APR-1995;
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95DK-0000477.
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. "X= Ala,
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5. 2.2e+03;
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               Modified-site
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                                                     Misc-difference
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147
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89
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87
                                                                                                                                                                                                                                                                                                                                                                       /label=
47
               /note=
149
                                                                                                                                                                                                                         /note= "possible insertion of Ala, Val, Gly, Phe, or Tyr" 93
                                                                                                                                                                                                                                         92
                                      /note= "insertion 148
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                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                             /label= H98X
/note= "X= Gly,
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
/note= "X= Ala, Asp,
       /label= D147X
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235
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267
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195
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373
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/note- "x- Gly,
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"X- unspecified
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                                                                            Asp,
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                                                                                                                                                                                                                                                                                                 Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lys,
                                                                             Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or Thr"
                                                                             Asn,
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16-NOV-1995;
21-APR-1995;
17-OCT-1995;
                                These mutant sequences are used to manufacture the 6 main CD types (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides, optionally in situ, e.g. during production of baked goods, to stabilise chemicals during their manufacture and in detergents. CD are known for their usefulness in foods, e.g. as a bread-improving agent, to encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals, pesticides or fungicides, to bind/remove lipophilic compounds such as cholesterol (e.g. in egg yolk or butter), in plastic laminates, films etc. and to make biodegradable plastics.
                                                                                                                                                                                                                        (also known as cyclodextrins) via an intramolecular transglycosylation reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a hydrophobic internal cavity that form inclusion complexes with many small hydrophobic molecules. These CGTase mutants have a modified substrate binding and/or product selectivity, compared to this sequence. The mutants are created using primer mutagenesis to modify the gene encoding this sequence. These sequences have greater product selectivity and/or reduced product inhibition (better yields) than wild-type CGTase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New variants of cyclo:malto:dextrin glucanotransferase (CGTase) - have altered substrate binding, useful for prodn. of cyclodextrin(s) or linear oligosaccharide(s), opt. formed in situ in e.g. baked
                                                                                                                                                                                                                                                                                                                                                                                             strain 251 (see AAW06773 for wild type sequence). CGTase catalyses the conversion of starch and similar substrates into cyclomaltodextrins
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW17568-W17579, and AAW17592-W17605 represent mutant versions of the cyclomaltodextrin glucanotransferase (CGTase) of Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1996;
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               goods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andersen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Page -; 161pp; English
689 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dijkhuizen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95DK-0001281.
95DK-0000477.
95DK-0001173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dijkstra BW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Der Osten
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5 ауху 8 Query Match Best Local S Matches 4

Local Similarity

Conservative

37.5%; 50 100.0%; Pr

Score 3; DB 1; Pred. No. 2.2 0; Mismatches

DB 17; L
). 2.2e+03;

Length 689; Indels

0;

Gaps

0;

Вр

97 ayxg 100

RESULT AAW17574 standard; protein; 689 AA 21

Bacillus CGTase variant gamma-cyclodextrin #2

30-JUN-1997 AAW17574;

(first

Cyclomaltodextrin glucanotransferase; CGTase; enzyme; Bacillus circulans; thermoanaerobacter; starch; cyclomaltodextrin; cyclodextrin; pasticide; transglycosylation; cyclic glucose oligomer; glucose oligosaccharide; cholesterol removal; food stabiliser; vitamin stabiliser; fungicide; plastic laminate; biodegradable plastic; mutein.

FTTTTTTXX

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Modified-site
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149
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147
  /label= N178Y
182
                                      /note=
171
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87
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                                                                      /label= S150A
/note= "X= Asn,
                                                                                                                                                                    /label= D147x
/note= "X= Ala,
                                                                                                                                                                                                                                                                                                                                                                                         /label= N93X
/note= "X= Gly,
                             'label= T168S
                                                     'label= Y167X
                                                                                                           /label= P149X
                                                                                                                          note= "X= Asn,
                                                                                                                                   /label= Q148X
                                                                                                                                                                                              /label= S146X
/note= "X= Pro,
                                                                                                                                                                                                                                                                   /label= H140x
/note= "x= Ala,
                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                  /label= N94X
/note= "X= Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= N88X
/note= "X= Pro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= R47X
/note= "X= Ala,
                                                                                                 'note=
                                                                                                                                                    'note= "insertion of
                                                                                                                                                                                                                        'note= "insertion of Pro,
                                                                                                                                                                                                                                                   'label= S145X
                                                                                                                                                                                                                                                                                             'label= D135L
                                                                                                                                                                                                                                                                                                              'note= "X= Gly,
                                                                                                                                                                                                                                                                                                                         /label= W101X
                                                                                                                                                                                                                                                                                                                                        'label= H98X
'note= "X= Gly,
                                                                                                                                                                                                                                                                                                                                                                                                                     /label= V92G
                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "possible insertion of Ala, Val, Gly, Phe, or Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= G91X
note= "X= Ala, Val,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= S90X
'note= "X= Gly, Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Y89X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "X= Asp,
                                                                                                 "X= Phe,
                                                                                                                                                                                                                                         "X= Ala, Glu,
                                            "X= Ala,
                                                                                                                                                                    Asp,
                                                                                                                                                                                              Ala,
                                              Phe,
                                                                                                 Leu,
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                                                                                                                                                                                                                                                                                                                                        Ala"
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                                                                        Ala,
                                                                                                                          Asp,
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  4444444444444444
                                                                                       16-NOV-1995;
21-APR-1995;
17-OCT-1995;
New variants of cyclo:malto:dextrin glucanotransferase (CGTase) - have altered substrate binding, useful for prodn. of cyclodextrin(s) or linear oligosaccharide(s), opt. formed in situ in e.g. baked
                                    WPI; 1996-485774/48.
                                                    Andersen C,
                                                                                                                          22-APR-1996;
                                                                                                                                            24-OCT-1996.
                                                                                                                                                            W09633267-AL
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                                                                                      95DK-0001281.
95DK-0000477.
95DK-0001173.
                                                                                                                          96WO-DK00179
                                                                                                                                                                                                                                                                                                                                       /label= F259X
/note= "X= Phe,
267
                                                                                                                                                                                                                                                                                                                                                                                                                   /label= L197x
/note= "X= Asp,
235
                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= D196X
/note= "X= Ala,
200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= F183X
/note= "X= Trp,
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= G179X
/note= "X= Ser,
183
                                                                                                                                                                                                                        /note=
378
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198
                                                                                                                                                                                                      /label= R375X
/note= "X= Ala,
                                                                                                                                                                                     'label = L600X
                                                                                                                                                                                                                                         'label= D373X
                                                                                                                                                                                                                                                        'label= D371X
'note= "X= Val,
                                                                                                                                                                                                                                                                                                   'label= N326X
'note= "X= Gln,
                                                                                                                                                                                                                                                                                                                               /label= E264Q
                                                                                                                                                                                                                                                                                                                                                                        /label= H233X
/note= "X= Gln,
                                                                                                                                                                                                                                                                                                                                                                                                   /label= K232X
/note= "X= Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "X= Leu,
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= N193X
'note= "X= Gly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "X= Pro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= G180X
/note= "X= Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= L195x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= T185X
                                                                                                                                                                                                                                                                                    label= T370N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= K192R
                                                                                                                                                                            "X= unspecified amino acid"
                                                                                                                                                                                                                                "X= Asp,
                                                     Dijkstra BW,
                                                                                                                                                                                                                               Glu,
                                                                                                                                                                                                                                                                                                                                              Trp,
                                                                                                                                                                                                      Pro,
                                                                                                                                                                                                                                                         Leu,
                                                                                                                                                                                                                                                                                                                                                                                                    Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                             Glu"
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                                                                                                                                                                                                                                                                                                                                                Ala"
                                                                                                                                                                                                                                                                                                                                                                          Ile"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trp,
                                                                                                                                                                                                                                                          Ile,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arg, Glu, Asp"
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                                                     Von
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RESULT :
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     small hydrophobic molecules. These CGTase mutants have a modified substrate binding and/or product selectivity, compared to this sequence. The mutants are created using primer mutagenesis to modify the gene encoding this sequence. These sequences have greater product selectivity and/or reduced product inhibition (better yields) than wild-type CGTase. These mutant sequences are used to manufacture the 6 main CD types (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides, optionally in situ, e.g. during production of baked goods, to stabilise chemicals during their manufacture and in detergents. CD are known for their usefulness in foods, e.g. as a bread-improving agent, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW17568-W17579, and AAW17592-W17605 represent mutant versions of the cyclomaltodextrin glucanotransferase (CGTase) of Bacillus circulans strain 251 (see AAW06773 for wild type sequence). CGTase catalyses the conversion of starch and similar substrates into cyclomaltodextrins (also known as cyclodextrins) via an intramolecular transglycosylation reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a hydrophobic internal cavity that form inclusion complexes with many
                                                                                                                                                                                               thermoanaerobactor; starch; cyclomaltodextrin; cyclodextrin; pesticide; transglycosylation; cyclic glucose oligomer; glucose oligosaccharide; cholesterol removal; food stabiliser; vitamin stabiliser; fungicide; plastic laminate; biodegradable plastic; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encapsulate/stubilise/solubilise vitamins, dyes, pharmaceuticals, posticides or fungicides, to bind/remove lipophilic compounds such as cholesterol (e.g. in egg yolk or butter), in plastic laminates, films etc. and to make biodegradable plastics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 34;
                                                                                                                                                                                                                                        Cyclomaltodextrin glucanotransferase; CGTase; enzyme; Bacillus circulans;
                                                                                                                                                                                                                                                                                                                      AAW17578 standard; protein; 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                   Modified-site
                                                                                                                              Modified-site
                                                                                                                                                                                                                                                           Bacillus CGTase variant gamma-cyclodextrin #3
                                                                                                                                                                                                                                                                                30-JUN-1997
                                                 Modified-site
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                                                                                                                                                           Key
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                                                                                                                                                                                                                                                                                (first entry)
                                                                                                /label R47X
/note "X Ala,
87
                                                                                                                                                  Location/Qualifiers
/notes "Xs
         'label- S90X
                            note- "x- Gly,
                                       /label~
                                                         /label- N88X
/note- "X- Asn,
                                                                                                                                      'label
                                                                                      label
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                                                                                                                                                                                                                                                                                                                                                                                                                       37.5%;
                                       x68X
                                                                                       187H
                                                                                                                                        F21Y
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Pred. No.
                                                                                                          Gln,
                             Ala,
                                                         Lys,
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                             Tyr,
                                                           His"
                                                                                                          His,
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                              Pro
                             or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 689
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92
                   200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "X= Ala, Glu, 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "X= Ala,
146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                           /note=
196
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188
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171
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150
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/note= "X= Ser,
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/note= "X= Phe,
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/label= L197X
/note= "X= Asp, Glu"
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                                                                                                                              /label= T185X
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(also known as cyclodextrins) via an intramolecular transplycosylation creaction. Cyclodextrins (CD) are cyclic glucose oligomers with a hydrophobic internal cavity that form inclusion complexes with many small hydrophobic molecules. These CGTase mutants have a modified substrate binding and/or product selectivity, compared to this sequence. The mutants are created using primer mutagenesis to modify the gene encoding this sequence. These sequences have greater product selectivity and/or reduced product inhibition (better yields) than wild-type CGTase. These mutant sequences are used to manufacture the 6 main CD types (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides, optionally in situ, e.g. during production of baked goods, to stabilise chemicals during their manufacture and in detergents. CD are known for their usefulness in foods, e.g. as a bread-improving agent, to encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals, pesticides or fungicides, to bind/remove lipophilic compounds such as cholesterol (e.g. in egg yolk or butter), in plastic laminates, films cetc. and to make biodegradable plastics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-1995;
21-APR-1995;
17-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of cyclo:malto:dextrin glucanotransferase (CGTase) - have altered substrate binding, useful for prodn. of cyclodextrin(s) or linear oligosaccharide(s), opt. formed in situ in e.g. baked
                                                                                                                                                                                                                                                                                                                                                                                                                            AAW17568-W17579, and AAW17592-W17605 represent mutant versions of the cyclomaltodextrin glucanotransferase (CGTase) of Bacillus circulans strain 251 (see AAW06773 for wild type sequence). CGTase catalyses the conversion of starch and similar substrates into cyclomaltodextrins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 40; Page -; 161pp; English
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_ X= Asp,
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"X= Gln,
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Best Local :
       painkiller
                       Generic enkephalin-like analgesic peptide
                                                                        AAP10370 standard; peptide; 4 AA
                                                                                                                                                                                                       Peptides SP3, SP4 and SP5 have Averence prepd. easily and in high yield. prophylaxis of hypertension.
                                        16-DEC-1992
                                                        AAP10370;
                                                                                                                                                                                                                                                                                                                                                                                                                                           07-DEC-1994
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                         Claim 1; Page 2; 5pp; Japanese
                                                                                                                                                                                                                                                       New tri-, tetra- and penta:peptide(s), e.g. Trp-Lys-Tyr - are ACE inhibitors useful for treatment or prophylaxis of hypertension
                                                                                                                                                                                                                                                                                 WPI; 1994-115194/14.
                                                                                                                                                                                                                                                                                                                                  19-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                   08-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                 JP06065288-A
                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                Angiotensin converting enzyme; ACE; inhibitor; SP5; SP4; SP3; hypertension; blood pressure.
                                                                                                                                                                                                                                                                                                                                                                                                                           ACE inhibitor
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100.0%; Pr
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b; Pred. No. 4.3
0; Mismatches
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d. They are useful for to
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| RESULT 2 US-08-079-445-3 : Sequence 3, Applicati ; Patent No. 5440016 ; GENERAL INFORMATION: | Query Match Best Local Similar: Matches 2; Cons Qy 1 wk 2 I Db 2 WK 3 | RESULT 1 US-09-461-697-405 Sequence 405, Application US Patent No. 6277974 GENERAL INFORMATION: APPLICANT: COGENT NEUROSCIE APPLICANT: Lo, Donald C. APPLICANT: Thomas, Mary Bet APPLICANT: Portbury, Stwart APPLICANT: Puranam, Kasturi APPLICANT: Puranam, Kasturi APPLICANT: NEATON: COMPOSI APPLICANT: NEATON: COMPOSI APPLICANT: Hard APPLICANT: NEATON: COMPOSI APPLICANT: HARD APPLICANT: NEATON: COMPOSI APPLICANT: HORNION: CELL DE TITLE OF INVENTION: CELL DE TITLE OF INVENTION: CELL DE TITLE OF INVENTION: CELL DE TITLE OF INVENTION: ONDS: 466 CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 1999-1 CURRENT FILING DATE: 1999-1 NUMBER OF SEQ ID NOS: 466 SOFTWARE: FASTSEQ for Windc SEQ ID NO 405 LENGTH: 3 TYPE: PRT ORGANISM: Homo sapiens US-09-461-697-405 | | 28 25 0 31 2 25 0 32 2 25 0 33 2 2 25 0 33 3 4 2 25 0 34 4 2 25 0 36 2 25 0 37 2 25 0 38 2 2 25 0 44 1 2 2 25 0 44 2 2 25 0 44 2 2 25 0 44 3 2 25 0 46 2 2 25 0 47 2 2 25 0 48 3 2 2 25 0 49 2 2 25 0 50 2 2 2 5 0 |
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| lication US/08079445)016 MATION: Blondelle, Sylvie E. Pinilla, Clemencia | 25.0%; Score 2; DB 4; L ity 100.0%; Pred. No. 1.6e+05 servative 0; Mismatches 0 | NCE, Inc. h D. TIONS AND METHODS ATTING CONDITIONS, ATTING 25,09/461,697 2-14 ws Version 4.0 | ALIGNMENTS | 4 2 US-08-488-659A-150 4 2 US-08-488-659A-151 4 2 US-08-488-659A-152 4 2 US-08-488-659A-53 4 2 US-08-671-47A-8 4 2 US-08-671-47A-8 4 2 US-08-651-179B-2 4 2 US-08-651-179B-3 4 3 US-08-651-179B-3 4 3 US-08-912-272-8 4 3 US-08-912-272-8 4 3 US-08-912-272-8 4 3 US-08-912-272-8 4 US-08-91-61-20-25 4 4 US-08-315-861-124 5 US-08-315-861-124 5 US-08-315-861-124 6 US-08-36-25-767-29 7 US-08-682-767-29 7 US-08-682-767-30 7 US-07-657-769B-36 5 1 US-07-630-163B-18 |
| | Length 3; 15; 0; Indels 0; Gaps | FOR DIAGNOSING DISORDERS, OR DISEASES INVOLV | | Sequence 150, App Sequence 151, App Sequence 153, App Sequence 8, Appli Sequence 1, Appli Sequence 2, Appli Sequence 114, App Sequence 114, Appli Sequence 114, Appli Sequence 124, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 26, Appli Sequence 27, Appli Sequence 28, Appli Sequence 29, Appli Sequence 30, Appli Sequence 30, Appli Sequence 30, Appli Sequence 30, Appli Sequence 30, Appli Sequence 30, Appli Sequence 30, Appli Sequence 30, Appli Sequence 30, Appli Sequence 30, Appli Sequence 36, Appli |

APPLICANT: APPLICANT: APPLICANT:

Pinilla, Clemencia Eichler, Jutta Houghten, Richard

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Query Match
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                                                                                                                                                                 Sequence 7, Application US/07840077A Patent No. 5443816
                                                                                                                                                  GENERAL INFORMATION:
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                                                                      APPLICANT: Zamora, Paul O. APPLICANT: Rhodes, Buck A. TITLE OF INVENTION: Pharma-
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LENGTH: 4 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
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N: 514
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                                                                        Pharmaceutical Preparation and
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HEMOLYTIC, ANTI-MELITTIN OR ANTI-ENZYMATIC ACTIVITY
                                                                                       Peptide-Metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=
/note= "
                                                                                                                                                                                                                                                                                                                                                                                                      /note= "C-terminal amino acid is amidated" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Xaa
/note= "Xaa=any amino acid"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08176938 Patent No. 5602099
APPLICATION NUMBER: US/08/176,938
FILING DATE: 04-JAN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sterner Ph.D., Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Schill
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                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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ZIP: 87109-5802
COMPUTER READABLE FORM:
                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Deborah A. Peacock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8
FILING DATE: 03-JAN-1992
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MEDIUM TYPE: Storage
MEDIUM TYPE: Storage
MEDIUM TYPE: IBM PC/XT/AT, IBM PS/2 or
ner-pos
                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 10036-2787
                                                                                                                                                                                                                                                           STATE:
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SYSTEM: PC-DOS/MS-DOS
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WordPerfect 6.0a for Windows
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                                                                                                              US/08/176,938
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                   1103326-080
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                                                                                                                                             Version #1.25
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Best Local Similarity 100.
Conservative
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Patent No. 5624894
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     ZIP: 22313-140.

COMPUTER READABLE FLOPPY disk

MEDIUM TYPE: Floppy disk

COMPUTER: IRM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

CONTROL APPLICATION UNMBER: US/08/428,488
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INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
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                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 27-APPLICATION: 51/
                                                                           TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                            NAME: Baumeister, Mary Katherine REGISTRATION NUMBER: 26,254 REFERENCE/DOCKET NUMBER: 028724-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Alexandria
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TYPE: amino acid
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 OTHER INFORMATION:
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                NAME/KEY: Modified-site
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                                                                                                                             4 amino acids
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212-354-8113
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VENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE VENTION: PEPTIDES BY SEQUENTIAL METABOLISM
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linear
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100.0%; Pred. No. 1.
Live 0; Mismatches
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/note "phenylglycine"
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/notes "1,2,3,4-tetrahydroisoguinoline-3-carboxylic acid"
/note: "Position 1
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RESULT 6
US-08-428-488-60
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Best Local Similarity
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-428-488-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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OTHER INFORMATION: OTHER INFORMATION:
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                                                          LOCATION:
                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 amino acids
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                                                                                             Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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BRAIN-ENHANCED DELIVERY OF NEUROACTIVE

REPTIDES BY SEQUENTIAL METABOLISM
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100.0%;
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                                                                                                                                                           /note=
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ester."
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Pred. No. 1.6e+
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                                                                                                                                                                                                                                                                                                 "Position
                           "Position
                                                                                                                                                              "Position
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                           4
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                        Arg (jPmc)-Cholesteryl
                                                                                                                                                                                                                                                                                             Trigonellyl-Ala."
                                                                                                                                                              Tyr (0-tBu)."
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RESULT 8
US-08-428-488-62
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US-08-428-488-61
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                                                                                                                                                                                            US-08-428-488-61
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Sequence 61, Apprix
No. 5624894
                                                                                                                   Best Local Similarity Matches 2; Conserv
                                                                                                                                               Query Match
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GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
NAME: 51.254
                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                        LOCATION: 4
OTHER INFORMATION:
                                                                                                                                                                                                                                                               OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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nes 2; Conserv
                                                                                                                                                                                                                                    NAME/KEY:
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                                                                                      5 ay 6
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                                                                                                                                                                                                                                                                                                                                                                              4 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BODOR, Nicholas S.
VENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE VENTION: PEPTIDES BY SEQUENTIAL METABOLISM
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                                                     peptide
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                                                                                                                                  100.0%;
                                                                                                                                               25.0%;
                                                                                                                                                                                                     /note= "Position 4 = Arg-Cholesteryl ester."
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                                                                                                                                                                                                                                                                                                                                                                                                             61:
                                                                                                                                  Score 2; I
; Pred. No.
                                                                                                                    0;
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Pred. No.
                                                                                                                                                                                                                                                              "Position 1 = Trigonelly1-Ala"
                                                                                                                    Mismatches
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o. 1.6e+05;
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b. 1.6e+05;
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                                                                                                                    Indels
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RESULT 9
US-08-428-488-71
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Best Local Similarity
Thes 2; Conserve
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                                                                                                                                                                                                     Sequence 71, Application US/08428488 Patent No. 5624894
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                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REGISTRATION NUMBER: 26,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
                                                                                                NUMBER OF SEQUENCES: 1
                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.U. bua
CITY: Alexandria
               COUNTRY:
                                 STATE:
                                                 CITY: Alexandria
                                                               STREET:
                                                                                 ADDRESSEE:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States ZIP: 22313-1404
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22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                          Virginia
                                                               P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Burns, Doane, Swecker & Mathis P.O. Box 1404
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BODOR, Nicholas S.

VENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE

VENTION: PEPTIDES BY SEQUENTIAL METABOLISM
                                                                                                                                                                                                                                                                                                                                                                           Conservative
               United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                 Burns,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                  Doane,
                                                                                                                                  BRAIN-ENHANCED DELIVERY OF NEUROACTIVE PEPTIDES BY SEQUENTIAL METABOLISM
                                                                                                                                                                                                                                                                                                                                                                     25.0%; Score 2; DB: 100.0%; Pred. No. 1.0 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Position 4 = Arg-Cholesteryl ester."
                                                                                                                  107
                                                                                  Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    028724-087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Position 1 = 1,4-Dihydrotrigonellyl-Ala."
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MEDIUM TYPE: Floppy

Floppy disk

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RESULT 10
US-08-428-488-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-08
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 71:
                                                                                                                                                                                                                                                             APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                         STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
APPLICATION NUMBER: US/08/428,488 FILING DATE: 27-APR-1995 CLASSIFICATION: 514
                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/01 FILING DATE: 27-APR-1995
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                                                                                                                                                           RY: United States 22313-1404
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P.O. Box 1404
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100.0%; Pred. No. 1.0
Live 0; Mismatches
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ER: 028724-087
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5624894
GENERAL INFORMATION:
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INFORMATION FOR
        REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                        SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Baumeister, Mary K
                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                           COUNTRY: United States ZIP: 22313-1404
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STATE: Virginia
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OTHER INFORMATION:
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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BODOR, Nicholas S.
IVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
IVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
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(703) 87 NO: 72:
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linear
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O. Box 1404
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100.0%; Pr
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methylsulfate."
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                                                               028724-087
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Pred. No.
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ches 0; Indel
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SEQUENCE CHARACTERISTICS: LENGTH: 4 amino acids

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; LOCATION: 4
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-428-488-73
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 74, Application US/08428488 Patent No. 5624894
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                     TELEFAX: (703) 836-200 INFORMATION FOR SEQ ID NO:
                             LOCATION: 1
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                  NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Baumeister, Mary K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 27-APR-1995 CLASSIFICATION: 514
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                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. Box CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
NAME/KEY: Modified-site
                                                           NAME/KEY:
                                                                                                            TOPOLOGY:
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P.O. Box 1404
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                                                           Modified-site
                                                                                                          linear
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                   (703) 836-6620
                                                                                          peptide
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3 836-2021

3 NO. 74:
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BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
PEPTIDES BY SEQUENTIAL METABOLISM
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                                                                                                                                                                                                                                                    028724-087
                             "Position 1 = 1,4-dihydrotrigonellyl-Pro."
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Query Match
Best Local Similarity
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Best Local Similarity
"hes 2; Conserv
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NAME/KEY:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
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                                                                                                                                                      FEATURE:
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CORRESPONDENCE ADDRESS:
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                                                                                             NAME/KEY: Peptide LOCATION: 4 OTHER INFORMATION: OTHER INFORMATION:
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SOFTWARE: PatentI
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CITY: San Diego
                                                                                                                                                                 OTHER INFORMATION:
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LOCATION:
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4370 La Jolla Village Drive, Suite
                                                                                                                                                                                                                                                                                                         4 amino acids
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                                                                                                                                                                                                                                                                                                                                                 (619) 535-8949
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                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                               linear
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n, Richard A.
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           25.0%; Score 2;
100.0%; Pred. No.
cive 0; Mismatc
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100.0%; Pred.
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the C-terminal."
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1.6e+05;
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. 1.6e+05;
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Conservative

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RESULT 15
US-08-487-006-152
: Sequence 152, Application US/08487006
; Patent No. 5641861
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US-08-487-006-151
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Best Local Similarity
Thehes 3; Conserv
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Patent No. 5641861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/487,006
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-TP 1706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dooley, Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: No. 5641861e1 Mu Opioid Receptor Ligands:
TITLE OF INVENTION: Agonists and Antagonists
NUMBER OF SEQUENCES: 222
                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
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CORRESPONDENCE ADDRESS:
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STATE: California
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1 YXG 3
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LOCATION: 4
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4370 La Jolla Village Drive, Suite 700
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US-08-487-006-153
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Best Local
                                                                                                                                GENERAL INFORMATION:
APPLICANT: Dooley Colette T.
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: No. 5641861e1 Mu Opioid Receptor Ligands:
TITLE OF INVENTION: Agonists and Antagonists
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: NO. 5641861e1 Mu Opioid I
TITLE OF INVENTION: Agonists and Antagonists
NUMBER OF SEQUENCES: 222
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CITY: San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/487,006 FILING DATE: 07-JUN-1995 CLASSIFICATION: 530
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ZIP: 92122
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                                                                                    CITY:
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                                                                 STATE: California
                                                                                                                   ADDRESSEE:
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4370 La Jolla Village Drive,
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Floppy disk
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100.0%; Pr/
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Pred. No. 1.6e+05;
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                                                                                                    Suite 700
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RESULT 17
US-08-454-950-7
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                       APPLICATION NUMBER: UFILING DATE: 31-MAY-1 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect 6.0a for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zamora, Paul O. APPLICANT: Rhodes, Buck A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
APPLICATION NUMBER: 07/840,077
FILING DATE: 20-FEB-1992
APPLICATION NUMBER: 07/816,477
FILING DATE: 03-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4261 Ballo
CITY: Albuquerque
                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb MEDIUM TYPE: Storage COMPUTER: IDM PC/XT/AT, IBM PS/2 or COMPUTER: IDM PC/XT/AT, IBM PS/2 or COMPUTER: IDM PC/XT/AT, IBM PS/2 or COMPUTER: IDM PC/XT/AT, IBM PS/2 or COMPUTER: IDM PC/XT/AT, IBM PS/2 or COMPUTER: IDM PC/XT/AT, IBM PS/2 or COMPUTER: IDM PC/XT/AT, IBM PS/2 or COMPUTER: IDM PC/XT/AT, IBM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or COMPUTER: IDM PS/2 or CO
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OPERATING SYSTEM: PC-1
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LOCATION:
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4261 Balloon Park
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          31-MAY-1995
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N: 530
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100.0%; Pr
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the C-terminal."
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Best Local Similarity
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                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,761
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/079,445
FILING DATE: 18-JUN-1993
ATTORNEY/ACENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-HP 9648
                                                                                              TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Eichler, Jutta
APPLICANT: Houghten, Richard A.
TITLE OF INVENTION: PEPTIDES HAVING ANTI-MICROBIAL,
TITLE OF INVENTION: HEMOLYTIC, ANTI-MELITIN OR ANTI-ENZYMATIC ACTIVITY
                               FEATURE:
                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blondelle, Sylvie E. APPLICANT: Pinilla, Clemencia
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ANTI-SENSE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
NAME/KEY:
                                                  TOPOLOGY:
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TYPE: amino acid
STRANDEDNESS: single
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                                                                amino acid
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4370 La Jolla Village Drive, Suite 700
                                                                                  4 amino acids
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NO: 7:
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                     ; MOLECULE TYPE: peptide US-08-338-8908-1
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US-08-338-890B-1
                                                         Best Loc
Matches
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/WINDOWS
SOFTWARE: WORDPERFECT SAVED AS ASCII (DOS) TEXT(*.*)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,890B
FILLING DATE: NOV. 14, 1994
CLASSIFICATION: 530
ATTORNET/AGENT INFORMATION:
NAME: MAILDOSKI, Lynn
DECTIFERATION NUMBER: 28,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08338890B Patent No. 5700905
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TELEFAX: (215)568-3439
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hirschmann, Ralph
APPLICANT: Spanevello, Rolando
APPLICANT: Nutt, Ruth
TITLE OF INVENTION: Synthetic Somatostatin Mimics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewicz and No. 5700905ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 38,788
REFERENCE/DOCKET NUMBER: UPI
TELECOMMUNICATION:
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LOCATION:
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ZIP: 19103
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                                                           Local Similarity es 2; Conserv
                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
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/noteo "XaaoKFmoc"
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RESULT 20
US-07-923-260A-11
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Best Local Similarity
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US-08-454-949-7
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                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08454949 Patent No. 5759516
COUNTRY: U.S.A.
ZIP: 87109-58072
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
MEDIUM TYPE: Storage
COMPUTER: IBM PC/XT/AT, IBM PS/2 or
COMPUTER: COMPATIBLES
OPERATING SYSTEM: PC-DOS or MS-DOS
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Zamora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 215-875-8394 INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEPAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard J. Weiser
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   APPLICANT: Rhodes, Buck A. TITLE OF INVENTION: Peptid TITLE OF INVENTION: Pharma
                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Inouye, TITLE OF INVENTION:
                                                                                                                                                 CITY: Albuquerque
                                                                                                                                                                   STREET:
                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 31-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                   E: RhoMed Incorporated 4261 Balloon Park
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                                                                                                                                                                                                                                                                                    Zamora,
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                                                                                                                                                                                                                                     Peptide-Metal Ion Pharmaceutical Preparation and Method
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                                                                   3.5 inch, 1.44
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SOFTWARE: WordPerfect 6.0a for Windows CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/01 FILING DATE: 31-MAY-1995

US/08/454,949

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RESULT 22
US-08-798-897-49
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APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/840,077
FILING DATE: 20-FEB-1992
APPLICATION NUMBER: 07/816,477
FILING DATE: 03-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (505) 243-254 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL: N
                                       NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (505) 242-9677
TELEPHONE: (505) 243-2542
NFORMATION FOR SEQ ID NO: 7:
                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
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                  GEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                              APPLICATION NUMBER: US/08/798,897 FILING DATE: February 11, 1997 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Deborah A. Peacock REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
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LENGTH:
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4 amino acids
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US-08-463-377-2
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US-08-463-224-2
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Best Local Similarity
"hes 2; Conserva
Sequence 2, Application US/08463377 Patent No. 5837499 GENERAL INFORMATION:
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Patent No. 5807824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Best Local
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,224
                                                                                                                                                                                                                         TOPOLOGY: li
                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: C5a Receptor Antagonists Having TITLE OF INVENTION: Substantially No. 5807824Agonist Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                              Local Similarity
nes 2; Conser
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CITY: Westfield
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                                                                                                                                                                                                                                                                                                                                                       NAME: Foley, Shawn P
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                                                                                                                                                                                                                                                               LENGTH: 4 amino acids
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600 South Avenue West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galakatos, Nicholas G
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 van Heeke,
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100.0%; Pr
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b; Pred. No. 1.6
0; Mismatches
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s; Pred. No. 1.6
0; Mismatches
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APPLICANT:

Boyar, William C van Oostrum,

Jan

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RESULT 25
US-08-441-871-63
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Bost Local Similarity
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TELEX: 139-125
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
FENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 63, Application US/08441871 Patent No. 5846765
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,871
FILING DATE: 16-MAY-1995
                                                                                                                                                                                                                                                                           APPLICANT: Matthews, David J.
APPLICANT: Wells, James A.
APPLICANT: Wells, James A.
APPLICANT: 201ler, Mark J.
TITLE OF INVENTION: Identification of No. 5846765el Substrates
NUMBER OF SEQUENCES: 152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patchtin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,377
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Galakatos, Nicholas G.
APPLICANT: Galakatos, Albert
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5837499Agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: FOLEY, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 46
                                                                                                                                                                                                     CITY:
STATE:
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Search completed: January 14, 2002, 07:57:30 Job time: 375 sec

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Best Local S
Matches 2
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TELECOMMUNICATION: INFORMATION:
TELEPHONE: 415/225-1249
TELEPHAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-APR-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-DEC-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 10-APR-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/7 FILING DATE: 09-AUG-1991
                                                                                                                                                                                                                                                                                                     NAME: Winter, Daryl B. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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2; Conserv
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14-JUN-1991
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05-APR-1995
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03-DEC-1991
                                                      25.0%; Score 2; DB
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| B56864 | A61514 | S08575 | PQ0445 | PH1468 | РН0771 | PH1457 | PH1469 | PH1462 | PH1467 | S74144 | S10626 | JS0424 | B61497 | 869123 | S26554 | S26559 | JS0423 | S42765 | UOGM2 | 160434 |
| dipeptidyl-peptida | glutathione transf | botulinum neurotox | urotensin II - lau | T-cell receptor be | T-cell receptor be | T-cell receptor be | T-cell receptor be | T-cell receptor be | T-cell receptor be | aggrecan - bovine | lipovitellin - Afr | urotensin II-B pep | seed protein ws-17 | proton-translocati | T-cell receptor be | T-cell receptor be | urotensin II-A pep | urotensin II - tel | urotensin II - lon | 68kDa neurofilamen |

ALIGNMENTS

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Nicodemia diversifolia chlorop C; Species: chloroplast Nicodemia diversifolia C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-Jan-2000 C; Accession: T13492 R; Olmstead, R.G.; Reeves, P.A. Ann. Mo. Bot. Gard. 82, 176-193, 1995 A; Title: Evidence for the polyphyly of the Scrophulariaceae based on chloroplast rbcL A; Reference number: Z17559 A; Accession: T13492 A; Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-698 COLM> A; Cross-references: EMBL:L36405; NID:g703196; PID:g703197; PIDN:AAAB4496.1 C; Genetics: A; Note: ndhF C; Superfamily: NADH dehydrogenase (ubiquinone) chain 5 C; Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0644
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few A:Reference number: PT0509; MUID:91277601
A:Accession: PT0644
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 CFEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor RESULT T13492 PT0644
T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment) DЬ οy Query Match Best Local S Matches 4 5 sfxg 8 |||| 664 SFXG 667 Local Similarity Conservative 37.5%; Score 3; DB: 100.0%; Pred. No. 3.: tive 0; Mismatches DB 2; Le Length 698 0 0; Gaps z 0 regions

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pev-kinin 1 - penaeid shrimp (Penaeus vannamei) (fragment) C;Species: Penaeus vannamei
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change
C;Accession: pD0029
R;Nieto, J.; Veelaert, D.; Derua, R.; Waelkens, E.; Cerstiaens,
Blochem. Biophys. Res. Commun. 248, 406-411, 1998
A;Tita: Identification of one tachykinin- and two kinin-related
A;Reference number: pD0027; MUID:98342103
A;Accession: pD0029
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                       neuromodulatory peptide wWamide-3 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S33246
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
S33246
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A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides
A;Reference number: S33244; MUID:93265912
A;Accession: S33244
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A;Molecule type: proto
A;Residues: 1-7 <MIN>
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A;Molecule type: protein
A;Residues: 1-7 <MIN>
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C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #tex
C;Accession: S33244
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FEBS Lett. 323,
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1993
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MUID:93265912
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leucokinin VI - Madeira cockroach (Species: Leucophaea maderae (Madeira coc C; Spate: 07-Sep-1990 #sequence_revision 07-C; Accession: JS0316 R.Holman, G.M.; Cook, B.J.; Nachman, R.J. Comp. Biochem. Physiol. C 88, 27-30, 1987 A; Title: Isolation, primary structure, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R-phycoerythrin gamma-E chain - red alga (Gastroclonium coulteri) (fragment) (Species: Gastroclonium coulteri
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: A37521; J22565
C;Accession: A37521; J22565
C;R;Klotz, A.V.; Glazer, A.N.
J. Biolz, Chem. 260, 4856-4863, 1985
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Thehes 2; Conserve
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S11078
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A37521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Egestad, B.; Estonius, M.; Danielsson, O.; Persson, B.; FEBS Lett. 269, 194-196, 1990 A;Title: Rast atom bombardment mass spectrometry and chemia;Reference number: S11074; MUID:90353571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 30-Jun-1991 #sequence_revision 30-Sep-1991 #text_change 05-Aug-1994
C;Accession: S11078
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C; Species: Pichia jadinii, Candida utilis
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07-Sep-1990 #text_change 20-Jun-2000
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No. 2.2e+05;
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5. 2.2e+05;
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C:Species: Leucophaca maderae (Madeira cockroach) C:Date: 31-Mar-1988 #sequence_revision 26-May-1994 C:Accession: A23967 R. Nachman, R.J.; Holman, G.M.; Cook, B.J. Blochem. Blophys. Res. Commun. 137, 936-942, 1986 A:Title: Active fragments and analogs of the insect A:Reference number: A23967; MUID:86289041 A:Accession: A23967
                                                                                                                                                      A:Status: preliminary
A:Molecule type: protein
A:Molecule type: protein
A:Mosidus: 1-8 <DUV>
A:Experimental source: thoracic ganglia
A:Note: sequence extracted from NCBI backbone (NCBIP:128479)
                                                                                                                                                                                                                                            R:Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A. Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A;Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequen A;Reference number: A47393; MUID:93211980
A;Accession: D47393
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D47393
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A; Residues: 1-8 <NAC>
A; Residues: 1-8 <NAC>
C; Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolldone carboxylic acid (Gin) #status experimental
F;8/Modified site: amidated carboxyl end (Leu) #status experimental
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                                                                                                                                                                                                                                                                                                                                                     nouropeptide callatostatin 4 - bluebottle fly (Calliphora vomitoria)
C;Species: Calliphora vomitoria
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
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A; Residues: 1-8 <HOL>
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A; Accession: JS0316
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C;Species: Petromyzon marinus (sea lamprey)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 18-Mar-1997
C;Accession: A01412
R;Sherwood, N.M.; Sower, S.A.; Marshak, D.R.; Fraser, B.A.; Brownstein, M.J.
J Biol. Chem. 261, 4812-4819, 1986
A;Title: Primary structure of gonadotropin-releasing hormone from lamprey brain.
A;Reference number: A01412; MUID:86168192
A;Accession: A01412
A;McCession: A01412
A;McCession: A01412
C;Comment: This hormone was isolated from the brain.
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxyl end (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental
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A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity A;Reference number: PT0222; MUID:91108337
A;Accession: PT0315
                                                                                                                                                                                                                                                                                                                                                                  gonadoliberin - sea lamprey
N;Alternate names: gonadotropin releasing hormone (GnRH)
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Best Local Similarity
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C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0315
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A; Residues: 1-8 <WER>
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A;Title: Differential splicing in the extracellular region of fibroblast growth facto A;Reference number: A42057; MUID:92107200
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C; Species: Mus musculus (house mouse)
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A; Residues: 1-9 < YAM>
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sperm-activating peptide (Ser-1, Ala-3, Gly-5 speract) - sea urchin (Hemicel C;Species: Hemicentrotus pulcherrimus C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
                                                                   RESULT
D60787
                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 1-10 <CON>
C; Superfamily: substance P precursor
C; Keywords: amidated carboxyl end; neuropeptide; tachykinin
F; 10/Modified site: amidated carboxyl end (Met) #status prec
                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Aug-2000
C;Accession: JN0024
R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
JN0024
                                                                                                                                                                                                                                                                                                                                                                            A;Title: [Arg3]substance P and neurokinin A A;Reference number: JN0023; MUID:88204263 A;Accession: JN0024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: potentiates thyroliberin-induced thyrotropin secretion C;Superfamily: thyroliberin precursor C;Keywords: hypothalamus; neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Bulant, M.; Ladram, A.; Montagne, J.J.; Delfour, A.; Nicolas, P. Biochem. Biophys. Res. Commun. 189, 1110-1118, 1992
A;Title: Isolation and amino acid sequence of the TRH-potentiating peptide from A;Reference number: JC1367; MUID:93111999
A;Accession: JC1367
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A;Residues: 1-10 <BUL>
A;Experimental source: hypothalamus
C;Comment: This neuropeptide corresponds to a region of the rat thyroliberin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thyroliberin potentiating neuropeptide - bovine N;Alternate names: thyrotropin-releasing hormone potentiating peptide; TRH-C;Species: Bos prinigenius taurus (cattle) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1997
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. 2.2e+03;
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2.2e+03;
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                                                 urchin (Hemicentrotus
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                                              pulch
Query Match
Best Local Similarity
"hehes 2; Conserv
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A;Description: may play a physiological role in the regulation of cardiovascular and A;Note: neurokinin A is derived by post-translational processing of preprotachykinin C;Superfamily: unassigned animal peptides C;Keywords: neuropeptide; amidated carboxyl end; tachykinin F;10/Modified site: amidated carboxyl end (Met) #status predicted
                                                                                                                                                                          Eur. J. Biochem. 206, 659-664, 1992
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related
A;Reference number: S23186; MUID:92298992
A;Accession: S23186
                                                                                                                                                                                                                                                                                         neurokinin A - Atlantic cod
C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Mar_1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related A;Reference number: S23186; MUID:92298992
A;Accession: S23307
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S23307
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C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 1-10 <SU2
C; Comment: This oligopeptide from egg jelly
at shows some, but not absolute, species res
                                                                                                     C; Function:
                                                                                                                     A;Residues: 1-10 <JEN>
A;Experimental source: brain
                                                                                                                                           A; Molecule type: protein A; Residues: 1-10 <JEN>
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A;Accession: D60787
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Live 0; Mismatches
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Conservative

100.0%; 25.0%;

Score 2; DB 2; Pred. No. 2.2 0; Mismatches

DB 2; Length 10; . 2.2e+03; ches 0; Indels

Indels

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A; Molccule type: protein
A; Residues: 1-10 < KOZ>
C; Superfamily: unassigned animal peptides
C; Keywords: amidated carboxyl end; neuropeptide
F; 10/Modified site: amidated carboxyl end (Met)
                                                                                                                                                                                                                                                                            R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H. Blochem. Biophys. Res. Commun. 177, 588-595, 1991
A;Title: Isolation of four novel tachykinins from frog (Rana A;Reference number: JE0426; MUID:91254337
A;Accession: JE0428
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ranatachykinin C - bullfrog
C;Specles: Rana catesbeiana (bullfrog)
C;Date: 31-Dcc-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C;Date: 31-Dcc-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C;Accession: C6103; JB0428
R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.
Regul. Pept. 42(Suppl.1), S12, 1992
A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain
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A; Accession: C61033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Rana catesbelana (bullfrog)
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A; Residues: 1-10 <KAN>
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                                                                                                                    Length 10;
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Best Local Similarity
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trpE protein - Bacillus amyloliquefaciens (fragment)
C;Species: Bacillus amyloliquefaciens
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 15-Oct-1999
C;Accession: I40032
                                                                                                                                                                                                                     C;Accession: $38305
C;Accession: $38305
R;Kamemura, K.; Furuichi, Y.; Umekawa, H.;
R;Kamemura, K.; Furuichi, Y.; Umekawa, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurokinin A-related peptide - laughing frog
C;Species: Rana ridibunda (laughing frog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
                                                                                                          A; Molecule t
A; Residues:
                                                                                                                                                                   A; Reference number: A; Accession: S38305
                                                                                                                                                                                   Biochim. Biophys. Acta 1158, 181-188, 193
A;Title: Purification and characterization of novel lectins from Great Northern bean, A;Reference number: S38304; MUID:94002183
                                                                                                                                                                                                                                                                                      lectin GNL2 alpha chain - kidney bean (fragment)
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-10 <RES>
A;Cross-references: GB:K02661; NID:g143775; PIDN:AAB05353.1; PID:g143776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Construction of a promoter-probe vector for Bacillus subtills host by using A; Reference number: I40032; MUID: 85006754 A; Accession: I40032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;YOShimura, K.; Uemura, J.; Seki, T.; Oshima, Y. J. Bacteriol. 159, 905-912, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 1-10 <WAN>
C;Superfamily: unassigned animal peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Date: 19-Mar-1997 #sequence_revision
C; Accession: S27178
                                                                                                                                              A; Status: preliminary
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Conservative

Mismatches

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FMRFamide-like protein - tobacco hornworm
C;Species: Manduca sexta (tobacco hornworm)
C;Decies: Manduca sexta (tobacco hornworm)
C;Decies: Manduca sexta (tobacco hornworm)
C;Date: 11. Feb-1993 #sequence_revision 11-Feb-1993 #text_change 17-Mar-1999
C;Accession: A43977
R;Kingan, T.G.; Teplow, D.B.; Phillips, J.M.; Riehm, J.P.; Rao, K.R.; Hildebrand, J.G.;
Peptides 11, 849-856, 1990
A;Title: A new peptide in the FMRFamide family isolated from the CNS of the hawkmoth, Ma Reference number: A43977; MUID:91045350
A;Raccession: A43977
A;Molecule type: protein
A;Residues: 1-10 <KIN>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;10/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein P7 - curled-leaved tobacco (fragment)
C:Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C:Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
C:Accession: D28027
C:Accession: D28027
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-A:Reference number: A94167
A:Accession: D28027
A:Accession: D28027
A:Residues: 1-10 <BAU>
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Matches 2
                                           TISSUE-Intestine;
MEDLINE-94023216; PubMed-8210506;
Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
"Four novel tachykinins in frog (Rana catesbeiana) brain
                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
RANATACHYKININ C (RTK C).
Rana catesbelana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibla; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                        TISSUE-Intestine;
MEDLINE-91254337; PubMed-2043143;
Kozawa H., Hino J., Minamino N., Kang
"Isolation of four novel tachykinins
              litestine.";
Regul. Pept. 46:81-88(1993).
-I- FUNCTION: TACHYKININS AR
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                                                                                                             SEQUENCE.
                                                                                                                                Biochem. Blophys. Res. Commun. 177:588-595(1991)
                                                                                                                                                 brain and intestine.
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                                                                                                                                                                                                                                                                                                                                                    TKNC_RANCA
P22690;
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RANRI
                                                                                                                                                                                                                                           NCBI_TaxID~8400;
                                                                                                                                                                                                                                                                                                                                                                                RANCA
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MOD_RES 10 10 AMIDATION.
SEQUENCE 10 AA; 1160 MW; 526B407059D5BAA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
PIR: S27178; S27178.
Interpro: IPR002040; Tachykinin.
PROSITE: PS00267; TACHYKININ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Primary structure and receptor-binding related peptide from frog gut.";
Biochem. J. 287:827-832(1992).
-I- FUNCTION: TACHYKININS ARE ACTIVE PER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rana ridibunda (Laughing frog) (Marsh frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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TISSUE~Skin;
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 EVAKE BEHAVIORAL RESPONSES,
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ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS ONSES, ARE POTENT VASODILATORS AND
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Ranidae; Rana
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P80580;
01-OCT-1996
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SEQUENCE
                                                                                                                                                                                                                                                                                       hydroxybenzoate.";
microbiology 142:2115-2120(1996).
-!- CATALYTIC ACTIVITY: 3-MALEYLPYRUVATE =
                                                                                                                                                                                                                                                                                                                                                                Robson N.D., Parrott S., Cooper R.A.;
"In vitro formation of a catabolic plasmid carrying Klebsiella pneumoniae DNA that allows growth of Escherichia coli K-12 on hudowards."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MALEYLPYRUVATE ISOMERASE (EC 5.2.1.4) (FRAGMENT).
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-!- SIMILARITY: BELONGS
PIR; JE0428; JE0428.
PIR; C61033; C61033.
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MEDLINE-88204263; PubMed-2452461;

Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;

"[Arg3]substance P and neurokinin A from chicken small intestine.";

Regul. Pept. 20:171-180(1988).

-:- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

SCCRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOT
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01-FEB-1991 (Rel. 17, Last sequence update)
01-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                          TRNB_ONCMY STANDARD; PRT; 10 AA.

TRNB_ONCMY STANDARD; PRT; 10 AA.

P28500;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NEUROKININ A (SUBSTANCE K) (NEUROMEDIN L).
ONCOTHYNCHOLS MYKISS (RAINDOW TROUT) (Salmo gairdneri), and
Gadus morhua (Atlantic cod).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID-8022, 8049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKNB_CHICK P19851;
Jensen J., Conlon J.M.;
"Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.";
Eur. J. Biochem. 206:659-664(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tachykinin; Neuropeptide; Amidation MOD_RES 10 10 AMIDAT SEQUENCE 10 AA; 1134 MW; 8A6B40
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InterPro; IPR002040; Tachykinin.
PROSITE; PS00267; TACHYKININ; 1.
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                                                     MEDLINE=92298992; PubMed=1376687;
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MOD_RES 10 10 AMIDATION (BY SIMILARITY).

SEQUENCE 10 AA; 1145 MW; 136B4062C9D5B440 CRC64;
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SEQUENCE:
TISSUE=Intestine;
MEDLINE=94023216; PubMed=8210506;
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Kozawa H., Hino J., Minamino N., Kangawa K.,
"Isolation of four novel tachykinins from fro
brain and intestine.";
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Rana catesbelana (Bull frog).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;

Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
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InterPro; IPR002040; Tachykini
PROSITE; PS00267; TACHYKININ;
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PIR; JE0427; JE0427.

PIR; B61033; B61033.

InterPro; IPR002040; Tachykinin.

PROSITE; PS00267; TACHYKININ; 1.
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Regul. Pept. 46:81-88(1993)
-!- FUNCTION: TACHYKININS A
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SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
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(Rana catesbeiana)
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20-MAR-1987 (Rcl. 04, Last sequence update)
20-MAR-1987 (Rel. 29, Last annotation update)
01-JUN-1994 (Rel. 29, Last annotation update)
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MOD_RES
SEQUENCE
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MEDLINE-86168192; PubMed-3514603;
Sherwood N.M., Sower S.A., Marsha
"Primary structure of gonadotropi
    Petromyzon
Eukaryota;
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InterPro; IPR002012; GnRH.
Pfam; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1.
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Eukaryota; Mctazoa; Chordata; Craniata;
Petromyzontiformes; Petromyzontidae; Pe
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GONADOLIBERIN I (GONADOTROPIN-RELEASING HORMONE
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FÜNCTION: STIMULATES THE SECRETION
FÜLLICLE-STIMULATING HORMONES.
SIMILARITY: BELONGS TO THE GNRH FAM
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SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                            1E4B36237B1735AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION
Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNRH FAMILY
                                                                                                                                                                                                                                                                                                                                  Mismatches
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Vertebrata; Hyperoartia;
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sing hormone
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.2e+03
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                                                        (GNRH-III)
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RESULY 19
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Needle;
MEDLINE-98418576; PubMed-9747804;
Costa P., Bahrman N., Frigerio J.-M.,
"Water-deficit-responsive proteins in
"Water-deficit-responsive proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR PINPS STANDARD; PRT; 10 AA.

PRIOR4;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE (RUBISCO ACTIVASE) (RA) (WATER STRESS RESPONSIVE PROTEIN 4) (FRAGMENT).

PINUS PINASTEI (MATILIME PINE).

EUKARYOCTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinasceae; Pinus.

NCBI_TaxID=71647;
                                                                                                                                                                                                                                                           proteins."; concaracterization o proteins."; concaracterization o Electrophoresis 20:1098-1108(1999)
                             Chloroplast; ATP-binding.
NON_TER 1 1
NON_TER 10 10
                                                                                                                                                                                                                                                                                                                            MEDLINE=99274088; PubMed=10344291;
Costa P., Plonneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Frigerio J.-M., Plomion C.;
"Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
MOD_RES
SEQUENCE
     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Needle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            releasing hormone from lamprey brain.";
Endocrinology 132:1125-114.
-i- FUNCTION: STIMULATES THE SECRETION OF BOTH
FOLLICLE-STIMULATING HORMONES.
-i- SIMILARITY: BELONGS TO THE GNRH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_TaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002012; GnRH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sower S.A., Chiang Y.-C., Lovas S., Conlon "Primary structure and biological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sower S.A., Chiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93178316; PubMed=8440174;
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                                                                                            PUNCTION: ACTIVATION OF RUBISCO (RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO ACCEPTANT STRUCTURE (BY SIMILARITY).

SUBCELLULAR LOCATION: CHLOROPLAST STROMA (BY SIMILARITY).

INDUCTION: BY WATER-STRESS.

SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
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     10
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  AA;
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1277 MW;
  1171
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  W.
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Pred. No. 1.2
0; Mismatches
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  C0A506D2C72B1EA6 CRC64;
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284B36237AA1F5A3 CRC64;
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of a
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Best Local :
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Primary structure and synthesis of a blocked myotropic neuropeptide isolated from the cockroach, Leucophaea maderae.", Comp. Biochem. Physiol. 85c:219-224(1986).
-i- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nachman R.J., Holman G.M., Cook B.J.;
"Active fragments and analogs of the insect neuropeptide leucopyrokinin: structure-function studies.";
Biochem. Biophys. Res. Commun. 137:936-942(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaea.
                                                  Peptides 12:1295-1302(1991)
-!- FUNCTION: CARDIOACTIVE |
-!- SIMILARITY: BELONGS TO
                                                                                                 "The identification and structure-activity relations cardioactive FMRFamide-related peptide from the blue
                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda;
Eumalacostraca; Eucarida; Decapo
Eubrachyura; Portunoidea; Portur
                                                                                                                                                                                                                            FMRFAMIDE-LIKE NEUROPEPTIDE.
Callinectes sapidus (Blue crab).
                                                                                                                                                                                                                                                     01-OCT-1994 (Rel. 01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                              P38495;
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87052651; PubMed=2877794;
Holman G.M., Cook B.J., Nachman R.J.;
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           Neuropeptide; Amidation. MOD_RES 9 9
                                                                                       sapidus
                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                            Krajniak K.G.;
                                                                                                                                        MEDLINE=92270479; PubMed=1815216;
                                                                                                                                                                           NCBI_TaxID=6763;
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nes 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
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                                      FAMILY
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; IPR001484; Pyrokini
PS00539; PYROKININ;
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 AA;
                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BELONGS TO THE PYROKININ FAMILY
                                                                                                                                                                                                                                                     30, Created)
30, Last sequence up
32, Last annotation
 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      949 MW;
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  WW.
                                                                                                                                                                                       ppoda; Crustacea; Malacostraca;
Decapoda; Pleocyemata; Brachyu
Portunidae; Callinectes.
                                                  PEPTIDE.
THE FARP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyu
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                        Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
Sphingiodea; Sphingidae; Sphinginae; Manduca.
NCBI_TaxID=7130;
                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-FEB-1994 (Rel. 28, Last sequence up
01-NOV-1995 (Rel. 32, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FARP_MANSE P18523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MANSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN
Neuropeptide; Amidation; Multigene family.
MOD_RES 10 10 AMIDATION (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARCINUSTATIN 19.
"A new peptide in the FMRFamide family isolated from the CNS of the hawkmoth, Manduca sexta."; peptides 11:849-856(1990).

-i- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING
                                                                                                                                                 MEDLINE-91045350; PubMed-2235684;
Kingan T.G., Teplow D.B., Phillips J.M.,
Hildebrand J.G., Homberg U., Kammer A.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and identification of multiple neuropeptides allatostatin superfamily in the shore crab Carcinus mae
                                                                                                                                                                                                                     SEQUENCE
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                                        Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
                                                                                                                                                                                                                                                                                                                                  Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., winstan Davey M., East P.D., Thorpe A.; "Lepidopteran peptides of the allatostatin superfamily."; Peptides 18:1301-1309(1997).
--- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                             01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
LEUCOKININ IV (L-IV)
                                                                                                                                                                                                                                                                                                                              Neuropeptide; Amidation.
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                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Larva;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
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30-MAY-2000 (Rel. 39, Last annotation updat
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SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
D47393; D47393.
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OR N.
D32879D5AB47740A CRC64;
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Pred. No. 1e+
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P13049;
P13049;
O1-JAN-1990 (Rel. 13, Created)
O1-FEB-1994 (Rel. 28, Last sequence update)
O1-FEB-1994 (Rel. 28, Last annotation update)
C1-FEB-1994 (Rel. 28, Last annotation update)
C1-FEB-1994 (Rel. 28, Last annotation update)
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MOD_RES
SEQUENCE
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P19988;
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Holman G.M., Cook B.J., Nachman R.J.;
"Isolation, primary structure, and synthesis of leucokinins V and V
"Isolation, primary structure, and synthesis of leucokinins V and V
myotropic peptides of Leucophaea maderae.";
Comp. Biochem, Physiol. 88c:27-30(1987)
-i- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-i- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
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Eukaryota; Metazoa; Arthropoda; Trachata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Biattaria;
Blaberoidea; Blaberidae; Leucophaea.
NCBI_TaxID=6988;
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01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
LEUCOKININ VI (L-VI).
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SEQUENCE
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"primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";

Comp. Biochem. Physiol. 84C:271-276(1986).

-i- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTII ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).

-i- SIMILARITY: TO THE OTHER LEUCOKININS.
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AL17_CARMA
P81820;
30-MAY-2000
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
CARCINUSTATIN 18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eumalacostraca; Eucarida; Decapoda; Pleocyemata Eubrachyura; Portunoidea; Portunidae; Carcinus. NCBI_TaxID=6759;
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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
                                                                                                                                                                                                                                                                                     Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyu
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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30-MAY-2000 (Rel. 39, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                                                                                                          allatostatin superfamily in the shore Eur. J. Biochem. 250:727-734(1997).
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                                                                                                                                                          "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
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                                                                                    Neuropeptide; Amidation; Multigene family.
MOD_RES 8 8 AMIDATION (POTENTIAL).
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FUNCTION: MAY ACT AS A NEUROTRANSMITTER
SIMILARITY: BELONGS TO THE ALLATOSTATIN
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Similarity 2; Conserv
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P41840;
01-NOV-1995
the blowfly Calliphora vomitorià.";
Cell Tissue Res. 276:367-379(1994).
-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
- ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
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TISSUE-Thoracic ganglion;
MEDLINE-93211980; PubMed=8460157;
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MEDLINE-
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Oestroidea; Calliphoridae; Calliphora.
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01-NOV-1995 (Rel. 32, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update)
CALLATOSTATIN 4 (LEU-CALLATOSTATIN 4).
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"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997)
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                                                                                                                                                                                                                                                     "Callatostatins: neuropeptides from the blowfly Calliphora with sequence homology to cockroach allatostatins."; proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
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Duve H., Thorpe A.
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                                                                                                                                                                         "Distribution and functional significance of Leu-callatostatins
                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
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Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto |
"WMamide-1, -2 and -3: novel neuromodulatory peptides iss
ganglia of the African glant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
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MOD_RES 7 7 7
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Achatinacea; Achatinidae;
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Achatinacea; Achatinidae; Achatina.
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P81818;
30-MAY-2000 (Rel. 39, Created)
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CARCINUSTATIN 15.
Carcinus maenas (Common shore crab) (Carcinus maenas (Common shore crab) (Carcinus maenas (Common shore crab)
                                                                                                                          "Isolation and identification of multiple neuropepti allatostatin superfamily in the shore crab Carcinus Eur. J. Biochem. 250:727-734(1997).
-I- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEURO-I-SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY. Neuropeptide; Amidation; Multigene family.
MOD_RES 8

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AMIDATION.
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01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.

NCBI_TaxID=6759;
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MEDLINE=93365912; pubMed=8495720;
MEDLINE=93365912; pubMed=8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto
"WWamide-1, -2 and -3: novel neuromodulatory peptides is
ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
PIR; S33244; S33244.
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata;
Achatinacea; Achatinidae; Achatina.
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AL14_CYDPO
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ALC4_LEUMA
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FARP_CARMA
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CON1_PETMA
GON1_PETMA
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TKNB_CANCA
UR2A_CATCO
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O63721 rattus norv
P72345 pseudomonas
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Ogbota homo sapien
P97889 rattus norv
O67605 squash leaf
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O44693 bacillus am
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SEQUENCE 23 AA; 2638 MW; AF86888FEF8029F8 CRC64;
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Čhordata; Cranlata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canldae;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
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MEDLINE=94198820; Pubmed~8185738;
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Best Local Similarity 100.
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-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENEATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
-!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                 MEDLINE-91123196; PubMed-1846858;
Inoue N., Uchida H.;
"Transcription and initiation of ColEl DNA replication in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Archosauria; Aves; Neognathae; Passeriformes; Sturnidae; Toxostoma.
NCBI_TaxID=99878;
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site-
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Zink R.M., Blackwell-Rago R.C.;
"Species limits and recent population history of the Curve-billed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                               MEDLINE-89210827; PubMed-3149585;
Stirling C.J., Szatmari G., Stewart G., Smith M.C., Sherratt
"The arguine repressor is essential for plasmid-stabilizing
specific recombination at the ColEl cer locus.";
EMBO J. 7:4389-4395(1988).
                                                                                                                                                         Chan P.T., Ohmori H., Tomizawa J., LeBowitz J.;
"Nucleotide sequence and gene organization of ColEl DNA.";
J. Biol. Chem. 260:8925-8935(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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EMBL; J01566; AAB59139.1; -.
                                                                                                                                              PubMed=2991225;
                                                                                                                                                                                                                                                                                                                                                                                                                                     56 AA; 6254 MW;
01-NOV-1996 (TrEMBLrel. 01, 01-MAY-1999 (TrEMBLrel. 10,
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Matches 4; Conserv
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                                          Escherichia coli.
                                                                                                 NCBI_TaxID=562;
                                                         Plasmid ColE1
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Leishmania major.
Eukaryota: Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID-5664;
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Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
NCBI_TaxID=6290;
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Blouin M.S., Yowell C.A., Courtney C.H., Dame J.B.;
"Substitution bias, rapid saturation, and the use of mtDNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
InterPro; IPR000179; Cyt_b_b6.
Pfam, PF00033; cytcotnome_bb. 1.
PROSTIE; PS00192; CYTCOTHROME_B.HEME; 1.
Electron transport; Heme; Mitochondrion; Respiratory chain;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
01-0CT-2000 (TREMBLrel. 15, Last annotation update)
POSSIBLE PROBABLE ECF-FAMILY SIGMA FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NADH DEHYDROGENASE SUBUNIT 4 (FRACMENT).
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100.0%; Pred. No. 2.3e+03;
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InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; Oxidored_q1; I.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
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-1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-1- COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

-1- SUBMIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.

EMBL: U86819; AAD12338.1; --

Interpre, PROTEIN (BY SIMILARITY).
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                           Barrell B.;
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                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                          Steppan S.J.; "Phylogenetic relationships and species limits within Phyllotis (Rodentia: Sigmodontinae): concordance between mtDNA sequence and morphology.";
                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00032; cytcohrome_bc; 1.
Pfam; PF00033; cytcohrome_bc; 1.
PROSTTE; PS00193; cytochrome_b_N; 1.
PROSTTE; PS00193; cytochrome_b_Nems; 1.
PROSTTE; PS00193; cytochrome_B_QO; UNKNOWN_1.
Transmembrane.
                                                                                                               37.5%; Score 3; DB 5; Length 271; 100.0%; Pred. No. 3.7e+03; ive 0; Mismatches 0; Indels
                       Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL390935; CAC00895.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                               271 AA; 30356 MW; B59E63D2D321EFF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCEAF9D0DBED2771 CRC64;
                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8; Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                        Phyllotis darwini (Darwin's leaf-eared mouse).
                                                                                                                                                                                                                                           290 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 3; DB 8;
; Pred. No. 3.9e
0; Mismatches
                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                            PRT;
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100.0%; Pre
0; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 290
290 AA; 32572 MW;
                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                 CYTOCHROME B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammal. 79:0-0(1998).
                                                                    271
                                                                                                   Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-UNM NK27558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
SEĞUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     Phyllotis.
NCBI_TaxID=56232;
              STRAIN-FRIEDLIN;
                                                                   271
                                                                                                                                                                                                                                                                                                                                    Mitochondrion.
                                                                                                                                                                        1111
154 SFXG 157
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                                                                                                                                                             5 sfxg 8
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                                                                    NON_TER
SEQUENCE
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NON_TER
SEQUENCE
                                                        NON_TER
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COMPLEX (COMPLEX II OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COMPLEX (COMPLEX II OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
C1-COPACTOR: TWO HEME GROUPS (BSZ AND BSS6) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
C1-COPACTOR: THE MAIN SUBMITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
C1-SIBUNIT: THE MAIN SUBMITS OF COMPLEX B-C3
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
C1-SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
REMBL: AF089009; AFF02229.1.
R FALLS (CYTOCHROME B-C): 1.
R FALLS (CYTOCHROME B-C): 1.
R FALLS (CYTOCHROME B-LHEME; 1.
R PROSITE; PS00193; CYTOCHROME B-HEME; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                  Lanyon S.M., Omland K.E.; "A molecular phylogeny of the blackbirds (Icteridac): flve lineages
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passerlformes; Icteridae; Agelalus.
NCBI_TaxID-044775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Fringillidae;
Emberizinae; Habia.
                                                                                                                                                                                                                                                                                                                                                                                                                       revealed by cytochrome-b sequence data.";
Auk 116:629-639(1999).
-:- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biogeography of a diverse radiation of neotropical birds."; Mol. Phylogenet. Evol. 8:334-348(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33128 MW; 8B62C22B82EE2ED5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.5%; Score 3; DB 8; L
100.0%; Pred. No. 4e+03;
Live 0; Mismatches 0
Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347 AA.
                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-98086775; Pubmed-9417892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       063418;
01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2001 (TrEMBLrel. 17, CYTOCHROME B (FRAGMENT).
                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                         CYTOCHROME B (FRAGMENT)
                                                                                                                                                                           Agelaius ruficapillus.
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297
297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 SFXG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Habia rubica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 sfxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
NON_TER
SEQUENCE
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37.5%; Score 3; DB 5; Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
NON_TER 1
NON_TER 385 38
SEQUENCE 385 AA; 4
                                                    Mammalia; Eutheria;
Spermophilus.
                                                                                                                                                                                                                                                                                                                                                              379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leishmania major.
                                                                           NCBI_TaxID=99840;
                                                                                                                                   Boqdanowicz S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 SFXG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                            5 sfxg 8
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LM12.753
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Q9GWR8
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0
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                                                              -!- COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).
-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RESKE PROTEIN (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.
EMBL; AF006233; AAC05054.1; -.
InterPro; IPR000179; CYL_D.66.
InterPro; IPR001609; Galanin.
Pfam; PF00033; CYTOCHROME_D.C; 1.
Pfam; PF00033; CYTOCHROME_D.C; 1.
PRINTS; PR0073; GALANIN.
PROSITE; PS00193; CYTOCHROME_B.QO; UNRNOWN.1.
Electron transport; Heme; Mitochondrion; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; ALL60371; CAC00227.1; -. NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBL_TaxID=5664;
          COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYMHESIS (BY SIMILARITY).

CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2
FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
POSSIBLE 75 KDA INVARIANT SURFACE GLYCOPFOTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 353;
                                                                                                                                                                                                                                                                                37.5%; Score 3; DB 8; Length 347; 100.0%; Pred. No. 4.5e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38247 MW; 3E427E2171CC7F24 CRC64;
                                                                                                                                                                                                                                                 347 AA; 38616 MW; 81208E4E94D37A8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Len . 4.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                           353 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.5%; Score 3; DB 5
100.0%; Pred. No. 4.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                  Query Match 37.5
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353
                                                      FERROCYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
'-haq 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-FRIEDLIN;
                                                                                                                                                                                                                              Fransmembrane.
                                                                                                                                                                                                                                                                                                                                                    107 SFXG 110
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01-MAY-2000 (
01-JUN-2001 (
                                                                                                                                                                                                                                                                                                                              5 sfxg 8
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                                                                                                                                                                                                                                      NON_TER
SEQUENCE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09TF74
C9TF74;
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Q9TF74
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"A molecular phylogeny of ground squirrels and prairie dogs.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- EUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAN GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
-!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Buğlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В.
                              Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOUND TO THE PROTEIN (BY SIMILARITY).

-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,

CYTOCHROME IL AND THE RIESKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B/B6 FAMILY.

EMBL, AF157875; AAD50159.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell
Oliver K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Electron transport; Heme; Mitochondrion; Respiratory chain; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.5%; Score 3; DB 8; Length 379; 100.0%; Pred. No. 4.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
Spermophilus erythrogenys (red-cheeked ground squirrel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL390114; CAC02470.1; -. InterPro; IPR001522; Desaturase. PRINTS; PR00075; FADDSATRABE. PRODOM; PD02221; Desaturase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42795 MW; B0C35BAFE3118854 CRC64;
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                                                                                                                                                                                                                                                                                                                             Harrison R.G., Sherman P.W., Yensen E., Hoffmann R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UDW-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 43.0 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000179; Cyt_b_b6.
Pfam; PF00032; Cytcohrome_b_c; 1.
Pfam; PF00033; Cytcohrome_b_N; 1.
PROSITE; PS00192; CYTOCHROWE_B_HENE; 1.
PROSITE; PS00193; CYTOCHROME_B_QO; UNKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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THE DIMEN (BY SIMILARITY).

THE DIMEN (BY SIMILARITY).

-1- SUBJUNIT: HOMODIMEN (BY SIMILARITY).

-1- SUBJUNIT: HOMODIMEN (BY SIMILARITY).

-1- SUBJUNIT: HOMODIMEN (BY SIMILARITY).

-1- SIMILARITY: TO THE ENDLASE FAMILY.

REMBL; AF6025805; AR887890.1; -.

R FSP; P5625; IPDZ.

R FSP; P5625; IPDZ.

R FSP; P5632; IPDZ.

R FRYBASE; PSP00031296; DDSE\DO.

R FNORT; PR00141; Enolase.

R PF00113; enolase: 1.

R PROSTIE; PS00164; ENOLASE: 1.
                          Gaps
                                                                                                                                                                                                                                                                            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO LARGE SUBUNIT).
                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENOLASE (EC 4.2.1.1) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
Genetica 0:0-0(1997).
-I- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE - PHOSPHOENOLPYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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0
                                                                                                                                                                                                                                               Drosophila pseudoobscura (Fruit fly).
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 413;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44404 MW; 11414BCC18644A94 CRC64;
           4.9e+03;
hes 0;
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                                                                                                                                              413 AA.
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Pred. No. 5.1
0; Mismatches
                       Mismatches
           Pred. No.
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                                                                                                                                             PRT;
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100.0%; Pre
0;
100.08; Pie
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NON_TER 1 1
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                       Conservative
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                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 AA;
      Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                        Ephydroidea; Dros
NCBI_TaxID=7237;
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247 SFXG 250
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360 SFXG 363
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                                                5 sfxg 8
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NON_TER
SEQUENCE
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Q9TID6
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whitten M., Williams N.H., Chase M.W.;
"Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with
special emphasis on Stanhopeinae: Combined molecular evidence.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF239478; AAK31875.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Asparagales, Orchidaceae, Epidendroideae, Maxillarieae, Stanhopelnae,
                                                                                                                                                                                                                                                                                                                                                                                ö
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Ericaceae; Pieris.
NCBI_TaxID=49157;
                                                                                                                                                                                                                                                                                    PROSITE: PSOULT: RUBISCO_LARGE: 1.
Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase; Oxidoreductase; Photorespiration; Photosynthesis.
SEQUENCE 475 AA; 52495 MW; 76F3CAOB4364B1C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                          Length 475;
                                                                                                                                                                                                                                                                                                                                                         37.5%; Score 3; DB 8; Length 475; 100.0%; Pred. No. 5.7e+03; 1.ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.5%; Score 3; DB 8; Length 510;
100.0%; Pred. No. 6e+03;
.ive 0; Mismatches 0; Indels
                                                          Kron K.A., Judd W.S., Crayn D.M.;
"Phylogenetic analyses of Andromedeae (Ericaceae subfam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61288 MW; C70C056B44F26B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                RuBisCO_large.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gongora gratulabunda
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510
510 AA;
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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                                                 SEQUENCE FROM N.A.
                                                                                  Vaccinioideae).";
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                           61 SFXG
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NON_TER
SEQUENCE
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707 AA;
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                                                                                                                                       664 SFXG 667
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| 503 KXXSF
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Q9MVG6
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Q9MVF7
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                                                                                                                        δ
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                                                                                                                                                                                                                             Whitten M., Williams N.H., Chase M.W.;
"Tribal and subtribal relationships of Maxillarieae (Orchidaceae) with special emphasis on Stanhopeinae: Combined molecular evidence."; submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF239484; AAK31881.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olmstead R.G., Reeves P.A.;
Ann. Mo. Bot. Gard. 82:176-193(1995).
-!- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.
-!- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS CHAINS.
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                            Directory Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Epidendroideae; Maxillarieae; Stanhopeinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Scrophulariaceae; Nicodemia.
NCBI_TaxID=28500;
                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                               Score 3; DB 8; Length 510;
Pred. No. 6e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  61361 MW; B03CD0D32738AAB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NADH DEHYDROGENASE SUBUNIT (FRAGMENT).
                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              698 AA
                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, L36405; AAA84496.1; -.
Mendel; 2471; Nicdi;ndhF;2471.
InterPro; IPR001064; Crystallin.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR0012128; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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PF01010; oxidored_q1_C; 1.
                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                 37.5%; £ 100.0%;
                                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicodemia diversifolia.
                                                                                                                                                                                                                                                                                                         510
                                                                                                                        MATURASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                         510 5
510 AA;
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                            Gongora sphaerica.
Chloroplast.
                                                                                                                                                                                                      NCBI_TaxID=125126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                    346 SFXG 349
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                                                                                                                                                                                                                                                                                                                                                                                       5 sfxg 8
sfxg 8
                                                                                                                                                                                                                                                                                               NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                              Gongora.
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                                                                                Q9BAX0;
                                                                       09BAX0
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Pfam;
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Q32665
                                                   RESULT
                                                              Q9BAX0
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SEQUENCE FROM N.A.
Alverson W.S., Whitlock B.A., Nyffeler R., Bayer C., Baum D.A.;
Alverson W.S., Whitlock B.A., Nyffeler R., Bayer C., Baum D.A.;
Phylogeny of the core Malvales: evidence from ndhF sequence data.";
Am. J. Bot. 86:1459-1471(1999).
-!- CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.
-!- SIMILARITY: TO NADH-UBLQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Muntingiaceae; Muntingia.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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0
                                                                                                                                                                                                                  Length 698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                      79217 MW; F4B4EBE4E7440A3D CRC64;
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ODMUGGS,
ODMUGGS,
OL-OCT-2000 (TrEMBLrel. 15, Created)
OL-OCT-2000 (TrEMBLrel. 15, Last sequence update)
OL-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NDH-PDHYDROGENASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-00T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                 DB 8; Le.,
Pfam; PF00662; oxidored_q1_N; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
Chloroplast; NAD; Oxidoreductase; Plastoquinone.
NON_TER 1 1
NON_TER 698 698
SEQUENCE 698 AA; 79217 MW; F4B4EBE4E7440A3D CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001750; Oxidored_q1.
InterPro; IPR002128; Oxidored_q1.
InterPro; IPR002128; Oxidored_q1_C.
InterPro; IPR003151; Oxidored_q1_N.
Pfam; PF01010; Oxidored_q1; 1.
Pfam; PF01010; Oxidored_q1_C; 1.
Chloroplast; NAD; Oxidored_q1_N; 1.
Chloroplast; NAD; Oxidored_q1_N; 1.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.5%; Score 3; DB 8; Le 100.0%; Pred. No. 7.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     707 AA
                                                                                                                                                                                                                     37.5%; Score 3; DB E 100.0%; Pred. No. 7.6 Live 0; Mismatches
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nes 5; Conservative
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Matches 4; Conservative
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Gaps

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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
                                                              SEQUENCE FROM N.A.

BEDLINE-81069885; PubMed-6254986;
Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
"Assembly of the mitochondrial membrane system. Structure and nucleotide sequence of the gene coding for subunit 1 of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycotes;
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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                    Saccharomycetales; Saccharomycetaceae; Saccharomyces
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PHOSPHODIESTERASE 10A7 (PDE10A7) (FRAGMENT).
HSPDE10A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 8 AA; 1019 MW; 4E21A9C449D5B73B CRC64;
                                                                                                                                                                                                                       7 AA; 859 MW; 75B7232362CDC460 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AA.
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                                                                                                                                       cytochrme oxidase..;
J. Biol. Chem. 255:11927-11941(1980).
EMBL, V00694; CAA24066.1;
NON_TER. 1
SEQUENCE 7 AA; 859 MW; 75B7232362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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SGD; S0003988; GIN11.
NON_TER 1
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Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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                                 NCBI_TaxID-4932;
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                                                         Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Luehea.
NCBI_TaxID=45194;
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Bacteria; Cyanobacteria; Chroococcales; Cyanothece.
NCBI_TaxID=41431;
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF003700; AAC35193.1; -.
NON_TER
SEQUENCE 7 AA, 849 MW; 7412C72AA9D5B030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 7;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
INSIDE INTRON 5 (FRAGMENT).
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUG-1998 (TrEMBLrel. 07, Last annotation update)
NIFK (FRAGMENT).
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Pfam; PF01010; oxidored_q1; 1.
Pfam; PF00662; oxidored_q1_N; 1.
Chloroplast; NAD; Oxidored_q1_N; 1.
717 717 717
SEQUENCE 717 AA; 81293 MW; DF845EF5B33D64A7
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Pred. No. 7.8e+03;
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; Pred. No. 4.76
0; Mismatches
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InterPro; IPR001750; Oxidored_q1.
InterPro; IPR002128; Oxidored_q1_C.
InterPro; IPR001516; Oxidored_q1_N.
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100.0%; Pre
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Best Local Similarity
Matches 2; Conserv
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469 KXXSF 473
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Best Local Similarity
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                                                    Fujishige K., Kotera J., Yuasa K., Omori K.;
"The human phosphodiesterase PDE10A gene. Genomic organization and evolutionary relatedness with other PDEs containing GAF domains.";
Eur. J. Biochem. 267:5943-5951(2000).
EMBI, ABO41779; BAB16368.1; -.
NON_TER B BSEQUENCE 8 AA; 966 MW; FD4B19D5A6C76446 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.; "Isolation and structural elucidation of eight kinins from the retrocerebral complex of the American cockroach, Periplaneta
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KININ-1 (PEA K-1).
Periplaneta americana (American cockroach).
Periplaneta americana, Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Blattoidea; Blattidae; Periplaneta.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KTNIN-2 (PEA-K-2).
Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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8 AA; 950 MW; 326365B449D5A774 CRC64;
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MEDLINE=98010462; Pubmed=9350979;
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100.0%; Pic
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MOD_RES 8 8
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                                                                                                                                                       Query Match
Best Local Similarity
Matches 2; Conserv
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Matches 2; Conserv
                               SEQUENCE FROM N.A.
         NCBI_TaxID=9606;
                                           PubMed=10998054;
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Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
"Isolation and structural elucidation of eight kinins from the
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KININ-3 (PEA-K-3).
Periplaneta americana (American cockroach).
Eukaryota: Mertazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neopters; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retrocerebral complex of the American cockroach, Periplaneta
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-!- PUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).
-!- SIMILARITY: BELONGS TO THE KININ FAMILY.
                                                                                                                                                                                                                                        Regul. Pept. 71:199-205(1997).
-i- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                 AMIDATION.
DC6365A5B9D5BDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AA; 909 MW; DC6365B449D5A76A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2; DB 5; Len; Pred. No. 4.7e+05;
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                                                                                                                                                                                                                                                                                        (MYOTROPIC ACTIVITY).
-!- SIMILARITY: BELONGS TO THE KININ FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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100.0%; Pred. No.
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Blattoidea; Blattidae; Periplaneta.
NCBI_TaxID=6978;
                                                                                                 TISSUE=CORPORA CARDIACA;
MEDLINE=98010462; PubMed=9350979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                     Neuropeptide; Amidation. MOD_RES 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-CORPORA CARDIACA;
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                                                                        SEQUENCE, AND FUNCTION
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Word size :

Searched:

Sequence:

Database :

1004321

Result Š

OM protein

Run on:

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Hyphozyma sp. strains CBS 648.91; phospholipase; fatty acyl; hydrolyse; oil degumming; wheat starch hydrolysate; breadmaking; dough.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "believed to be a glycosylated Asn residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyphozyma sp. strain CBS 648.91 phospholipase fragment #8.
                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                           AAG72750
AAG72752
AAY76127
                                                                      AAW48932
AAR8242
AAR8243
AAY05839
AAR405842
AAR4256
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AAP71285
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                  AAB6379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW62083 standard; peptide; 31 AA.
97WO-DK00490
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AAW62083
2224
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H. pylori cytoplas
Human colon cancer
Interleukin-13 bin
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Staphylococcus aur
                                                                     (without alignments)
7.281 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             нурьогута sp.
                                                             ; Search time 81.39 Seconds
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                               522463 segs, 74073290 residues
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                                                            January 14, 2002, 07:56:29
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    protein search, using sw model

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AAW77559
AAY12820
AAG76222
AAM40785
AAB21195
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AAB53916
AAW56254
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Gapop 60.0 , Gapext 60.0
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40 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        5 sfxg 8
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                                                                                                                                                                                                                                                                                                                                   components.
 Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW77559;
                                                                                                                                                                                                                                                                                                                                                         Sequence
            Duan RD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW77559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
 Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a new phospholipase peptide fragment, from strain CBS 648.91 of a Hyphozyma. The phospholipase can hydrolyse both fatty acyl groups in a phospholipid (PL), has an optimum temperature about 50 degrees Celsius (measured for 10 min at pH 34) and optimum pH about 3 (measured at 40 degrees Celsius for 10 min). The phospholipase is used to hydrolyse acyl groups in (lyso)PL, particularly (lyso)lecithin. Specifically it is used: (a) to improve filterability of aqueous solutions or slurines of carbohydrate origin (especially wheat starch hydrolysate) containing PL; (b) in breadmaking (added to the dough) to improve elasticity; and (c) to reduce PL content (degum) in edible oils. The phospholipase lacks lipase activity and is effective at very low PH, so does not cause enzymatic/alkaline hydrolysis of triglycerides. It is not membrane bound so can be produced and purified on a commercial
                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein; gene therapy; cancer; tumor; fetal deficiency; neurodegenerative disorder; developmental abnormality; blood disorder; immune system disease; autoimmune disease; leukemia; inflammation;
                                             phospholipase from Hyphozyma strain and related DNA - hydrolyses a expl residues in phospholipid, useful for degumming edible s, and to improve dough quality or filterability of carbohydrate
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     allergy; Alzheimer's disease; cognitive disorder; schizophrenia; obesity; osteoporosis; arthritis; infection; AIDS; diabetes; asthma; connective tissue disorder; transplant rejection; sepsis; acne; psoriasis; cardiovascular disorder; reproductive disorder; food additive; food preservative; storage capability.
                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                            Length 31;
                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide sequence derived from a human secreted protein.
                                                                                                                                                                                                                                                                                                                                            37.5%; Score 3; DB 19; Le
100.0%; Pred. No. 4.2e+02;
iive 0; Mismatches 0;
 ż
  Tsutsumi
  Stringer MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY40039 standard; Peptide; 40 AA.
                                                                                                         Claim 3; Page 18; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0076051.
98US-0076052.
98US-0076053.
98US-0076054.
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                                                                                                                                                                                                                                                                                                                                                                    Conservative
 Hasida M,
                        WPI; 1998-272208/24.
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                             AA;
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26-FEB-1998;
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Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-SEP-1999
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                                                                      oils, and
                                                         both acyl
                                                                                                                                                                                                                                                                                                             Sequence
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AAY40001-92 are derived from human secreted proteins. The

polynucleotides and their corresponding secreted polypeptides are useful

for preventing, treating or ameliorating medical conditions, e.g. by

protein or gene therapy. Pathological conditions can also be diagnosed by

determining the amount of the new polypeptides in a sample or by

cetermining the presence of mutations in the polynucleotide. Specific

uses include developing products for the diagnosis or treatment of

cancer, tumors, neurodegenerative disorders, developmental abnormalities

and fetal deficiencies, blood disorders, sepsis, diseases of the immune

system, autoimmune diseases, inflammation, allergies, Alzheimer's and

cognitive disorders, schizophrenia, obesity, osteoporosis, arthritis,

infections, AlDS, connective tissue disorders, transplant rejection,

diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,

and reproductive disorders. The polypeptides or polynucleotides can

also be used as food additives or preservatives, such as to increase

or decrease storage capabilities, if at content, lipid, protein,

carbohydiate, vitamins, minerals, cofactors or other nutritional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus protein; immune response induction; eye infection;
                                                                                                                                                                                     New human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Rosen CA;
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Ruben SM,
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Ebner R,
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 39; 246pp; English.
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Brewer LA,
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    Florence K,
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                                                                                                                                                                                                                           This sequence represents a Staphylococcus aureus protein of unknown function, and is encoded by a DNA sequence of the invention. The DNA sequences of the invention. The DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, contral nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytckine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemocactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                               New nucleic acid sequences from Staphylococcus aureus WCHU29 - useful in vaccines and for treatment of bacterial infections of e.g. respiratory tract and central nervous system
                                                                  Rosenberg M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                 especially useful in the treatment of H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.5%; Score 3; DB 19; Length 42; 100.0%; Pred. No. 5.1e+02; ive 0; Mismatches 0; Indels
                                                     Knowles DJC;
Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lacroix B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted protein SEQ ID NO:410.
                                      Black MT, Burnham MKR, Hodgson JE,
Lonetto MA, Nicholas RO, Pratt JM,
Ward JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duclert A, Dumas Milne Edwards J,
                                                                                                                                                                                                      Claim 11; Page 252; 390pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY12820 standard; Protein; 58 AA.
          (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-IB01231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                       WPI; 1998-252940/23.
N-PSDB; AAV53359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEST ) GENSET
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34 sfxg 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 5' EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9906549-A2
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                                                                                                                                                      AAX51459 to AAX51691 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY12681 to AAY12913, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They proteins obtained may have cytokine activity, cell products and therapy. The proliferation/differentiation activity, hemmatopolesis regulating activity, tissue growth regulating activity, rememberatic/ chemokinetic activity, hemmatory activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forenace, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                        New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from testis, ovary, uterus and spleen tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 58;
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100.0%; Pred. No. 6.2e+02;
iive 0; Mismatches 0;
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                                                                                                                       Claim 34; Page 465; 522pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG76222 standard; Protein; 84 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0157137.
99US-0163280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-2000; 2000WO-US26524.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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1999-153779/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-235357/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 AA;
                   N-PSDB; AAX51598
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03-NOV-1999;
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N-PSDB; AAI59941
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                                                                                                           The invention
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26-JAN-1999;
26-JAN-1999;
26-JAN-1999;
01-FEB-1999;
01-FEB-1999;
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| 78 sfxg 81
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11-FEB-1999;
11-FEB-1999;
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                                                       therapy and vaccine production. N and P may be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                     AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang D;
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                         present invention. N.B. pages 7053 of the sequence listing were N.B. pages 666 to 682 and page 7053 of the sequences listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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Zhang J;
                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                      Length 84;
                                                                                                                                                                                                                                                                                                                             0; Indels
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Yang Y,
                                                                                                                                                                                                                                                                                                     37.5%; Score 3; DB 22; Le
100.0%; Pred. No. 7.8e+02;
ive 0; Mismatches 0;
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
Claim 11; Page 8423-8426; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM40785 standard; Protein; 114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polypeptide SEQ ID NO 5716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0693036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                   84 AA;
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09-JUL-2000;
19-JUL-2000;
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Zhao QA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiallergic; antiasthmatic; nootropic; neuroprotective; anticonvulsant; vulnerary; asthma; inflammation; allergy; Chôdiak Higashi syndrome; CHS; Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes; digestion disorder; wound healing disorder; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exocytosis pathway protein; Exo protein; antiparkinsonian; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders
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                                                                                                                                                                                                          Example 2; SEQ ID NO 5716; 10078pp; English.
                                                                                                                                           such as central nervous system injuries
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990S-0118179.
990S-0119286.
990S-0119998.
990S-0119759.
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99US-0117308.
99US-0117309.
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Best Local Similarity
2001-442253/47.
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WPI; 1997-298052/27.
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                                                                                                                                                                                                                                                                                                Sequence
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Exc proteins and their agonists and antagonists are useful in the diagnosis, treatment or prevention of exocytosis-mediated disorders cuch as asthma, inflammation, allergies, Chediak-Higashi Syndrome (CHS), Alzheimer's disease, Parkinson's disease, Huntington's disease, The nucleic acids, antagonists or agonists of Exc proteins are useful in gene therapy. The nucleic acids are also useful for generating transgenic or knock-out animals which can be used in the care of the companion of therapeutically useful reagents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                 New nucleic acids encoding Exo proteins which are useful in the diagnosis, treatment or prevention of exocytosis-mediated disorders such as asthma, inflammation and allergies
                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                            Score 3; DB 21; Length 115;
Pred. No. 9.5e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     37.5%; Score
100.0%; Pred. No. 5...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. pylori cytoplasmic protein 24039587.aa.
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/note- "encoded by AAW"
                                                                                                                              Disclosure; Page 167; 305pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW20281 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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95US-0487032.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
          (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori.
                                                  WPI; 2000-482908/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 115
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
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                                                               N-PSDB; AAA89574
                                                                                                                                                                                                                                                                                                                                                                                                                     107 sfxg 110
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                       5 sfxg 8
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                                                                                                                                                                                                                                                                                                                              Seguence
                               Luo Y;
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This sequence is a H. pylori cytoplasmic protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial by machine and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be production H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                               Helicobacter pylor1 nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylor1 infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition.
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100.0%; Pred. No. 1e+03;
ive 0; Mismatches 0; Indels
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Mellgaerd BL;
                                                                                                                                                                                                                                                                                               Claim 61; Page 482; 1481pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW24625 standard; Protein; 129 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
Smith D,
                                                              WPI; 1997-052306/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                    N-PSDB; AAT67763
Berglindh OT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 sfxg 116
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09-185908-1c.oligo.rag

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WPI; 2000-587534/55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 sfxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW56254;
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Matches
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  δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pMPX vectors to construct a series of shotgun subclone libraries. The purified DNA samples were then
                                                                                                                                                                                          Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA mass isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The ORF/protein reference number for this sequence was obtained from the related specification, WO9640893.
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                                                   Helicobacter pylori nucleic acid sequences and related proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; colon cancer; colon cancer antigen; diagnosis; detection; diadentification; cytostatic; cardioactive, neuroprofective; vulner immunomodulatory; muscular; gynaecological; gastrointestinal nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; refroductive cardiovascular disorder; cardiovascular disorder;
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                                                                                                                                                                     This sequence is a H. pylori cytoplasmic protein. Helicobacter pylori has been strongly linked to c duodenal ulcer disease. The nucleic acid sequenc
                                                                           used for diagnostics and therapeutics
                                                                                                                    Claim 10; Page 129; 1481pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 sfxg 8
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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have expostatic, cardiacative, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, culnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, and treatment and diagnosis of colon disorders, such as colon cancer. The colon disorders, such as colon cancer. The colon disorders and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune diseases, and cardiovascular disorders, renal disorders, infectious diseases, and cardiovascular disorders, renal disorders, infectious diseases, and cardiovascular disorders and the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                               Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                         Claim 11; Page 2017; 2104pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Unknown
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nes 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 AA;
N-PSDB; AAC98673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1111
135 sfxg 138
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antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                  Example 1; Page 592-593; 799pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burnham MK,
Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toxic shock syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-424969/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT84187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 sfxg 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9730070-A1
                                                                                                                                                                                                                                                                                                                                                                         e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 sfxg B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pratt JM,
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW28289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The IL-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one IL-13 activity. They can be used for treating IL-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered IL-13 after IL-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autolmmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gastric cancer associated antigen protein sequence SEQ ID NO:870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                     New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as asthma or for diagnosis or detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast cancer; gastric cancer; prostate cancer; diagnosis; associated antigen; cytostatic; cancer vaccine.
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Pred. No. 1.18+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         2hang
                                                                                                                                                                                                                                                                      Simpson RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB63508 standard; Protein; 174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 45-48; 69pp; English
                                                                                                                                                                                                                      (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.5%; Sc
Best Local Similarity 100.0%; P.
Matches 4; Conservative 0;
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99US-0153454.
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                                                                                                                                             97AU-0005374
96AU-0002262
                                                                                                  97WO-AU00591
                                                                                                                                                                                                                                                                      Hilton DJ, Nicola NA,
                                                                                                                                                                                                                                                                                                                 WPI; 1998-207062/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA;
                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV22697
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10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
WO9810638-A1
                                                                                                                                                  27-FEB-1997;
                                                                                                  10-SEP-1997;
                                                                                                                                                                      10-SEP-1996;
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                                                  19-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer
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represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB6323 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic accids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used to isolate antimicrobial compounds, and in vaccines against S. aureus infection
                                                                                                                                                                                                                                                                               Gaps
AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicholas RO;
                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                         Length 174;
                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of an encyl-acyl carrier protein.
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Ward JM;
                                                                                                                                                                                                                                         37.5%; Score 3; DB 22; Lc
100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "encoded by ANT"
Misc-difference 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encoded by NTG"
Misc-difference 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encoded by CNG"
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, Rosenberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW28289 standard; Protein; 194 AA.
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4; Conservative
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                                                                                                                                         Best Local Similarity
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Best Local Similarity
                                                                     AĄ;
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                                                                                                                                                                                                              1111
214 sfxg 217
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                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2001
                                  e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-APR-2001.
                                                                                                                                                                                            5 sfxg 8
                                                                                                                                                                                                                                                                                                                                                      AAG72280;
                                                                     Sequence
                                                                                                                        Query Match
                                                                                                                                                         Matches
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AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate cancer associated antigen protein sequence SEQ ID NO:1153.
                                           The present sequence represents a Staphylococcus aureus protein, that, based on homology with an E. coli protein, is believed to be an enoy1-acyl carrier protein. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding breast, gastric and prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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0
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                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                    Score 3; DB 18; L. Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
            Claim 6; Page 586-587; 989pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                    37.5%; ;
100.0%;
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99US-0153454.
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                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-025274/03
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 sfxg 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                        5 sfxg 8
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                                                                                                                                                                                                                                                                                                    Sednence
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acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation.
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                                                                                                                                                                                                                                      Length 217;
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                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                         DB 22;
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                                                                                                                                                                                                                                         37.5%; Score 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG72280 standard; Protein; 229 AA.
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(YEDA ) YEDA RES & DEV CO LTD.
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24-FEB-2000; 2000US-0184809.
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                                                                                                                                                                                                                                                                                                             Conservative
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17
                    Matches
                                        S
                                                          a
                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/Ainhibin activity, cancer diagnosis and therapy, drug screening, assays, for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed
                                                                                                                                                       nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                Wang D;
                                                                                                                                                                 peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Hemenstatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemctactic; chemckinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acids and polypeptides, useful for treating disorders is central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                              en R, Ma Y, (
u C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Chen R,
                                                                    AAM41776 standard; Protein; 297 AA
                                                                                                                                   Human polypeptide SEQ ID NO 6707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Asundi V,
Wang Z, Wehrman T,
Zhou P, Goodrich R
                                                                                                                                                                                                                                                                                                                                           2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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2000US-0598042.
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                                                                                                             22-OCT-2001 (first entry)
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N-PSDB; AA160932.
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183 sfxg 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification
                                                                                                                                                                                                                              Homo sapiens.
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09-JUL-2000;
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03-AUG-2000;
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8
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                                                                                                                                                                                                          Leukaemia.
5 sfxg
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                                                                                          AAM41776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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The present sequence is a polypeptide from the human olfactory receptor data exploratorium (HORDE). It was used as a query sequence in a database search of olfactory receptor (OR)-like sequences. The invention relates to isolated polynucleotides encoding polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory sensation. The polynucleotides can be used in screening for olfactory primary scents and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This chables the construction of a scent representation (also called a scent ingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
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                 Length 297;
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                       DB 22; LG . 1.7e+03;
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                       Score 3; DB 22
Pred. No. 1.76
0; Mismatches
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37.5%; Sco.
100.0%; Pre
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(YEDA ) YEDA RES & DEV CO LTD.
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2000US-0184809.
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                                                                                Conservative
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                       Query Match
Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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                                                                                                                                                                                        256 sfxg 259
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24-FEB-2000;
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5 sfxg 8

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AAY76127 standard; Protein; 354 AA.

foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; therapy.

Human; secreted protein; cancer; tumour; developmental abnormality;

Human secreted protein encoded by gene 4.

(first entry)

23-MAR-2000

AAY76127;

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The present sequence is a polypeptide from the human olfactory receptor data exploratorium (HORDE). It was used as a query sequence in a database search of olfactory receptor (OR)-like sequences. The invention relates to isolated polynucleotides encoding polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory sensation. The polynucleotides can be used in screening for olfactory primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of cetect these primary scents. The methods also enable determination of cetect these primary scents. The methods also enable determination of cetect these primary scents. The methods also enable determination of secondary scents are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent ingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties of different
                                                                                                                                                                                                           Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2434.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yanai I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sensation for identifying olfactory agonists and antagonists
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100.0%; Pred. No. 1.8e+03;
tive 0; Mismatches 0;
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                                                                                                   AAG72752 standard; Protein; 312 AA.
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2000US-0184809.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  WO200127158-A2
              167 sfxg 170
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                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                      AAG72752;
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98US-0085920. 98US-0085921. 98US-0085922. 98US-0085923.

12-MAY-1998 12-MAY-1998 18-MAY-1998 18-MAY-1998 18-MAY-1998 18-MAY-1998 18-MAY-1998 18-MAY-1998 18-MAY-1998

98US-0085105. 98US-0085180. 98US-0085906

99WO-US09847

06-MAY-1999;

12-MAY-1998 .2-MAY-1998

18-NOV-1999.

Homo sapiens. WO9958660-A1. 98US-0085924. 98US-0085928. 98US-0085925. 98US-0085927.

18-MAY-1998; 18-MAY-1998;

(HUMA-) HUMAN GENOME SCI INC

Ruben SM,

Olsen

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human genes. The genes and their corresponding secreted by the 97 human genes. The genes and their corresponding secreted by the 97 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliocrating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developing products for the and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences shown in AAY76224 to AAY76424 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                              New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 358-359; 475pp; English.
                                                                                                                      Ebner R;
Florence K, Ni J,
Shi Y, Young PE, V
Endress GA, Ebner
                                                                                                                                                                                                                      WPI; 2000-062296/05.
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                                                                                                                      Lafleur DW,
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354 AA;

Sequence

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Gaps

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Indels

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4; Conservative

Matches

167 sfxg 170

AAY76127 RESULT

5 sfxg 8

ōλ g

Rosen CA, Carter KC, Moore PA; Wei F, Brewer LA, Soppet DR;

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"this residue is Ala in HPV11 and Ser in HPV6b"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "this residue is Ala in HPV11 and Ile in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "this residue is Ile in HPV11 and Val in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "this residue is Thr in HPV11 and Ala in HPV6b"
                                                                                                                       "this residue is Gly in HPV11 and Ser in HPV6b"
                                                                                                                                                             "this residue is Asn in HPV11 and Gly in HPV6b"
                                                                                                                                                                                                      "this residue is Ser in HPV11 and Thr in HPV6b"
                                                                                                                                                                                                                                            "this residue is Ala in HPV11 and Gly in HPV6b"
                                                                                                                                                                                                                                                                                    "this residue is His in HPV11 and Asn in HPV6b"
                                                                                                                                                                                                                                                                                                                            /note= "this residue is His in HPV111 and Gln in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                            "this residue is Lys in HPV11 and Thr in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "this residue is Gln in HPV11 and Pro in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "this residue is Asp in HPV11 and Asn in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "this residue is Met in HPV11 and Leu in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "this residue is Phe in HPV11 and Tyr in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "this residue is Thr in HPV11 and Ser in HPV66"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "this residue is Pro in HPV11 and Ala in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "this residue is Thr in HPV11 and Ala in HPV6b"
/note⇔ "this residue is Asp in HPV11 and Thr in HPV6b"
                                       "this residue is Leu in HPV11 and Ile in HPV6b"
                                                                               "this residue is Val in HPV11 and Ile in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                     "this residue is Ser in HPV11
and Lys in HPV6b"
                                         /note-
                                                                    Misc-difference 274 /note
                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                               Misc-difference 284
/note=
                                                                                                                                                                                                                                                                                       /note-
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                             Misc-difference 273
                                                                                                           Misc-difference 277
                                                                                                                                                                                           Misc-difference 281
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                                                       0
                                                       Gaps
                                                                                                                                                                                                                                                                                    Human papillomavirus type 16; HPV16; virus-like particle; VLP;
HPV16Dd202E; H16.U4 antibody; H16.V5 antibody; identification;
HPV16 type; characterisation; HPV type 16 infection; HPV11; HPV6b.
                                                       .,
                        Ouery Match 37.5%; Score 3; DB 21; Length 354; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 170 / note "this residue is Tyr in HPV11" / note and Lys in HPV60 and Lys in HPV60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 53
/note= "this residue is Lys in HPV11
and Arg in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
/note= "this residue is Val in HPV11
and Ala in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 131
/note= "this residue is Gly in HPV11
and Ser in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "this residue is Ser in HPV11 and Thr in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "this residue is Asn in HPV11 and Arg in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 246
/note= "this residue is Tyr in HPV11
and Phe in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263
/note= "this residue is Thr in HPV11
and Glu in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                              /note= "this residue is Lys in HPV11 and Thr in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 49
/note= "this residue is Tyr in HPV11
and Phe in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 119
/note= "this residue is Leu in HPV11
and Phe in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "this residue is Ser in HPV11 and Pro in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "this residue is Leu in HPV11 and Ile in HPV6b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "this residue is Val in HPV11 and Thr in HPV6b"
                                                                                                                                                                                                                                                         Human papillomavirus consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                ney Location/Qualifiers
Misc-difference 28
                                                                                                                                                                           AAW48932 standard; protein; 500 AA.
                                                                                                                                                                                                                              08-OCT-1998 (first entry)
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∕note≕
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                                                                                                                                                                                                                                                                                                                                          Human papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 271
                                                                                                          173 sfxg 176
                                                                               5 sfxg 8
                                                                                                                                                                                                     AAW48932;
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AAW48932
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The invention relates to an isolated transcription factor gene which is expressed in a recombinant maturing dicot seed and which encodes a transcription factor protein which targets a promoter of a gene encoding seed storage proteins, lectins or oil-body proteins. The transcription factors isolated are Pv-Seed factor-1 (ROM1) and Vicilin-box binding protein-1 (ROM2). These factors bind to 7S-globulin (b-phaseolin) or lectin (PHA-L) promoters. The transcription factor gene is useful for enhancing or reducing expression of seed storage protein, lectin or oil-protein genes in dicot seed crops. The present sequence represents the amino acid sequence of bZIP2 (basic leucine zipper) ORF2 protein.
protein that targets promoters of genes encoding seed storage proteins are useful for modulating seed storage protein expression in dicot seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brevican; chrondroitin sulphate proteoglycan; glial cell; axon; neurofibromatosis; gliosis.
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41..50
/note= "unidentified amino acids"
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                                                                                                                                                                                                                                                                                                                                                                                                               37.5%; Score 3; DB 22; Lo
100.0%; Pred. No. 2.5e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "unidentified amino acid" Misc-difference 74..75
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                                                                               Disclosure; Columns 35-38; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "unidentified 290
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                                                         The present sequence represents a consensus sequence between human papillomavirus type 11 (HPV11) and HPV6b. The specification decribes a synthetic HPV16 virus-like particle (VLP) which contains a Glu substitution for the naturally occurring Asp at position 202. The protein is designated HPV16bd202E. The novel VLP HPV:D202E binds H16.44 antibody but not H16.V5 antibody and thus allows specific identification of HPV16 types. The new VLPs are used in the characterisation of HPV type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription factor; seed storage protein; lectin; oil-body protein; Pv-Seed factor-1; ROM1; Vicilin-box binding protein-1; ROM2; 7S-globulin; phaseolin; PHA-L; bean; nuclear protein; promoter; ORF; bZIP; basic leucine zipper.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                        - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel, transcription factor gene which encodes transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                      Human papillomavirus type 16 D202E virus-like particles characterising HPV16 type infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 3; DB 19
Pred. No. 2.46
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of bZIP2 ORF2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYMA-) UNIV MARYLAND BALTIMORE COUNTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB48242 standard; Protein; 552 AA.
                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.5%; 100.0%;
                                        96US-0032633.
97WO-US22023
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                                                                                 & CO INC
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                                                                                                                                                                WPI; 1998-348266/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-079619/09.
N-PSDB; AAC84565.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phaseolus vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 kxxsf 442
                                                                               (MERI ) MERCK
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05-DEC-1997;
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                                        09-DEC-1996;
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                                                                                                                       Ludmerer S;
                                                                                                                                                                                                                                                                                                                                                                                                                                       types. The infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB48242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Gaps

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Length 552; Indels

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Banana ripening fruit Gluc. translated polypeptide.
(first entry)
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                                                                                                                                                             23-SEP-1998;
                                                                                                                                                                             25-SEP-1997;
02-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-1999
                                                                                                                                            01-APR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                  Banana;
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                                                                                                                                                                                                                                                                                                                                                                    used in
                                                                                                                                                                                                                                                                                                                                                                                                           Brevican was isolated from the proteoglycan soluble fraction of rat brain. The fraction containing the core protein was purified and the sequences of the N-terminus and internal tryptic peptides were detd., giving the sequence shown in AAR85443. Brevican is used to modulate axonal growth and to raise antibodies useful for detecting gliosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                   Mammalian brevican protein - directs/inhibits axonal growth, treatment of neuro-fibromatosis and in detection of gliosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 3; DB 16; Length 908;
Pred. No. 3.5e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                    Yamaguchi Y;
                                                                                         /note="unidentified amino acids" 561..581
/note= "unidentified amino acids"
                                                                                                                                                                             "unidentified amino acids"
                                                                                                                                                                                                              note- "unidentified amino acids"
                                                                                                                                                                                                                      897..898
/note= "unidentified amino acids"
                                                                                                                                                                                              "unidentified amino acids"
                       /note= "unidentified amino acid"
                                                                                                                                                             "unidentified amino acids'
/note= "unidentified amino acid"
Misc-difference 395
                                       /note- "unidentified amino acid"
                                               Misc-difference 439..440 /note= "unidentified amino
                                                                                                                         Misc-difference 718..720
                                                                         "unidentified amino
                                                                                                                                                                                                                                                                                                                                   Yamada H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY05839 standard; Protein; 1186 AA
                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 45-47; 73pp; English.
                                                                                                                                                                                                                                                                                                                 (LJOL-) LA JOLLA CANCER RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.5%; Sco.
100.0%; Pre
0;
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866..867
                                                                 447.490
/note= "u
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751..800
                                                                                  524..530
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                                                                                                                                                                        /note=
835
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Best Local Similarity
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Misc-difference 324
                               Misc-difference 413
                                                                                                                   Misc-difference 603
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                                                                                                                                                                                                                                                                                                                                   Shimonaka M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                          /note= "the X residues in this sequence correspond to in-frame stop codons in reading frame 1 of Gluc. DNA"
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fruit ripening; glucanase; differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.5%; Score 3; DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 15A-E; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BOYC-) BOYCE THOMPSON INST PLANT RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY05842 standard; Protein; 2466 AA.
                                  fruit development; transgenic plant.
                                                                                                                                                        Location/Qualifiers
1..1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated banana DNA molecules
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-244425/20
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                                                                                                                                                                                                     Misc-difference 1.
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                                                                                                    Ausa acuminata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 kxxsf 121
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Search completed: January 14, 2002, 07:56:30 Job time: 725 sec
                                    JP06065288-A.
                                                                                    19-AUG-1992;
                                                                                                              19-AUG-1992;
                                                             08-MAR-1994.
             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                             /note= "the X residues in this sequence correspond
                                                                                                              to in-frame stop codons or degenerate codons in reading frame 1 of ENDO. DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiotensin converting enzyme; ACE; inhibitor; SP5; SP4; SP3; hypertension; blood pressure.
         Banana; fruit ripening; glucanase; differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 3; DB 2C; Pred. No. 6.46
                                                                                                                                                                                                                                                   (BOYC-) BOYCE THOMPSON INST PLANT RES.
                       fruit development; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                              Claim 14; Fig 16A-J; 143pp; English.
                                                                      Key Location/Qualifiers
Misc-difference 1..2466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           directly in the transformed fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.5%; Scor.
100.0%; Pre
0; !
                                                                                                                                                                                                                                                                                                                                      New isolated banana DNA molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR42556 standard; peptide; 3 AA.
                                                                                                                                                                                                  98WO-US03343.
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                                                                                                                                                                                                                                                                            Clendennen S, May G;
                                                                                                                                                                                                                                                                                                 WPI; 1999-244425/20.
N-PSDB; AAX25613.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACE inhibitor SP3.
                                                Musa acuminata,
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Peptides SP3, SP4 and SP5 have ACE inhibiting activity. They can be prepd. easily and in high yield. They are useful for treatment or prophylaxis of hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                           New tri-, tetra- and penta:peptide(s), e.g. Trp-Lys-Tyr - are ACE inhibitors useful for treatment or prophylaxis of hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                             25.0%; Score 2; DB 1
100.0%; Pred. No. 4.3
:ive 0; Mismatches
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92JP-0220270.
                                        92JP-0220270
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 60.0 , Capext 60.0
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    /cgn2_6/ptiodata/2/1aa/5A_COMB.pep:*
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/cgn2_6/ptiodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptiodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptiodata/2/1aa/B_COMB.pep:*
/cgn2_6/ptiodata/2/1aa/backfiles1.pep:*
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US-09-295-186-8
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US-08-889-8418-30
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| RESULT 1 US-08-764-157 Sequence 8, Patent No. GENERAL IN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICAN APPLICA COMPUTER MEDIUM COMPUTER TELEPH TELEPH TELEPH TYPE: TOPOLO MOLECULE FEATURE: | | 5 9 9 8 7 6 5 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 |
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| ,7-8 5830863 SNEORMATION: NT: Buck, SNET: Harbeson NT: Hassman NT: Hassman NT: Hassman NT: Hassman NT: Hassman NT: Hassman NT: Hassman NT: Hassman NT: Hassman NT: Hassman NT: Hassman NT: Gincinnati Continnati | | 22222222222222222222222222222222222222 |
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| .25 | | Sequence 3, Appli Sequence 1, Appli Sequence 109, App Sequence 117, App Sequence 117, App Sequence 117, App Sequence 117, App Sequence 62, Appli Sequence 117, App Sequence 117, App Sequence 117, App Sequence 408, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli |

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; NAME/KEY: Modified
; LOCATION: 7
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-764-157-8
US-08-987-519-3
, Sequence 3, Application US/08987519
, Patent No. 5952216
; GENEWAL INFORMATION:
, APPLICANT: Ludmerer, Steven
, TITLE OF INVENTION: Synthetic HPV16 Virus-Like
; FILE REFERENCE: 19853
                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Xaa at position 5 US-09-295-186-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hasida, Miyoko
APPLICANT: Tsutsumi, No. 6127137iko
APPLICANT: Tsutsumi, No. 6127137iko
APPLICANT: Halkier, Torben
APPLICANT: Stringer, Mary Ann
TITLE OF INVENTION: An Acidic Phospholipase, Pri
TITLE OF INVENTION: Methods of Using Thereof (A:
FILE REFERENCE: 4953.204-US
CURRENT APPLICATION NUMBER: US/09/295,186B
CURRENT FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: 1215/96
PRIOR FILING DATE: 1996-10-31
PRIOR APPLICATION NUMBER: PCT/DK97/00490
PRIOR FILING DATE: 1997-10-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 31
TYPE: PRT
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Matches 4; Conserv
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(Leu-NH2)"
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amino acid"
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having a 1-methylene group, in place of a
1-carbonyl group, bonded to the alpha nitrogen"
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pred. No. 1.6
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s; Pred. No. 69;
0; Mismatches
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                                                                                                                                          US-08-796-899-28
                                                                                                                                                          RESULT
              Sequence 28, Application US/08796899
Patent No. 6160202
GENERAL INFORMATION:
APPLICANT: BUSTOS, Mauricio M
APPLICANT: BUSTOS, Mauricio M
APPLICANT: CHERN, Maw Shenq
TITLE OF INVENTION: TRANSCRIPTIO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/987,519
CURRENT FILING DATE: 1997-12-09
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 501
TYPE: PRT
                                                                                                                                                                                                                                                                                      Matches
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| 13 2 S47365 | 13 2 S47362 | 13 2 S47359 | ν | | | | | 13 1 MTCMAD | | 12 2 PH1459 | | | Ν | Ν | | 2 | | N | 12 2 S26546 | 2 |
| T-cell antigen rec | T-cell antigen rec | T-cell antigen rec | T-cell antigen rec | Ig heavy chain CRI | osteoclast function | equinatoxin 1A - : | melanotropin alpha | melanotropin alpha | T-cell receptor be | T-cell receptor be | T-cell receptor be | Ig H chain V-D-J ı | T-cell antigen rec | T-cell antigen rec | coagulation factor | Ig heavy chain - | T-cell receptor be | T-cell receptor be | T-cell receptor be | fructose-bisphosph |

ALIGNMENTS

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phenol 2-monooxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (frag C;Species; Pseudomonas sp. C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993 C;Accession: A37832 C;Accession: A37832 C;Accession: A37832 C;Accession: A37832 C;Accession: A37832 C;Accession: A37832; MUID:91072331 A;Reference number: A37832; MUID:91072331 A;Residues: A37832; MUID:91072331 A;Residues: 1-4 <POW> C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                dnaZX-like protein - Bacillus subtilis (fragment)
c;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C;Accession: I40469
                                          A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                     R;Struck, J.C.; Hartmann, R.K.;
Mol. Genet. 215, 478-482,
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A; Start codon: GTG
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1989
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Query Match Best Local Similarity

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Score Pred.

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DB 2; Length 5; 2.2e+05;

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Biochim. Biophys. Acta 828, 380-382, 1985
A;Title: Amino acid sequence around the reactive serine residue A;Reference number: A60139; MUID:85175165
A;Mocleonie +----
neuromodulatory peptide wWamide-2 - giant African snail
(;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-
C;Accession: S33245
R;Minakata, H; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated
A;Reference number: S33244; MUID:93265912
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homo ydrolase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] S-C;Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enz F;5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 22-Jan 1993 #sequence_revision 22-Jan-1993 #tC;Accession: A60139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-7 <CHA>
C:Superfamily: hypothalamic heptapeptide
C;Keywords: hypothalamus
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981
C;Accession: 401417
R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, Horm. Metab. Res. 13, 228-232, 1981
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R;Egestad, B.; Estonius, M.; Danielsson, O.; Persson, B.; Cederlund, E.; Kaiser, R.; FEBS Lett. 269, 194-196, 1990
A;Title: Fast atom bombardment mass spectrometry and chemical analysis in determinati A;Reference number: S11074; MUID:90353571
A;Accession: S11078
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A; Title: Integration of human papillomavirus type
A; Reference number: I56695; MUID: 87311896
A; Accession: I56695
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                                                      RESULT
B27867
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homeotic protein Ultrabithorax - fruit fly (Drosophila melanogaster) (fragment) C;Species: Drosophila melanogaster C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 23-Feb-1997
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neuropeptide Grb-AST B3 - two-spotted cricket
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: C57444
R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the A:Reference number: A57444; MUID:95403341
A:Accession: C57444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuropeptide Grb-AST B2 - two-spotted cricket C;Species: Gryllus bimaculatus (two-spotted cricket) C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996 C;Accession: B57444 R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995 A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the A;Reference number: A57444; MUID:95403341 A;Accession: B57444
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A;Molecule type: protein
A;Residues: 1-9 <LOR>
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B57444
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A;Cross-references: FlyBase:FBgn0003944
C;Keywords: DNA binding; nucleus; trans
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A;Title: The structure of a
A;Reference number: A91072
A;Accession: B27867
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R; Saarl, G.;
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A; Residues: 1-8 <SAA>
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Best Local
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2; Conserv
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                                                             Conservative
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                                                                          25.0%;
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Pred. No.
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NO. 2.2e+05;
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cytokeratin 4 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
C;Accession: 146016
R;Blessing, M.; Jorcano, J.L.; Franke, W.W.
EMBO J. 8, 117-126, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity A;Reference number: PT0222; MUID:91108337
A;Accession: PT0324
A;Molecule type: DNA
A;Residues: 1-9 < YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                A;Title: Enhancer elements directing cell-type-specific A;Reference number: I46016; MUID:89231609
A;Accession: I46016
A;Status: preliminary; translated from GB/EMBL/DDBJ
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I46016
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
C;Accession: PT0324
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A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity A;Reference number: PT0222; MUID:91108337
A;Accession: PT0238
A;Mclecule type: DNA
A;Residues: 1-9 <- YAMN
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
                                                                                      A;Molecule type: DNA
A;Residues: 1-9 <BLE>
A;Cross-references: EMBL:X14478; NID:g303; PIDN:CAA32640.1; PID:g577897
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PT0324
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0238
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Best Local S
Matches 2
   Query Match 25.0
Best Local Similarity 100
Matches 2; Conservative
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Mismatches

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A;Statuq: preliminary; not compared with A;Molecule type: DNA A;Residues: 1-9 <WHE> C;Keywords: T-cell receptor
                                                                                                                                                                           T-cell receptor gamma chain (2t.23) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Date: 03-Feb-1994 #sequence_revision (03-Feb-1994 #text_change)
C:Accession: G41946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;ACCression. 7: Kelsoe, G. R;Jacob, J; Kelsoe, G. submitted to the EMBL Data Library, Ju submitted to the EMBL studies on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan 1994 #sequence_revision
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A; Residues: 1-9 < LAK>
C; Keywords: aldehyde-lyase;
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J. Biol. Chem. 245, 2140-2141, 1970
A;Title: The carboxyl-terminal structure of rabbit liv
A;Reference number: A28924; MUID:70166720
A;Accession: A28924
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                                                                                     A;Title: Rearrangement and junctional-site A;Reference number: A41946; MUID:92049316 A;Accession: G41946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X67387; NID:g50113; PIDN:CAA47799.1; PID:e51594; PID:g1333871 C;Keywords: heterotetramer; immunoglobulin
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A; Accession: S36850
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 07-Feb-1997
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A; Residues: 1-9 < JAC>
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b. 2.2e+05;
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). 2.2e+05;
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                                                                                                                             of T-cell receptor gamma
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R;Matsuo, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.
Biochem. Biophys. Res. Commun. 45, 822-827, 1971
A;Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-pha A;Reference number: A90176; MUID:72065376
A;Rotnents: annotation; Synthesis
A;Note: the synthetic and natural hormones have the same physicochemical and bio R;Babb, Y.; Arimura, A.; Schally, A.V.
Biochem. Biophys. Res. Commun. 45, 483-487, 1971
Biochem. Biophys. Res. Commun. 45, 483-487, 1971
A;Title: On the tryptophan residue in porcine LH and FSH-releasing hormone. A;Reference number: A90175; MUID:72117544
A;Contents: annotation
A;Note: TTp-3 appears to be essential for biological activity
C;Comment: This hypothalamic hormone stimulates the secretion of both luteinizin C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental
                                                               A; Molecule type: protein
A; Residues: 1-10 <BUR>
A; Residues: 1-10 <BUR>
A; Note: the natural and synthetic hormones have the
C; Comment: This hypothalamic hormone stimulates the
C; Superfamily: gonadoliberin
                                                                                                                                                                                                                     R:Burgus, R.; Butcher, M.; Amoss, M.; Ling, N.; Monahan, M.; Rivier, J.; Fellows, F
Proc. Natl. Acad. Sci. U.S.A. 69, 278-882, 1972
A;Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing
A;Reference number: A93780; MUID:72094314
                                                                                                                                                                                                                                                                                                                 C;Species: Ovis orientalis aries, Ovis C;Date: 31-Dec-1991 #sequence_revision C;Accession: A93780; A01411
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A;Title: Structure of the porcine LH- and FSH-releasing hormone.
A;Reference number: A90172; MUID:72114303
A;Accession: A01411
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C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 18-Mar-1997
C:Accession: A01411
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C;Superfamily: gonadoliberin C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid F;L/Modified site: pyrolidone carboxylic acid (Gln) #status experimental F;10/Modified site: amidated carboxyl end (Gly) #status experimental
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31-Dec-1991 #text_change 18-Mar-1997
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ches 0; Indels
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Query Match

25.0%;

Score

2;

DB 1;

Length 10

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T-cell receptor beta chain V-D-J region - rat (fragment) C; Species: Rattus norvegicus (Norway rat) C; Date: 09-Oct-1992 #sequence_revision 19-Oct-1995 #text_change 30-May-1997 C; Accession: PH0948; PH0897; PH0899; PH0899 R; Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B. J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experime A; Reference number: PH0891; MUID:92078857
A;Accession: PH0848
                                                                                                                                                                                   RESULT
PH0948
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Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983
A;Title: Characterization of a teleost gonadotropin-releasing hormone
A;Reference number: A21114; MUID:83195140
A;Accession: A21114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gonadoliberin - chum salmon
C:Species: Oncorhynchus keta (chum salmon)
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 18-Jun-1993
C:Accession: A21114
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A21114
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A; Residues: 1-10 <LOV>
A; Residues: 1-10 <LOV>
C; Superfamily: gonadoliberin
C; Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (Gin) #status experimental
F; 10/Modified site: amidated carboxyl end (Gly) #status experimental
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Thes 2; Conserve
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A;Title: Primary structure of two forms of gonadotropin-release Primary structure of two forms of gonadotropin-release Primary and A;Reference number: A60066; MUID:91352338
A;Accession: A60066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: gonadotropin-releasing hormone I
C;Specles: Alligator mississippiensis (American alligator)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
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A; Residues: 1-10
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2; Conservative 0;
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Mismatches 0;
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o. 1.8e+03;
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A; Accession: A34662
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-11 <FUJ>
C; Keywords: amidated carboxyl er
F; 11/Modified site: amidated ca.
                                                                                                      R; Fujimoto, K.; Ohta, N.; Yoshida, M.; Kubota, I.; N
Biochem. Biophys. Res. Commun. 167, 777-783, 1990
A; Title: A novel cardio-excitatory peptide isolated
A; Reference number: A34662; MUID:90211261
                                                                                                                                                                         Achatina cardio-excitatory peptide-1 - giant African snail C;Species: Achatina fulica (giant African snail) C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 11-Jul-1997 C;Accession: A34662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgelin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: O3-May-1994 #sequence_revision O3-May-1994 #text_change 31-Oct-1997
C;Accession: A40693
R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.
J. Cell Biol. 121, 1065-1073, 1993
A;Title: Purification and properties of transgelin: a transformation and shape A;Reference number: A40693; MUID:93273790
A;Accession: A40693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: aorta c; Comment: This protein gels actin and is c C; Superfamily: smooth muscle protein SM22; C; Keywords: actin binding; cytoskeleton
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A40693
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A; Residues: 1-10 <GO1>
A; Experimental source:
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A; Residues: 1-10 <GO4>
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A; Residues: 1-10 <GO3>
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68XDa neurofilament - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I60434
R;Reeben, M.; Neuman, T.; Palgi, J.; Palm, K.; Paalme, V.; Saarma, M.
J. Neurosci. Res. 40, 177-188, 1995
A;Title: Characterization of the rat light neurofilament (NF-L) gene promoter and identi
A;Reference number: I60434; MUID:95264348
A;Accession: I60434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell receptor gamma chain (1t.57) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: B41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-599, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316
A;Accession: B41946
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A; Gene: NF68
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A;Molecule type: DNA
A;Residues: 1-11 <RES>
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Copyright (c) 1993 - 2000 Compugen Ltd
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CXA2_CONAL
PL2_PERAM
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CAT9_FASHE
CXA1_CONAL
CXA3_CONAL
RIPW_CREAM
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"WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from

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| 95720; Nobayashi M | ed) sequence update) annotation update) can snail). si Gastropoda; Pulmona chatina. | PRT; 7 AA. | | Score 2; DB 1; Pred. No. 1e+05; 0; Mismatches | 632B45B1FB5059A0 CR | 3778; rimura A., Redding n J.W., Cohn D.V., nthesis of a hepte porcine hypothala (1981). | ta; Craniata; Verteb .iodactyla; Suina; Su | ed) sequence update) annotation update) | PRT; 7 AA. | ALIGNMENTS | TLANM_STRMU TLANM_HETFU CYSP_TRIFO TX2_HETFU CS33_ARAHY FEDG_AMYME FIBG_CANFA | FIBB_ANTAM NRLA_ACISP PSBF_SYNVU CYSP_TRIVA | RIPX_CUCPE RLC1_HALMA VR90_BORPE | CRP_MUSCA LPP3_HUMAN PYRR_PYRAP |
| ,, Nomoto K.; | onata; Stylommatopho <i>ra;</i> | | | Length 7; 0; Indels 0; Gaps 0; | :RC64; | T.W., Coy D.H., Schally A.V.; peptide with in vitro | brata; Euteleostomi; uidae; Sus. | | | | P80666 streptococc P82850 heterometru P33403 tritrichomo P82851 heterometru P80926 arachis hyp P80707 amycolatops P12800 canis famil | $\omega \omega \omega \sigma$ | 000 | 224 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993)
-i- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
PIR; S33245; S33245.
                                                                                                                                                                                                                                                                                                                         TISSUE-Cerebral ganglion, and Thoracic ganglion, MEDLINE-98121193; PubMed-9461295; Duve H., Johnsen A.H., Maestro J.-L., Scott A.G
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Eumalacostraca; Eucarida; Decapo
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                                      Eukaryota; Metazoa; Chordata; Craniata; vertebuata, Archosauria; Crocodylidae; Alligatorinae; Alligator
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TISSUE-Brain;
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                                                      Alligator mississippiensis (American alligator).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                               NCBI_TaxID=8496;
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Decapoda; Pleocyemata; Brachyura;
Portunidae; Carcinus.
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                                                                                        (GNRH-I)
                                                       Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GON3_ONCKE STANDARD; PRT; 10 AA.
P20367; P81751;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GONADOLIBERIN III (GONADOTROPIN-RELEASING HOR
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MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                           SEQUENCE,
SPECIES=C.
                                                                                                                        Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G., Chang J.P., Rivier J.E., Sherwood N.M.;
Chang J.P., Rivier J.E., Sherwood N.M.;
Primary structure and function of three gonadotropin-releasing hormones, including a novel form, from an ancient teleost, herrical endocrinology 141:505-512(2000).

-i- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND FOLLICLE-STIMULATING HORMONNES.
                                                                                                                                                                                                                                                                                 Sherwood N., Eiden L., "Characterization of a Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ONCKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                      Pfam; PF00446; GnRH;
                                                                                  PIR; A21114; A21114.
InterPro; IPR002012; GnRH.
                                                                                                                                                                                                                          SEQUENCE, AND FUNCTION.
SPECIES=C.pallasii; TISSUE=Brain,
MEDLINE=20114351; PubMed=10650929;
                                                                                                                                                                                                                                                                                                                             MEDLINE=83195140; PubMed=6341999;
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                                            Hormone;
                                                       PROSITE;
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    \begin{array}{c} 10 \\ 1230 \end{array}
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     W.
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284B23D7286B45A3 CRC64;
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284B3233786B45A3 CRC64;
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                              PYRROLIDONE CARBOXYLIC
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Euteleostei;
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                                                                                                                                                                                                                                                                                                                                                                                                  Oncorhynchus
                                                                                                                                                                                                                                                                                                     Rivier J., Vale W.; asing hormone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mississippiensis).";
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        STRAIN-FERUSSAC: TISSUE-Heart atrium;

MEDLINE-90211261; PubMed-2322251;

Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi
"A novel cardio-excitatory peptide isolated from the atria of the
African giant snail, Achatina fulica.";

Biochem. Biophys. Rcs. Commun. 167:777-783(1990).

-i- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE.
                                                                                                                                                                           CEP1_ACHFU STANDARD; PRT; P2790; P2790; Ol-AUG-1991 (Rel. 19, Created) Ol-AUG-1991 (Rel. 19, Last sequence up Ol-DEC-1992 (Rel. 24, Last annotation CARDIO-EXCITATORY PEPTIDE-1 (ACEP-1).
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Sanchez J.-C., Roug
Hoogland C., Appel
                                                                                                               SEQUENCE
                                                                                                                                  Achatinacea; Achatinidae; Achatina.
NCBI_TaxID=6530;
                                                                                                                                                      Achatina fulica (Giant African snail).
Eukaryota: Metazoa: Mollusca: Gastropoda: Pulmonata;
                                                                                                                                                                                                                                                ACHFU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P99027:
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
60S_ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                             -1- PTM: PHOSPHORYLATED (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE L12P FAMILY SWISS-2DPAGE; P99027; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cowthorne
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NON_TER 10 10
SEQUENCE 10 AA; 1186 MW; 07121F
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nilarity 100.0%;
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Appel R.D.,
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Binz P.-A.,
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Pred. No. 9.6
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IN THE ELONGATION STEP
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BUCCAL MUSCLE
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STRUCTURE BY NMR.

MEDLINE-99324017; PubMed=10395477;

MEDLINE-99324017; PubMed=10395477;

Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;

"Solution structure of alpha-conotoxin ImI by 1H nu
resonance.";

J. Med. Chem. 42:2364-2372(1999).

-!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P50983;
01-OCT-1996
01-OCT-1996
20-AUG-2001
                                                                                                          Maslennikov I.V., Shenkarev Z.O., Zhmak M.N., Methfessel C., Tsetlin V.I., Arseniev A.S.; "NMR spatial structure of alpha-conotoxin ImI scaffold in snail and snake toxins recognizing acetylcholine receptors."; FEBS Lett. 444:275-280(1999).
                                                                                                                                                                STRUCTURE BY NMR.
MEDLINE-99158061;
Maslennikov I.V.,
                                                                                                                                                                                                                            other conotoxins receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   McIntosh J.M., Yoshikami D., Mahe E., Nielsen
Gray W.R., Olivera B.M.,
"A nicotinic acetylcholine receptor ligand of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Mollusca; Gastropoda
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=35631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus imperialis (Imperial cone).
Conus imperialis (Imperial cone).
Fukarvota: Metazoa; Mollusca; Gastropoda; Caenogastropoda;
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01-OCT-1996 (Rel. 34,
20-AUG-2001 (Rel. 40,
ALPHA-CONOTOXIN IMI.
                                                                                                                                                                                                                                                                Rogers J.P., Luginbuhl Wemmer D.E.;
                                                                                                                                                                                                                                                                                                                                   acetylcholine receptor blockade: alpha 7 and alpha 9 receptors.";
                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION.
MEDLINE=95379776; PubMed=7651351;
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                                                                                                                                                                                                                   Biochemistry
                                                                                                                                                                                                                                        "NMR solution structure of alpha-conotoxin ImI and comparison other conotoxins specific for neuronal nicotinic acetylcholine
                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR. MEDLINE-99212205;
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11 AA; 1305
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       MLA_CAMDR STANDARD; PRT; P01198; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence up 20-AUG-2001 (Rel. 40, Last annotation MELANOTROPIN ALPHA (ALPHA-MSH)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis
NCBI_TaxID=28377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dores R.M., Lancha A., Rand-Weaver M., Jankelow L., Adamczy "Detection of a novel sequence change in the major form of isolated from the intermediate pituitary of the reptile, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Pituitary;
MEDLINE-92270473;
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Camelus dromedarius (Dromedary) (Arabian camel),
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Ol-FEB-1991 (Rel. 17, Last sequence update)
Ol-NOV-1995 (Rel. 32, Last annotation update)
OLOTROPIN DI (EC 3.4.22.-) (FRAGMENT).
Calotropis gigantea (Madar) (Dowstring hemp).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Apocynaceae; Asclepiadoideae;
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SEQUENCE
                                                                                                                                                     Bhattacharya D., Sengupta A., Sinha N
"Chemical modification and amino term
from Calotropis gigantea.";
Phytochemistry 26:633-636(1987).
-!- SIMILARITY: BELONGS TO PEPTIDASE
PAPAIN FAMILY OF THIOL PROTEASES.
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"Isolation, characterization, and amino acid
melanotroplus from camel pituitary glands.";
Biochemistry 14:947-952(1975).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus
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Dixon J.S., Li C.H.;
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PROSITE; PS00139; THIOL_PROTEASE_CYS; PA
PROSITE; PS00639; THIOL_PROTEASE_ASN; PA
PROSITE; PS00640; THIOL_PROTEASE_ASN; PA
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NCBI_TaxID=4066;
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MEDLINE=75146434; PubMed=1125179;
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                                   ΑA,
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AMIDATION.
FF991CA958BB09C1
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21-JUL-1986 (Rel. 01, Last
20-AUG-2001 (Rel. 40, Last
TRP OPERON LEADER PEPTIDE.
TRPL OR TRPEE OR B1265 OR Z
Escherichia coli, and
Escherichia coli 0157:H7.
SEQUENCE FROM N.A.
MEDLINE=82150258; PubMed=7038627;
Yanofsky C., Platt T., Crawford I
Horowitz H., van Cleemput M., Wu
                                                                                                                                                    LPW_ECOLI P03053;
                                                                                                                                                                                                                                                                                                                                                                                                                                        LPW_CITFR P03056;
                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-83007061; PubMed-6749821;
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01-MAY-1991
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                                                  NCBI_TaxID-562,
                                                              Escherichia.
                                                                     Bacteria; Proteobacteria;
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Last annotation update)
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MW; 5B792A473E8048E7
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Pred. No. 1.2
0; Mismatches
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   Wu A.M
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EMBL; J01714; AAA57296.1; -. EMBL; AC0494; CAA00361.1; -. EMBL; AC0424; AAC74347.1; -. EMBL; AE005380; AAC36550.1; -. EMBL; AF002556; BAB35260.1; -. EMBL; AF002556; BAB35260.1; -. PIR; AC0389; LFECW. ECOGene; EG11274; trpL. ECOGene; EG1274; trpL. Tryptophan biosynthesis; Leader SEQUENCE 14 AA; 1723 MW; 5B7
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MEDLINE=76240562; Pul
Squires C., Lee F., 1
Yanofsky C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Posfai G., Hackett J., Lim A., Dinalanta E.T., Potamousis K.,

Posfai G., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-K12 / MG1655;

MEDLINE-97426617; PubMed-9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
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"Attenuation in the Escherichia coli tryptophan op
secondary structure involving the tryptophan codor
proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; pubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=80101455; PubMed=118451;
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                                                                                                                                                                                                                                                                                            or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Res. 8:11-22(2001). FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF TRYPTOPHAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409:529-533(2001).
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                                                                                                                                                                                                                                                                                         email to license@isb-sib.ch).
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K., Mayhew G.F
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21-JUL-1986 (Rel. (
21-JUL-1986 (Rel. (
01-FEB-1995 (Rel. 3
TRP OPERON LEADER H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regions of the tryptophan operons of Escherichia coli typhimurium.";
J. Mol. Biol. 121:193-217(1978).
-i- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF TOF TRYPTOPHAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=78196931; PubMed=351195;
Lee F., Bertrand K., Bennett G.N., Yanofsky C.;
"Comparison of the nucleotide sequences of the initial transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRPL OR TRPEE.
Salmonella typhimurium
                                                             Eukaryota; Metazoa; Mollusca; Gas
Neogastropoda; Conoidea; Conidae;
                                                                                     Conus aulicus (Court cone).
                                                                                                                                                                                                                                                                                                                                      Tryptophan biosynthesis; Leader peptide. SEQUENCE 14 AA; 1635 MW; 49F22A47362248E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             EMBL; M24960;
PIR; A03590; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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           TISSUE=Venom;
                                                NCBI_TaxID=89437;
                                                                                                                                                                                                                                                                                                                                                                StyGene; SG10400; trpL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=602;
MEDLINE=99003392; PubMed=9786965;
                        SEQUENCE, AND SYNTHESIS
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llarity 100.0%;
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PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                        NOT_ANNOTATED_CDS.
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01, Last
31, Last
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Pred. No.
                                                             Gastropoda; Caenogastropoda;
dae; Conus.
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o. 1.2e+03;
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RESULT 16
PH2_PERAM
Query Match
Best Local Similarity
Thehes 2; Conservi
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Best Local Similarity
"-+ches 2; Conserv
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"Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic acetylcholine receptors and nicotine-evoked norepinephrine release.";

J. Neurosci. 18:8571-8579(1998).

-i-FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-J/BETA-4 SUBUNITS.

-i- MASS SPECTROMETRY: MM-1572.5; METHOD=ELECTROSPRAY.

POSTSYNAPTIC neurotoxin; Acetylcholine receptor inhibitor; Amidation;
                      Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
                                                                       01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
15-JUL-1999 (Rel. 38,
UNKNOWN PROTEIN FROM 2
                                                                                                                                     _MAIZE
UC08_MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattoidea; Hlattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDE HORMONE 2 (PEA-VEAACID 2).
Periplaneta americana (American cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PH2_PERAM STA
P82695;
20-AUG-2001 (Rel.
                                                                                                            P80614;
01-OCT-1996
                                                                                                                                                                                                                                                                                                               Neuropeptide.
SEQUENCE 15 AA; 1603 MW;
                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2000) t-i- FUNCTION: UNKNOWN.
Panicoideae; And NCBI_TaxID=4577;
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s; Pred. No. 1.3
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o. 1.3e+03;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-TOV-1997 (Rel. 35, Last annotation update)
PUTATIVE CATHEDSIN-LIKE ENZYME (EC 3.4.22.-) (NEWLY EXCYSTED JUVENILE PROTEIN 9) (FRAGMENT).
Easciola hepatica (Liver fluke).
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SEQUENCE.
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"The maize two dimensional gel protein database: towards an
                                                                                                                                                                                                                                                           InterPro; IPR000169; Thiolprot_act_site.
PROSITE; PS00139; THIOL_PROTEASE_CYS; PA
PROSITE; PS00639; THIOL_PROTEASE_HIS; PS
PROSITE; PS00640; THIOL_PROTEASE_ASN; PA
                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO PAPAIN FAMILY OF THIOL MEROPS; CO1.033; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 213:169-174(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95366993; PubMed-7639732;
Tkalcevic J., Ashman K., Mceusen E.;
"Fasciola hepatica: rapid identification of newly excysted juvenile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                           Hydrolase;
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1785 MW;
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tospermata; Mediofusata;
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P56639;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DISULFID DISULFID
                                                                                           "Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic acetylcholine receptors and nicotine-evoked norepinephrine releas J. Neurosci. 18:8571-8579(1998)
J. Neurosci. 18:8571-8579(1998)
-I- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THE BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THE NICOTINIC ACETYLCHOLINE RECEPTORS ENOCKS MAMMALIAN NICOTINIC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
-I- MASS SPECTROMETRY: MW-1667.6; METHOD-ELECTROSPRAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P56641;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
ALPHA-CONOTOXIN AUIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetylcholine receptors and nicotine-evoked norepinephrine released. 18:8571.8579(1998)

ON NEUROSCI. 18:8571.8579(1998)

IN HEUROSCI. 18:8571.8579(1998)

IN PROVIDE ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THE BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3, JET7A-4 SUBUNITS.

ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3, JET7A-4 SUBUNITS.

THANSS SPECTROMETRY: MM-1725.6; METHOD-ELECTROSPRAY.
                                                                                                                                                                                                                                                                                                            Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
Olivera B.M., McIntosh J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID-89437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Luo S., Kulak J.M., Cartier Olivera B.M., McIntosh J.M.;
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Luo S., Kulak J.M., Cartier G.E.,
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Eukaryota; Metazoa; Mollusca; Gastropoda
Neogastropoda; Conoidea; Conidae; Conus.
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                                                      Venom.
                                                                           Postsynaptic
                                                                                                                                                                                                                                                                                                                                                               TISSUE=Venom; 
MEDLINE=99003392; PubMed=9786965;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, AND SYNTHESIS.
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                                                                           neurotoxin;
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16
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8
                                                                           Acetylcholine receptor
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Pred. No.
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1E310FEB8FDC7001 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update;
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b. 1.4e+03;
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Ol-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
RIBOSOME-INACTIVATING PROTEIN TRICHOKIRIN (RRNA N-GLYCOSIDASE)
(EC 3.2.22) (FRAGMENT).
Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Characterization and use for preparation of immunotoxins.";
Eur. J. Biochem. 176:581-5861-586(1988).
-:- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- PTM: GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Casellas P., Dussossoy D., Falasca A.I., Barbieri L., Guillemot J.C., Ferrara P., Bolognesi A., Cenini P., Stirpe "Trichokirin, a ribosome-inactivating protein from the seed: Trichosanthes kirilowii Maximowicz. Purification, partial reharacterization and use for preparation of immunotoxins.";
Actinomycetales;
Corynebacterium.
NCBI_TaxID=1718;
                                                  Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                01-JAN-1988 (Rel. 06, Crea
01-JAN-1988 (Rel. 06, Last
20-AUG-2001 (Rel. 40, Last
TRP OPERON LEADER PEPTIDE.
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PROSITE; PS00275; SHIGA_RICIN; PARTIAL.
Protein synthesis inhibitor; Hydrolase;
NON_TER 16 16
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SY 14
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Pred. No. 1 4e+03;
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           PH3_PERAM STANDARD; PRT; 17 AA.

PB2696;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PBFTIDE HORMONE 3 (PEA-VEAACID 1).
Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
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                                                                                                                                                                                                                                                                                                                                                                           Tryptophan SEQUENCE
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PIR; A29834; A29834.
PIR; A24723; A24723.
PIR; S13087; S13087.
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EMBL; M17892; AAB59110.1; -.
EMBL; M16663; -, NOT_ANOTATED_CDS.
EMBL; X55994; CAA39466.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heery D.M., Dunican L.K.;
"Nucleotide sequence of the Corynebacterium glutamicum trpE gene.";
Nucleic Acids Res. 18:7138-7138(1990).
-!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=ATCC 13059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88032866; PubMed=3667535; Matsui K., Miwa K., Sano K.;
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PubMed=2263476;
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MEDLINE-20140865; PubMed-10676456;
Predel R., Eckert M., Holman G.M.;
"The unique neuropeptide pattern in abdominal perisympathetic organs of insects.";
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Abbondanza A., Bolognesi A., Falasca A.I., Rossi C.A.;
"Purification and partial characterization of a mitogenic lectin from
the latex of Euphorbia marginata.";
Biochim. Biophys. Acta 1158:33-39(1993).
-i- FUNCTION: LECTIN THAT BINDS GALACTOSE, GALACTOSE-CONTAINING SUGARS
AND GENTIOBIOSE. IT IS STRONGLY MITOGENIC FOR HUMAN T LYMPHOCYTES.
-i- SUBUNIT: HOMODIMER.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Malpighiales; Euphorbiaceae; Euphorbia.
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SEQUENCE 17 AA; 1807 MW;
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-I- FUNCTION: UNKNOWN.
-I- MASS SPECTROMETRY: MW-1651.35; METHOD-MALDI.
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SIMILARITY: TO E.MARGINATA LECTIN.
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                                                                                                                                                           MEDLINE=98054539; PubMed=9392829;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
Davey M., East P.D., Thorpe A.;
                                                                                                                                                                                              TISSUE-Larva;
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b. 1.5e+03;
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Search completed: January 14, Job time: 708 sec 2002,

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Oghyda reishmania
Oz7953 balaenopter
Oghz74 homo sapien
Ogyv3 trypanosoma
Ogb52 schoenoceph
O1898 homo sapien
O34909 locusta mig
O958z4 spinacia ol
O62721 rattus norv
Ogbyf9 homo sapien
O28093 bos taurus
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O91a14 gallus gall
O9uc46 homo sapien
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RESULT Q9GVM9 ID Q9 AC Q9 DT 01 В Š RESULT Query Match Best Local S Matches 4 Q9GVM9 PRELIMINARY; Q9GVM9; 01-MAR-2001 (TrEMBLrel. 16, MEDLINE-94250349; PubMed-8192865; Moodward J., Brown J.P., Evans B.R., Affholter K.A.; Moodward J., Brown J.P., Evans B.R., Affholter K.A.; "Papain digestion of crude Trichonderma reesei cellulase: purification and properties of cellobiohydrolase I and II core proteins."; Biotechnol. Appl. Biochem. 19:141-153(1994). HSSP; P07987; ICB2. HSSP; P07987; ICB2. 01-MAY 2000 (TremBLrel. 13, Created) 01-MAY-2000 (TremBLrel. 13, Last sequence update) 01-OCT-2000 (TremBLrel. 15, Last annotation update) CELLOBIOHYDROLASE II CORE PROTEIN, CBH II CP-3.2.1.91. Trichoderma reesei (Hypocrea jecorina). Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; Hypocreaceae; Hypocrea. NCBI_TaxID=51453; SEQUENCE. Q9UR79; Q9UR79 5 syxg 8 4 SYXG N Similarity 100.0%; | 4; Conservative 0; 7 PRELIMINARY; 37.5%; Score 3; DB;; Pred. No. 6. 0; Mismatches Created) PRT; DB 3; Length 38; b. 6.7e+02; ches 0; Indels 77 38 A AA. Indels 0 Gaps

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Q91947
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GLUTATHIONE PEROXIDASE (FRAGMENT).
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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01-MAR-2001 (TrEMBLrel.
HYPOTHETICAL 8.1 KDA PROLM12.1312.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Lussier J.G.;
"Cow glutathione peroxidase.";
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Q9GWB2; O1-MAR-2001 (TrEMBLrel. 16, Created)
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PROBABLE SINGLE STRAND-SPECIFIC NUCLEASE (FRAGMENT).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                  Balaenoptera physalus (Finback whale) (Common rorqual)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticet
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MOTITA Y., Mitani H., Naruse K.;
MOTITA Y. atthes eya3 homoLogue partial sequence.
"Oryzias latthes eya3 homoLogue partial sequence.
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ dat
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   Balaenopteridae;
NCBI_TaxID=9770;
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131 AA;
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Pred. No. 1.8e+03;
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o. 1.9e+03;
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
EMBL, AF217787; AAF43005.1; -.

InterPro; IPR000889; Glut_peroxidase.

Pfam; PF00255; GSHPX; 1.

PRINTS; PR01011; GLUTPROXDASE.

PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
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NON_TER
SEQUENCE
                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EXTRACELLULAR GLUTATHIONE PEROXIDASE.
HOMO Sapiens (Human).
Eukbryota: Mctazoa: Chordata: Craniata: Vertebrata:
Mammalla: Eutheria: Primates: Catarrhini: Hominidae
  SEQUENCE FROM N.A. Wickstead B., Ersf
                                Eukaryota; Euglenozoa;
NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                   Comhair S.A.A., Thomassen M.J., Erzurum S.C.; "Differential induction of nitric oxide synthase 2 and extracellular gluthatione peroxidase in airways of healthy individuals exposed to 100% O2 or cigarette smoke.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gatesy J., Hayashi C., Cronin M., Mol. Biol. Evol. 0:0-0(0).
EMBL; U53900; AAB08405.1; -.
Interpre; IPR001508; Casein.
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                                                       Trypanosoma
                                                                               VARIANT SURFACE GLYCOPROTEIN.
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                                            Trypanosomatidae;
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SEQUENCE
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF207634; AAK21842.1; ...
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TISSUE-PLACENTA;
Lee C.C., Yazdani A., Wehnert M., Bailey J
Coolbaugh M.I., Chinault C.A., Baldini A.,
Caskey C.T.H.;
                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-AUG-1998 (TrEMBLrel. 07, (CLONE XP6AllB) (FRAGMENT).
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Spermatophyta; Magnollophyta;
Rapateaceae; Schoenocephalium.
NCBI_TaxID=142441;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NADH DEHYDROGENASE F (FRAGMENT).
                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                     SEQUENCE FROM
                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                              Q15898;
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79703 MW;
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Primates;
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0; Mismatches
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9D5C330AF1167836 CRC64;
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Catarrhini; Hominidae;
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01-MAY-2000 (TREMBLRel. 13, Last annotation update)
PHOTOSYSTEM I REACTION CENTER SUBUNIT IV, PSI-E.
Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac
Spermatophyta; Magnoliophyta; eudicotyledons; core eudico
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
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Lagoutte B., Vallon O.; "Purification and membrane topology of PSI-D of the photosystem I reaction center."; Eur. J. Biochem. 205:1175-1185(1992).
SEQUENCE 8 AA; 1082 MW; 2145BB1324069044
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NCBI_TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                         McCracken A., Uhlenbusch I., Gellissen G.;
"Structure of the cloned Locusta migratoria mitochondrial genome:
restriction mapping and sequence of its ND-1 (URF-1) gene.";
Curr. Genet. 11:625-630(1987).
EMBL; X05286; CAA28905.1; -.
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01-JUN-2001 (TrEMBLrel. 17, L;
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Q62721;
                                               SEQUENCE FROM N.A. Should be supported by the results of the reproductor activity and protein binding sites of the respuences of the human cytokeratin 19 gene."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databasement and 45973; BAB40770.1; -.
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01-NOV-1996 (TrEMBLrel.
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                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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EMBL: U17178; AAA86692.1; -.
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
CYTOKERATIN IV GENE UPSTREAM REGION (FRAGMENT).
                                                                                                                                                                                                                                Lutz P.G., Moog-Lutz C., Houzel-Charavel A., (Submitted (JUN-1998) to the EMBL/GenBank/DDBJ EMBL; AJ007030; CAA07429.1; -.
                                                                                                                                                                                                                                                                                                                                  STRAIN-SV129 D3;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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01-MAY-2000 (TrEMBLrel. 13, Last anno
PROTEINASE 3 (FRAGMENT).
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"Enhancer elements directing cell-type-specific cytokeratin genes and changes of the epithelial transfections of hybrid cytokeratin genes.";
EMBO J. 8:117-126(1989).
EMBL; X14478; CAA32640.1; -
EKFaLIn; Intermediate filament.
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Eukaryota; Metazoa; Chordala; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
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NCBI_TaxID=9913;
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Q9U046;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 17, Last annotation update)
01-UN-2001 (TrEMBLRel. 17, Last annotation update)
FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 2 ISOFORM
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Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
"Isoform Diversity among Fibroblast Growth Fa
Is Generated by Alternative Promoter Usage an
Splicing.";
J. Biol. Chem. 275:2589-2597(2000).
EMBL; AF199609; AAF31396.1; -.
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Eukaryota; Metazoa; Chordata;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Catarrhini;
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MEDLINE=98315113; PubMed=9649539;
Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska
Sueltmann H., Figueroa F., Klein J.;
"Linkage relationships and haplotype polymorphism among cichl
                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B LOCUS 4 (FRAGMENT).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroide.
Cichlidae; Oreochromis.
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MHC CLASS II B LOCUS 1 (FRAGMENT)
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLING=98315113; PubMed=9649539;

Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-
Sueltmann H., Figueroa F., Klein J.;

"Linkage relationships and haplotype polymorphism
class II B loci.";
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Genetics 149:1527-1547(1998).
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EMBL; AF049992; AAC41331.1; -.
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B LOCUS 4 (FRAGMENT).
01-cochromis niloticus (Nile tilapia) (Tilapia nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroide:
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O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS II B LOCUS 4 (FRAGMENT).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Cukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroide;
Cichlidae; Oreochromis.
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"Linkage relationships and haplotype polymorphism class II B loci.",
Genetics 149:1527-1547(1998).
EMBL; AF049995; AAC41334.1; -.
                                                                                                                                                  MEDLINE=98315113; PubMed=9649539;
Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska
Sueltmann H., Figueroa F., Klein J.;
"Linkage relationships and haplotype polymorphism among cichl
"Class II B Loci.";
Class II B Loci.";
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NCBI_TaxID=8128;
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Macey J.R., Schulte J.A. II, Larson A.;

"Evolution and information content of the mitochondrial genomic structural features illustrated with acrodont lizards.";

Syst. Biol. 49:257-277(2000).
       Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B. Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.; "Evaluating Trans-Tethys migration: An example using phylogenetics."; Syst. Biol. 49:233-256(2000). EMBL, AF128495; AAG00722.1; -.
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Curr. Genet. 12:247-250(1987).
EMBL; X05881; CAA29303.1;
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
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"The gene for the 9 kd polypeptide, a possible apoprotein iron-sulfur centers A and B of the photosystem I complex,
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STRAIN-BRIGHT YELLOW 4; TISSUE-LEAVE;
MEDLINE-88210537; PubMcd-3329576;
Hayashida N., Matsubayashi T., Shinozaki K.,
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Mol. Biol. Evol. 14:30-39(1997).
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EMBL; AF128500; AAG00737.1; -.
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l AA;
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                                                                                                                                                                                           11
1341 MW;
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el. 16, Last annotation update)
SUBUNIT I (FRAGMENT).
                                                                                                   25.0%;
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                                                                                                          .0%;
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                                                                                   Mismatches
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.1e+03;
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Title:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Word size :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      January 14, 2002, 07:56:31;
: /SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT: *
:/SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search time 81.39 Seconds (without alignments)
7.281 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | ø | | | COMMENSATION | |
|--------|-------|-------|-----------------|----|--------------|--------------------|
| Result | | Query | | | | |
| NO. | Score | Match | Match Length DB | | ID | Description |
| 1 | 3 | 37.5 | 7 | 19 | AAW65247 | Peptide containing |
| 2 | ω | 37.5 | 24 | 20 | AAW74457 | Fibroblast growth |
| ω | ω | 37.5 | 24 | 21 | AAY90893 | Fibroblast growth |
| 4 | ω | 37.5 | 34 | 22 | AAM15839 | Peptide #2273 enco |
| տ | ω | 37.5 | 34 | 22 | AAM28350 | Peptide #2387 enco |
| Ó | ω | 37.5 | 34 | 22 | AAM03577 | Peptide #2259 enco |
| 7 | ω | 37.5 | 53 | 11 | AAR08007 | Modified murine ep |
| 80 | w | 37.5 | 72 | 22 | AAG77776 | Human colon cancer |
| 9 | w | 37.5 | 90 | 21 | AAG28199 | Arabidopsis thalia |
| 10 | w | 37.5 | 96 | 21 | AAG28198 | Arabidopsis thalia |
| 11 | ω | 37.5 | 104 | 14 | AAR38596 | Human lambda light |

| | 49 | 48 | 47 | | 45 | | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 |
|-----|----------|------------|----------|----------|----------|------------------|--------------------|--------------------|----------|----------|----------|----------|----------|--------------------|-------------------|----------|-------------------|----------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|----------|----------|------------|--------------------|-----|-----|--------------------|----------|----------|-----------|--------------------|--------------------|
| N | N | N | N | 2 | Ν | 2 | Ν | ۵ | 2 | 2 | 2 | N | N | N | Ν | N | 2 | 2 | N | 2 | N | ω | ω | ω | w | ω | w | ω | ω | ω | ω | ω | ω | ω | ω | ω | ω | ω |
| 5. | <u>ა</u> | 5 | 5 | 5 | | | | 5 | 5 | 5 | 5 | | 5 | 5 | 5 | ū | 5 | 5 | 5 | 5 | 5 | 7. | 7. | 7. | 7. | 7. | .7 | .7 | 7. | .7 | 7. | 7. | 7. | 7. | | 37.5 | 37.5 | 37.5 |
| 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | w | ω | ω | ω | ω | ω | w | 685 | 685 | 685 | 684 | 684 | 684 | 533 | 329 | 280 | 230 | 226 | 226 | 164 | 158 | 129 | 105 | 104 |
| 7 | տ | w | w | N | | 2 | | | | | N | | | 2 | 22 | 19 | 19 | 17 | 17 | 16 | 15 | 17 | 17 | 17 | 17 | 17 | 17 | 15 | 21 | 21 | 18 | 21 | 16 | 21 | 22 | 22 | 21 | 19 |
| 135 | AAP40339 | AAP20210 | AAP20208 | AAP10625 | AAP10620 | AAP10401 | AAP10433 | AAP10599 | AAP10386 | AAP10375 | AAP10373 | AAP10372 | AAP10370 | AAP10154 | AAB92005 | AAW41282 | AAW56219 | AAR90601 | AAR98547 | AAR84691 | AAR48523 | AAW17590 | AAW17586 | AAW17582 | AAW17589 | AAW17585 | AAW17581 | AAR44893 | AAB08730 . | AAB08728 | 43 | | AAR72680 | AAG28197 | AAG75907 | 573 | AAG02234 | AAW58496 |
| of | e of er | lgesic and | ic an | ö | - | Agonist peptide. | Analgesic tetrapep | N-adamantane tetra | ana | in-like | lin-like | - | w | Sequence of trypto | FMRF neuropeptide | ptosi | Anti-inflammatory | errin | e fo | Bovine lactoferrin | Lactoferrin derive | | Thermoanaerobacter | Thermoanaerobacter | Thermoanaerobacter | Thermoanaerobacter | 7 | heria | acid | Amino acid sequenc | - | | Human plasma gluta | _ | colon | colon car | Human secreted pro | Human lambda light |

ALIGNMENTS

| > | e e x | PX | FΤ | FΤ | FT | FT | FΤ | FT | ΤŢ | FT | FH | XX | SO | × | KW | ΚW | × | DE | × | DΤ | × | AC | XX | ID | AAW | RESC |
|----|-----------------------|------------------------|----------------------|---------------|------------------|---------------|----|---------------|------------------------------|--------------------|----|----|---------------|---|------------------------------------|---------------------------|---|---|---|------------------------------|---|--------------|----|--------------------------------------|----------|----------|
| AA | XX PD 28-MAY-1998. | xx PN W09822125-A1. | FT /note= "Glu(OBz)" | Modified-site | | Modified-site | | Modified-site | | FT Modified-site 1 | | | OS Synthetic. | | KW APC; substrate; peptidomimetic. | | | DE Peptide containing 6-peptidylamino-1-naphthylenesulphonamide moiety. | | DT 02-OCT-1998 (first entry) | | AC AAW65247; | | ID AAW65247 standard; peptide; 7 AA. | AAW65247 | RESULT 1 |
| | | | | , | honamide moiety" | | | • | d by t-butoxycarbonyl (BOC)" | | | | | | , | ein C; blood coagulation; | | lenesulphonamide moiety. | | | | | | | | |

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RESULT
AAW74457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               дδ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to peptidomimetics containing 6-peptidylamino-1-naphthalenesulphonamide moleties. They are peptidomimetics of natural substrates for activated protein C (APC), whose substrates are promoters of the blood coagulation process. The present sequence represents a specifically claimed peptidomimetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptidyl-amino-1-naphthalene-sulphonamide compounds - are peptidomimetics of natural substrates for activated protein C, useful as promoters of the blood coagulation process
                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                         Agonist identification;
Graves' disease; thyroi
Identifying agonists of orphan receptors from their effect on
                        WPI; 1999-105468/09
                                               Behan DP,
                                                                                                       14-APR-1997;
                                                                                                                                                      22-OCT-1998
                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                       adenylate cyclase const
thyrotropin stimulating
                                                                                                                                                                                                                                                                                            schizophrenia;
                                                                                                                                                                                                                                                                                                                                          Fibroblast growth factor 3 receptor mutational cassette
                                                                                                                                                                                                                                                                                                                                                                   12-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                         AAW74457;
                                                                                                                                                                                                                                                                                                                                                                                                               AAW74457 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-312167/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Butenas S, Mann KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-1996;
                                                                     (BEHA/) BEHAN D P.
(CHAL/) CHALMERS D T.
                                                                                                                               14-APR-1998;
                                                                                                                                                                             WO9846995-A1
                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BUTE/) BUTENAS S. (MANN/) MANN K G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 wrxxs 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 wrxxs 6
                                                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 37.5%; Sy Similarity 100.0%; Similarity 100.0%; Sy Conservative O;
                                              Chalmers DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                 se; thyroid adenoma; hypertension; cardiomyopathy;
   Kaposi's sarcoma; fibroblast growth factor receptor;
lase constitutive activator; thyrotropin receptor;
                                                                                                       97US-0839449
                                                                                                                               98WO-US07496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0031359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US21075
                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                    /label= Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50pp; English.
                                                                                                                                                                                                                                                                        hormone; beta-adrenergic receptor
                                                                                                                                                                                                                                                                                                                    orphan receptor; constitutively active OR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 3; DB 1; Pred. No. 4.3
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               24 AA
                                                                                                                                                                                                  Asp, Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 19; Lc..
40.4.3e+05;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 7;
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 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT
AAY90893
Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, thyroid adenoma, hypertension, cardiomyopathy, schizophrenia, major depression, Kaposi's sarcoma and many others tabulated). It is based on identification of agents that reduce receptor activation, rather than compounds that antagonise the normal ligand. Once identified, (inverse) agonists can be used to study OR function. The method does not require knowledge of the endogenous receptor ligand or receptor function, and identifies directly compounds that inhibit the activated receptor, i.e. able to block both ligand-dependent and independent activation, rather than only the ligand-dependent process, as is the case with compounds identified by ligand-dependent assays. It should accelerate drug discovery at a wide range of OR and since activated receptors have a greater response to the agents, potential drugs are more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutational cassette. The invention relates to a method for the identification of candidate compounds as agonists, including inverse or partial, of an orphan receptor (OR), which comprises: (i) applying test compound to constitutively active OR; and (ii) measuring its effect on OR. The method is particularly used to identify inverse agonists of G protein-coupled OR, i.e. potential therapeutic agents for treating conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which constitutively active OR are implicated (e.g. Graves, conditions in which conditions in which constitutively active OR are implicat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identification; modulator; cell surface membrane receptor; treatment; orphan receptor; antithyroid; antidiabetic; neuroleptic; antidepressa cytostatic; G protein-coupled receptor agonist.
                                                        Behan DP,
                                                                                                                                                                        13-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibroblast growth factor 3 receptor mutational cassette #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY90893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY90893 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constitutively active receptor - particularly therapeutically active inverse agonists at G protein coupled receptors, without requiring knowledge of endogenous ligand or receptor function
                                                                                                             (AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                             12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                             WO200021987-A2
                                                                                                                                                                                                                                                                                     20-APR-2000.
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                                                        Chalmers DT;
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                                                                                                                                                                                                                             99WO-US23935
                                                                                                                                                                        98US-0170496
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  /label= Glu, Asp, Gln,
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100.0%; Pr
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Pred. No.
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b. 2.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antidepressant;
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WPI; 2000-317935/27

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method for directly identifying a compound having inverse agenist activity, partial agenist activity or agenist activity to a constitutively active orphan receptor (ORR). The method comprises determining the efficacy of the compound by contacting it with the ORR. A compound identified by the above method having inverse agenist activity to ORR is useful for the treatment of diseases characterised by constitutive activation of the receptor e.g. Graves' disease, male precoclous puberty, Jansen's disease, retinitis pigmentosa, hypoparathyroidism, neuropsychiatric diseases, schizophrenia, major depression, and cancerous growth in Kaposi's sarcoma. The method can identify (I) directly without prior knowledge or use of receptor ligands and is useful for accelerating drug discovery at a broad range of ORR. The present sequence represents a fibroblast growth factor 3 receptor invalidational cassette, which is used in the exemplification of
Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying compounds with inverse agonist activity to orphan receptor: useful for treating e.g. Graves' disease, and schizophrenia, involves contacting candidate compounds with constitutively activated receptors
                                             WPI; 2001-488901/53.
                                                                                                                                                               03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                             26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                          04-FEB-2000;
                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                  W0200157278-A2
                                                                                                                                                                                                                                                                                                                                                                            cervical
                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #2273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM15839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM15839 standard; Protein; 34 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 47; 110pp; English.
                                                                                                     (MOLE-)
                                                                                                                                                  27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention.
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                                                                                                     MOLECULAR DYNAMICS INC.
                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 AA;
                                                                                                                                2000US-01B0312.
2000US-0207456.
2000US-060840B.
2000US-0632366.
2000US-0236687.
2000US-0236589.
2000US-0236583.
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                                                                                                                                                                                                                                                                                                                                                                                                                      encoded by probe for measuring cervical gene expression
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                                                                       Chen W,
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b. 2.7e+02;
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RESULT AAM28 AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AS AAM28 AA
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Best Local
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                WPI;
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genetic disorder.
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                                                                                                                                                                                     Claim 27;
                                                                                                                                                                                                                                   analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #2387 encoded by probe for measuring placental gene expression.
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| 18 syxg
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                                                                                                                                                                                                                                        genome-derived single exon nucleic acid zing gene expression in human placenta -
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                                                                                                                                                                                     SEQ
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                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                 Hanzel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                     ID No
                                                                                                                                                                                                                                   expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                 DK,
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                                                                                                                                                                                     28619;
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                                                                                                                                                                             654pp;
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Pred. No.
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                                                                                                                                                                                English.
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                                                                                                                                                                                                                                                        probes
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                                                                                                                                                                                                                                                              useful
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Best Local
                                                                                                                                   The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                 Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-2001
                                                                                                 breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                           Novel single exon nucleic acid probe used to measuring in a human breast -
                                                                                                                                                                                                                                                                                                                              WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; human; breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #2259
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                                                            Sequence
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory disease; proliferative breast disease; non-carcinoma tumour
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                                                                                                                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                SEQ ID No 12317; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
                                                                34
                                                                                                                                                                                                                                                                                                                                                                                                    ; 2000US-0180312
2000US-0207456
; 2000US-0608408
; 2000US-0632366
; 2000US-0632366
; 2000US-0234369
; 2000US-0236359
; 2000US-0024263
 37.5%; So ilarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.5%;
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 Score 3; DB 2; Pred. No. 3.5
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŘΑ
                                                                                                                                                                                                                                                                                                                                                      Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for measuring breast gene
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DB 22; Le..
lo. 3.5e+02;
0;
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3.5e+02;
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                        Length 34;
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   Indels
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  0;
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  Gaps
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   0;
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RESULT
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                                                                                           AAG77776
                                                                                                     RESULT
                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
      Human; colon cancer; colon cancer antigen; diagnosis;
                         Human colon cancer antigen protein SEQ ID NO:8542.
                                             03-SEP-2001
                                                                                                                                                                                                                                                     The human rEGF is used to treat oversecretion of gastric acid epithelial wound. EGF is modified to increase its chemical stability. Its storage life is improved without diminishing biological activity. The proteins may be prepared by traditi
                                                                                                                                                                                                                                                                                                      Claim 9; Page 25; 32pp; English.
                                                                                                                                                                                                                                                                                                                       greater stability and improved storage life.
                                                                                                                                                                                                                                                                                                                                Human epidermal growth factor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified murine epidermal growth factor; stability; storage; epithelial wounds; gastric acid secrection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR08007 standard; protein; 53
                                                                AAG77776;
                                                                                 AAG77776
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                   chemical or recombinant means.
See also AAR08004.
                                                                                                                                                                                                                                                                                                                                                     WPI; 1990-361427/48.
                                                                                                                                                                                                                                                                                                                                                                        Nascimento CG,
                                                                                                                                                                                                                                                                                                                                                                                                            12-MAY-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified murine epidermal growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1991
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                                                                                                                               5 syxg
||||
9 syxg
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                                                                                 standard; Protein;
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                                                                                                                                                                                                                   53 AA;
                                                                                                                                                                     Conservative
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                                            (first entry)
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                                                                                                                                                                37.5%; 50
100.0%; Pro
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                                                                                  72
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Pred. No.
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                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                  is substituted at position
                                                                                                                                                                              DB 11; L
b. 4.6e+02;
                                                                                                                                                                                      Length 53;
                                                                                                                                                                      Indels
        detection;
                                                                                                                                                                                                                                                         traditional
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                                                                                                                                                                                                                                                                                     or
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                                                                                                                                                                    Gaps
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0;

colorectal carcinoma

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AAG28199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon CC cancer-associated nucleic acid molecules (N) and proteins (P), where CC the proteins are collectively known as colon cancer antigens. The colon CC cancer antigens have cytostatic activity and can be used in gene CC therapy and vaccine production. N and P may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate P CC expression. For example, N and P may be used to treat disorders CC associated with decreased expression by rectifying mutations or deletions CC in a patient's genome that affect the activity of P by expressing CC inactive proteins or to supplement the patients own production of P. CC Additionally, N may be used to produce the colon cancer-associated Ps, CC by inserting the nucleic acids into a host cell and culturing the cell CC by inserting the proteins. N and P can be used in the prevention, diagnosis CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 CC and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
    EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPT; 2001-235357/24.
N-PSDB; AAH37183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1999;
03-NOV-1999;
                             Arabidopsis thaliana
                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 33328
                                                                                                                                               17-0CT-2000 (first entry)
                                                                                                                                                                                                             AAG28199 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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99US-0163280.
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100.0%; Pred. No. 5.7e+02;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                              Indels
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 08-JUN-1999
10-JUN-1999
11-JUN-1999
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14 - WAZ 1999
14 - WAZ 1999
18 - MAY - 1999
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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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19-APR-1999,
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23-APR-1999,
23-APR-1999,
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05-MAR-1999,
09-MAR-1999,
23-MAR-1999,
25-MAR-1999,
29-MAR-1999,
01-APR-1999,
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08-APR-1999;
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99US-0132484
99US-0132485
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99US-0130510.
99US-0130891.
99US-0131449.
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99US-0126264.
99US-0126785.
99US-0127462.
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99US-0132407
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99US-0128714
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02-JUL-1999; 06-JUL-1999; 08-JUL-1999; 09-JUL-1999; 12-JUL-1999; 13-JUL-1999; 14-JUL-1999;

14-JUL-1999; 15-JUL-1999; 16-JUL-1999;

16-JUL-1999; 19-JUL-1999;

19-JUL-1999; 19-JUL-1999; 19-JUL-1999;

19-JUL-1999; 19-JUL-1999;

20-JUL-1999; 21-JUL-1999;

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RESULT 10
AAG28198
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Best Local S
Matches 4
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24-SEP 1999
28-SEP 1999
29-SEP 1999
04-OCT 1999
05-OCT 1999
07-OCT 1999
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13-OCT 1999
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29 - CCT - 1999
                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 33327.
                                                                                                                                                                                                                                                                                   AAG28198;
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                                           25-FEB-2000; 2000EP-0301439
                                                                        06-SEP-2000
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                                                                                                                                  Arabidopsis thaliana
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syxg
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99US-0123180.
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| 9US-014069 9US-014082 9US-014128 9US-014118 9US-014215 9US-014205 9US-014239 9US-014239 9US-014239 9US-014239 | 99US-0138540 99US-0138847 99US-0139452 99US-0139453 99US-0139454 99US-0139456 99US-0139457 99US-0139457 99US-0139457 99US-0139467 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0139763 99US-0139763 99US-0139763 99US-0139817 99US-0139817 99US-0139817 | 903-01324 903-01324 903-013421 903-013421 903-013421 903-013476 903-013512 903-013512 903-013535 903-013535 903-013535 903-013535 903-013535 903-013535 903-013535 | 9US-012554 9US-012578 9US-012626 9US-012678 9US-012873 9US-0128873 9US-013087 9US-013087 9US-013089 9US-013144 9US-013248 9US-013248 |
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| 9US-015236 9US-015307 9US-015401 9US-015477 9US-015473 9US-015547 9US-015548 9US-015548 9US-015645 9US-015645 | 99US-0147935 99US-0148171 99US-0148341 99US-0148365 99US-0149368 99US-0149175 99US-0149723 99US-0149723 99US-0149723 99US-0149930 99US-01510884 99US-01510884 99US-0151088 99US-0151088 99US-0151088 | 908-014514 908-014514 908-014521 908-014521 908-014521 908-014591 908-014638 908-014638 908-014638 908-014730 908-014730 908-014730 908-014730 | 908-014400 908-014400 908-014430 908-014433 908-014433 908-014433 908-014433 908-014433 908-014433 908-014488 908-014488 |

99US-0157865

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RESULT 1
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Best Local
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07-OCT-1999;
08-OCT-1999;
                                                                                                                                                               Antibody; variable domain; light; L; heavy; H; c affinity; antigen; immunogenicity; humanisation;
        W09311794-A
                                        Misc-difference 89..92
                                                                   Misc-difference 87
                                                                                            Misc-difference 32
                                                                                                                      Misc-difference
                                                                                                                                Key
                                                                                                                                               Homo sapiens
                                                                                                                                                                                       Human lambda light chain subgroup 4 (hL4).
                                                                                                                                                                                                                                          AAR38596 standard; peptide; 104 AA.
                                                                                                                                                                                                          28-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-OCT-1999;
18-OCT-1999;
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les 4; Conserv
                                                                                                                                                                                                                                                                                                     5 syxg 8
                                                                                                                                                                                                                                                                                    syxg 47
                                                                                                                                                                                                                                                                                                                        Conservative
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99US-0160814
99US-0160815
99US-0160981
99US-0160981
99US-0160981
99US-0160989
99US-0161405
99US-0161406
99US-0161361
99US-0161361
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99US-0159295.
99US-0159329.
99US-0159330.
99US-0159331.
99US-0159637.
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99US-0161992.
99US-0161993.
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99US-0159584.
99US-0160741.
99US-0160767.
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99US-0158232
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                                                                                                    /note= "residue conserved in less than 50%
    known sequences of hL4"
                                                                                                                             Location/Qualifiers
                                 /note=
                                                          /note=
                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                37.5%;
                       "residues conserved in less than 50% of the known sequences of hL4"
                                                                          "residue conserved in less than
known sequences of hL4"
                                                "residue conserved in less than 50% known sequences of hL4"
                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                Score 3; DB 21; L
Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                       H; consensus;
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RESULT 12
AAW58496
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The consensus amino acid sequences for the subgroups of light chains (hK1 - AAR38590, hK3 - NGK, hK2 - GST, hL1 - AAR38591, hL2 - AAR38592, hL3 - AAR38593, hL6 - AAR38594, hK4 - AAR38595, hL4 - AAR38596, and hL5 - AAR38597) and heavy chains (hH3 - AAR38598, hH1 - AAR38599 and hH2 - AAR38600) of human variable domains may be used to prepare, for example, a modified mouse antibody variable domain that retains the affinity of the natural domain for antigen while exhibiting reduced immunogenicity in humans.

Unlike other methods of humanisation, which advocate the replacement of entire antibody framework regions with those of human antibodies, this method involves only the introduction of human residues into those positions not critical for antigen binding. This ensures that the binding properties of the modified antibody
                                                   /note=
Misc-difference 89
                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin; depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis; autoimmune disease; rheumatoid arthritis; type I diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies prepn. used for treatment of auto-immune diseases replacement of critical residues to reduce immunogenicity but retain binding affinity, etc.
                         Misc-difference
                                                                                                                                       Misc-difference
                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                   Synthetic.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lambda light chain subgroup 2 consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW58496 standard; protein; 104 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                            /note=
90
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32
/note=
                                                                                                                                                                                                                                                                         Location/Qualifiers
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100.0%; Pred. No.
                                                   "not
"not specified"
                                                                                                          "not
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5. 7.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                         a method has been developed of depleting CD5+ cells in an animal. The comprises administering a cytotoxic protein containing a modified immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig conclude or an immunoconjugate or fusion protein containing an anti-CD5 Ig conclude or an immunoconjugate or fusion protein containing an anti-CD5 Ig conclude or an immunoconjugate or fusion protein containing an anti-CD5 Ig molecule, and where the modified Ig variable domain comprises at CC least one of (a) a modified heavy chain variable region (see AAW58478 or CC CAAW58480), and (b) a modified heavy chain variable region (see AAW58479 CC or AAW58481), where AAW58478 and AAW58479 are humanised forms of the H65 Ight and heavy chain variable domains with low risk amino acid substitutions [i.e. low risk of reducing antigen-binding specificity.] CC and AAW58480 and AAW58481 are humanised forms of the H65 Ight and heavy chain variable domains with moderate risk amino acid substitutions and are present in humanised H65 antibody ha3 (ATCC HB 11206). The method is CC customatosus, rheumatoid arthritis, psoriasis or type I diabetes. The present sequence represents a consensus amino acid sequence for light chain subgroups of human antibody variable domains, from the present revertion.
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                         Query Match
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13-DEC-1991;
14-DEC-1992;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Column 55-56; 77pp; English
                                       gene therapy;
                                                     Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                   06-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
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                                                                                    Human secreted protein, SEQ ID NO: 6315.
                                                                                                                                               AAG02234;
                                                                                                                                                                        AAG02234 standard;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                 (first
                                        chromosome mapping.
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92WO-US10906.
95US-0472788.
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100.0%; Pr
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p; Pred. No. 7.2
p; Mismatches
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RESULT 1
AAG75733
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Best Local
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                                                                          29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                05-APR-2001
                                                                                                                                                                                                                                                               WO200122920-A2
                                                                                                                                                                                                                                                                                                                                                                     Human; colon cancer; colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human colon cancer antigen protein SEQ ID NO:6497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-2001
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                                                                                                                                                           28-SEP-2000;
                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic, forensic, gene therapy and chromosome mapping procedures
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99US-0163280
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100.0%; Pr
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0; Mismatches
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to 5'ESTs and
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(HUMA-) HUMAN

GENOME SCI INC

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders
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         N-PSDB;
             WPI; 2001-235357/24.
N-PSDB; AAH35312.
                                                                                                                 29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                      WO200122920-A2
                                                                                                                                                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                        Human colon cancer antigen protein SEQ ID NO:6671
                                                                                                                                                                                                                                                                                                                                                        03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                 AAG75907 standard; Protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 7974-7975; 9803pp; English.
                                                       Rûben SM,
                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                            28-SEP-2000;
                                                                                                                                                                                         05-APR-2001
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                                                                                                                                                                                                                                                                                colorectal
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                                                                                                                                                                                                                                                                                            colon cancer; colon cancer antigen; diagnosis; detection;
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                                                        Barash SC,
                                                                                                                                                                                                                                                                                carcinoma
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                                                                                                                                                            2000WO-US26524.
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99US-0163280.
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and/or treating colorectal cancers -
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Best Local Similarity
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25-FEB-1999

05-MAR-1999

09-WAR-1999

23-MAR-1999

25-MAR-1999

25-MAR-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG28197 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 33326
                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG28197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                       25-FEB-2000;
                                                                                                                                                                                                                                                                      06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                  termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                       2000EP-0301439
99US-0127462.
99US-0128714.
99US-0128714.
99US-0129845.
99US-0130077.
99US-0130047.
99US-0130610.
99US-0130891.
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99US-0126785
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99US-0123180
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No. 9.5e+02;
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| 10-MAY-1999; 21-MAY-1999; 22-MAY-1999; 22-MAY-1999; 23-MAY-1999; 26-MAY-1999; 27-MAY-1999; 28-MAY-1999; 28-MAY-1999; 29-MAY-1999; 20-JUN-1999; 21-JUN-1999; 21-JU | 28-APR-1999; 30-APR-1999; 30-APR-1999; 04-MAY-1999; 05-MAY-1999; 06-MAY-1999; 07-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; |
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| 990S-0134941 990S-0135134 990S-0135533 990S-0135629 990S-0136692 990S-0137522 990S-0137522 990S-0137522 990S-0139453 990S-0139453 990S-0139453 990S-0139455 990S-0139455 990S-0139455 990S-0139455 990S-0139455 990S-0139457 990S-0139461 990S-0139461 990S-0139461 990S-0139461 990S-0139461 990S-0139461 990S-0140853 990S-0140853 990S-0140823 990S-0140823 990S-0140823 990S-0140823 990S-0140823 990S-014085 990S-014085 990S-014085 990S-014085 990S-014085 990S-014085 990S-014085 990S-014085 990S-014085 990S-014085 990S-014085 990S-014085 990S-0144333 990S-0144333 990S-0144333 990S-0144333 | 908-011 908-011 908-011 908-011 908-011 908-011 908-011 908-011 |
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| R 28-JUL-1999 R 02-AUG-1999 R 02-AUG-1999 R 04-AUG-1999 R 04-AUG-1999 R 06-AUG-1999 R 06-AUG-1999 R 06-AUG-1999 R 09-AUG-1999 R 11-AUG-1999 | 21-JUL-1999; 99US-014481 21-JUL-1999; 99US-014508 21-JUL-1999; 99US-014508 22-JUL-1999; 99US-014508 22-JUL-1999; 99US-014508 22-JUL-1999; 99US-014519 22-JUL-1999; 99US-014519 23-JUL-1999; 99US-014521 23-JUL-1999; 99US-014521 23-JUL-1999; 99US-014521 23-JUL-1999; 99US-014521 23-JUL-1999; 99US-014521 23-JUL-1999; 99US-014521 27-JUL-1999; 99US-014531 27-JUL-1999; 99US-014591 |

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22-CCT-1999
25-CCT-1999
25-CCT-1999
25-CCT-1999
25-CCT-1999
The deduced amino acid sequence of the human plasma glutathione peroxidase as published (J. Biochem., 108, 1990,145-148). Immu
                           Disclosure; Fig 1; 33pp; French.
                                               New immunogenic oligo:peptide of human plasma glutathione peroxidase - and derived antibodies that do not recognise other forms of the enzyme and are useful in immunoassays, e.g. to detect selenium deficiency
                                                                                                               Chaudiere
                                                                                                                                                                                                                    W09506719-A
                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                           Human glutathione peroxidase; plasma; antibody; immunoassay; kidney; selenium deficiency; liver disease; graft rejection; hepatic cancer.
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28-OCT-1999;
                                                                                             WPI; 1995-115435/15.
                                                                                                                                 (BIOX-) BIOXYTECH SA. (BIOX-) BIOXYTECH.
                                                                                                                                                             03-SEP-1993;
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26-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0160741.
99US-0160767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0159584
                                                                                                                                                                                                                                               Location/Qualifiers 73
                                                                                                                                                                                                                                      /note= "unknown amino acid"
                                                                                                                                                                                                                                                                                                                                                                               peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.5%;
                                                                                                               Α,
                                                                                                               Malette P;
                                                                                                                                                                                                                                                                                                                                                                               226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 3; I
                                                                                                                                                                                                                                                                                                                                                                               AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Immunogenic

Indels

0;

Gaps

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Query Match
Best Local Similarity
Whiches 4; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB22828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                        peroxidase, nucleic of human pGPxH. The human pGPxH.
                                                                                                    This sequence represents human plasma glutathione peroxidase (pGPxH). The invention relates to this novel human glutathion peroxidase, nucleic acid encoding it, and to recombinant procof human pGPxH. The invention also encompasses applications if
                                                                                                                                                                                                                                                         Yu L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptides (e.g. see AAR72679) were derived from hydrophobicity/flexibility profiles of the published sequence. Peptides containing this sequence can be conjugated to carrier proteins and used to produce antibodies. The antibodies can be used to detect plasma glutathione peroxidase in immunoassays e.g. for detection of selenium deficiency or in diagnosis of certain kidney or liver diseases e.g. graft
                                                                                                                                                               Claim 2; Page 20-21; 26pp; Chinese.
                                                                                                                                                                                        New human glutathione peroxidase and use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasma glutathione peroxidase H; pGPxH; human; recombinant production.
                                                                   Sequence
                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                         29-OCT-1998;
                                                                                                                                                                                                                                                                                                                               29-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                      14-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                            CN1256312-A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB22828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB22828 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rejection or certain hepatic cancers.
                                                                                                                                                                                                                                                                                  (UYFU-) UNIV FUDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 syxg 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 syxg 8
                                                                                                                                                                                                                        2000-533631/49
DB; AAA90423.
                                                                                                                                                                                                                                                          Tu Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                   226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226
        37.5%; Score 3; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glutathione peroxidase H (pGPxH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                          Fu Q;
                                                                   ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                         98CN-0121973
                                                                                                                                                                                                                                                                                                                               98CN-0121973
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 73
                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                 "Encoded by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3; Pred. No.
            Mismatches
                                                                                                                                                                                                  its code sequence, preparation
                      DB 21; L
o. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; I
. 1.2e+03;
                                 Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                              glutathione
                                                                                                      production
ons for
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RESULT 19
AAW08430
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                                                                                                   The present sequence represents the representative construct fusion T6 CC which is involved in the rapumycin-dependent activation of signal CC transduction. This is involved in the construction of transcription CC factor fusion proteins, which in turn are involved in the production of canimal cells containing at least two recombinant DNAs. One DNA should cencode a chimeric protein which is capable of binding to rapamycin, or a capamycin analogue, and comprises at least one rapamycin binding domain CC (RBD) and at least one protein domain heterologous to it; the second crocombinant DNA should encode a second chimeric protein which is capable of forming a complex with rapamycin, or a rapamycin analogue, and the CC first chimeric protein and comprises at least one FKBP:rapamycin binding CC (FRB) domain and at least one domain heterologous to it. Contacting these genetically engineered cells with rapamycin or analogues, and the complex (between the fusion proteins, and the cc used for regulating biological events such as gene transcription, capamycin), and intracellular signal transduction pathway leading to ce.g. gene expression or appopical events such as gene transcription, and complex (between the fusion proteins, and the continuation of intracellular signal transduction pathway leading to ce.g. gene or inhibition of function of a gene whose cut, blockade of a gene or inhibition of function of a gene product. They are used cc recombinant proteins and viruses.
Query Match 37.5%; Score 3; DB Best Local Similarity 100.0%; Pred. No. 1. Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion protein; rapamycin binding domain; RBD; FKBP; FKBP; FKSO6-binding protein; FRB domain; genetic engineering; regulation; transcription; signal transduction; apoptosis; inhibition; virus; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New rapamycin-responsive transfected cells - contg. recombinant DNA encoding fusion proteins which act as biological switches for regulating biological events
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clackson T, Gilman MZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW08430 standard; Protein;
                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Page 109; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ARIA-) ARIAD GENE THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9641865-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rapamycin; responsive transfected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rapamycin-dependent activation of signal transduction fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW08430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    syxg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74
                                                                                               230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0598776.
95US-0481941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US09948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell;
                   DB 18; Le
o. 1.2e+03;
                                       Length 230;
   Indels
   0;
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   Gaps
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RESULT 2
AAB08728
                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                            The present sequence represents a consensus B7RP1 (B7 related protein-1) polypeptide. The specification also describes a CRP1 (CD28 related protein-1) polypeptide. The polypeptides are involved in T-lymphocyte activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are predicted to be a type I transmembrane protein. The nucleic acids are useful for regulating T cell activation or proliferation in an animal. The polypeptides are useful for treating, preventing ameliorating or diagnosing a T-cell mediated disorder in an animal. They can also be used to identify test molecules that bind to the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRP1; CD28 related protein-1; B7RP1; B7 related protein-1; T-lymphocyte activation; type I transmembrane protein; T cell activation; T cell proliferation; T-cell mediated disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 161-162; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-FEB-1999;
08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a consensus B7RP1 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB08728 standard; Protein; 280
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids encoding in the treatment, prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-543476/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yoshinaga SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JAN-2000; 2000WO-US01871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200046240-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB08728;
265 syxg 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 syxg 229
                                            5 syxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
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                                                                                                                                                                                                           280 AA;
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0244448
99US-0264527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Xaa represent unspecified amino acids"
                                                                                                                37.5%;
                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                Score 3; DB 21; Pred. No. 1.4e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑA
                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins CRP-1 and B7RP1 are useful diagnosis of T cell mediated disorde
                                                                                                                                Length 280;
                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
                                                                                           Gaps
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RESULT :
 XEXTX
                                                                                                                                      Дb
                                                                                                                                                         20
                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                        The present sequence represents a consensus B7RP1 (B7 related protein-1) polypeptide. The specification also describes a CRP1 (CD28 related protein-1) polypeptide. The polypeptides are involved in T-lymphocyte activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are predicted to be a type I transmembrane protein. The nucleic acids are useful for regulating T cell activation or proliferation in an animal.
          Diphtheria toxin (delta-147-148; H21X) mutant.
                                                                            AAR44893 standard; Protein; 533
                                                                                                                                                                                                                                                          The polypeptides are useful for treating, preventing ameliorating or diagnosing a T-cell mediated disorder in an animal. They can also be used to identify test molecules that bind to the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-1999;
08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRP1; CD28 related protein-1; B7RP1; B7 related protein-1; T-lymphocyte activation; type I transmembrane protein; T cell activation; T cell proliferation; T-cell mediated disorder.
                                  22-JUN-1994
                                                       AAR44893;
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 167-168; 174pp; English
                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful in the treatment, prevention and diagnosis of T cell mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-543476/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200046240-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB08730 standard; Protein;
                                                                                                                                     312 syxg
                                                                                                  22
                                                                                                                                                          ű
                                                                                                                                                 eyxg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                4;
                                                                                                                                                                                            Similarity
                                                                                                                                     315
                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SK
                                                                                                                                                                                                                                      329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of a consensus B7RP1 polypeptide
                                                                                                                                                                                 Conservative
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US01871
                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0244448
99US-0264527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                           37.5%; 5c.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Xaa
                                                                                                                                                                               Score 3; DB 2; Pred. No. 1.5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unspecified amino acids"
                                                                                                                                                                                           DB 21; L. 1.5e+03;
                                                                                                                                                                                0;
                                                                                                                                                                                                    Length 329
                                                                                                                                                                               Indels
                                                                                                                                                                               0;
                                                                                                                                                                               Gaps
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XXX AC XXX
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В
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                                                                                                                                                                                                                                         AAW17581
                                                                              RESULT
                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                              Oligonucleotide-directed mutagenesis of the wild-type diphtheria gene results in deletion of the codons for val-47 and active site residue Glu-148. The resulting mutein is not toxic, making it useful in diphtheria vaccines. The risk of reversion to toxicity is much lower for the 147-148 double mutant than for the prior art 148 single mutant, while its immunogenicity is not impaired. The 147-148 mutein opt. has other amino acid residues substd. or deleted, e.g. wild-type His(21) in fragment A. The specification includes the wild-type DT amino acid sequence (see AAR44888) but does not include any mutant sequences; the wild-type sequence was modified according to the description in the claims to give AAR44893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Protein
01-JUL-1997
                                                    AAW17581 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9325210-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reversion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DT; protein exotoxin; NAD-dependent ADP-ribosyltransferase; vaccine; diphtheria toxoid; deletion mutant; mutein; variant; double mutant;
                           AAW17581;
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; ; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       transformed cells, useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA encoding diphtheria toxin deletion mutants - wit toxicity and low risk of reversion, and derived toxoids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-007178/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collier RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1992;
                                                                                                                     19
                                                                              23
                                                                                                                                              5 syxg 8
                                                                                                                   syxg
                                                                                                                                                                        Similarity 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ54341
                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation; site-directed mutagenesis.
                                                                                                                                                                                                                                         533
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Killeen K,
(first entry)
                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-0901712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93WO-US04606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Diphtheria toxin mutant; Val(147) and
Glu(148) have been deleted and His(21)
is substd. by any other amino acid or
is absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                    protein; 684 AA
                                                                                                                                                                                   37.5%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "any amino acid
or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mekalanos
                                                                                                                                                                        0;
                                                                                                                                                                                      Score 3;
Pred. No.
                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۲.
                                                                                                                                                                                      ). DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other than wild-type His
                                                                                                                                                                                                 15;
                                                                                                                                                                                      .1e+03;
                                                                                                                                                                                                 Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ted and His(21) amino acid or
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                        0;
                                                                                                                                                                        Gaps
                                                                                                                                                                         0;
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Cyclomaltodextrin glucanotransferase; CGTase; enzyme;

starch; cyclomaltodextrin; cyclodextrin; pesticide;

Thermoanaerobacter CGTase variant beta-cyclodextrin

#1.

Bacillus circulans;

thermoanaerobacter;

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Modified-site
                      Modified-site
                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transglycosylation; cyclic glucose oligomer; glucose oligosaccharide; cholesterol removal; food stabiliser; vitamin stabiliser; fungicide; plastic laminate; biodegradable plastic; mutein.
                                  Modified-site
                                                       Modified-site
                                                                              Modified-site
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87
                                                                                                                       /note-
147
                                                                                                                                                                                                                                       /note-
95
  /note-
169
                                  /label- D148x
/note- "X- Gly,
151
                                                                         149
/label- T147X
                                                                                                                                           /note-
146
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47
                     /label≎ P149W
152
                                                      150
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
21
              /label- T150x
                                                                  /note-
                                                                                            /note-
                                                                                                   /label-
                                                                                                               /note: "possible insertion of Pro,
                                                                                                                                    'label⊹ S145X
                                                                                                                                                       /label~ H140X
                                                                                                                                                                    'label⇔ D135L
                                                                                                                                                                                /labelo W101x
/noteo "Xo Gly, Ala"
                                                                                                                                                                                                /notes "X= Gly,
102
                                                                                                                                                                                                            /label∽ H98x
                                                                                                                                                                                                                        /label~ S94X
/note~ "X~ Gln,
                                                                                                                                                                                                                                            /label- G93x
/note- "X- Gly,
                                                                                                                                                                                                                                                               /label⊹ G92V
                                                                                                                                                                                                                                                                            /label= F91ax
/note= "X= Ala, Val,
                                                                                                                                                                                                                                                                                                /note∘ "x∘ Ala,
                                                                                                                                                                                                                                                                                                       /label∵ T91X
                                                                                                                                                                                                                                                                                                                   /labelo S90X
/noteo "Xo Gly,
                                                                                                                                                                                                                                                                                                                                              /note-
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                                                                                                                                                                                                                                                                                                                                                                 'note-
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                                                                                                                                                                                                                                                                                                                                                                                            /label⊹ L87X
                                                                                                                                                                                                                                                                                                                                                                                                       /label ~ K47X
/note ~ "X ~ Gln,
                                                                                                                                                                                                                                                                                                                                                                                                                                   ∕label- v21x
                                                                                                                                                                                                                                                                                                                                                                label- P88X
note- "X- Pro,
                                                                                                                                                                                                                                                                                                                                      "X~ Asp,
absent"
                                                                                    "Xo Pro, Ala, Phe,
                                                           "X: Ala, Leu, Ile,
Thr, or absent"
                                                                                                                                               "X- Ala, Arg,
                                                                                                                                                                                                                                                                                                                                                                                   "X∪ Ile,
        "Xo Ala,
                                                                                                                           "X Ala, Glu, Trp, Leu
                                                                                                                                                                                                                                                                                                                                                                                                                            "X- Phe,
        Ser"
                                                                                                                                                                                                     Ala"
                                                                                                                                                                                                                                                                                               Val,
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                                         Asn, Ala,
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                                                                                                                                                                                                                                                                                                                   Ala,
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absent"
                                         Gln"
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                                                                 Gly,
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                                                                                                               Ile,
                                                                 Tyr,
                                                                                           Ile,
                                                                                                                                                                                                                        Ser,
                                                                                                               Gln,
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                                                                 Arg,
                                                                                          Arg,
                                                                                                               or
                                                                                            Glu,
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 16-NOV-1995;
21-APR-1995;
17-OCT-1995;
(NOVO ) NOVO-NORDISK AS
                                                                 W09633267-A1
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                                       22-APR-1996;
                                                    24-OCT-1996
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            95DK-0001281.
95DK-0000477.
95DK-0001173.
                                       96WO-DK00179
                                                                                                               /label= Y373X
/note= "X= Asp,
376
                                                                                                                                   /note= "X= Ala, 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Y167X
/note= "X= Ala,
170
                                                                             /label= L600x
/note= "X= unspecified amino acid"
                                                                              /note=
                                                                                                /label= R375X
/note= "X= Ala,
                                                                                                                                                            'note=
                                                                                                                                                                  /label=
                                                                                                                                                                               /label= N326X
/note= "X= Gln,
                                                                                                                                                                                                                'note-
                                                                                                                                                                                                                                     /note-
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/note= "X- Ala,
                                                                                                                                                                                                                                                                                                                                    /label= N193X
/note= "X= Gly,
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/note= "X= Pro,
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/note= "X= Gly,
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                                                                                                                                                                                                                label= Y259X
note= "X= Phe,
                                                                                                                                                                                                                                                                                                                                                                                         label= F183X
note= "X= Phe,
                                                                                                                                                                                                                                   abel= H233X
ote= "X= His,
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ote= "X= Lys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Y178N
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"X= Thr,
                                                                                                                                                                                                                                                                                                                  "X= Leu,
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                                                                                                                                        Gly"
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                                                                                                                                                                                                                                                                                                                                                                      Asp"
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AAW17585
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                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                       modify the gene encoding this sequence. These sequences have greater product selectivity and/or reduced product inhibition (better yields) than wild-type CGTase. These mutant sequences are used to manufacture the 6 main CD types (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides, optionally in situ, e.g. during production of baked goods, to stabilise chemicals during their manufacture and in detergents. CD are known for their usefulness in foods, e.g. as a bread-improving agent, to encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals, pesticides or fungicides, to bind/remove lipophilic compounds such as cholesterol (e.g. in egg yolk or butter), in plastic laminates, films etc. and to make biodegradable plastics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence). CGTase catalyses the conversion of starch and similar via an substrates into cyclomaltodextrins (also known as cyclodextrins) via an intramolecular transglycosylation reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a hydrophobic internal cavity that form inclusion complexes with many small hydrophobic molecules. These CGTase mutants have a modified substrate binding and/or product selectivity, compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW17580-W17591, and AAW17606-W17652 represent mutant versions of t cyclomaltodextrin glucanotransferase (CGTase) of Thermoanaerobacter thermosulphurigenes sp. ATCC 53627. (see AAW06772 for wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New variants of cyclo:malto:dextrin glucanotransferase (CGTase) - have altered substrate binding, useful for prodn. of cyclodextrin(s) or linear oligosaccharide(s), opt. formed in situ in e.g. baked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                 cholesterol
                                                                                                                                                             Cyclomaltodextrin glucanotransferase;
                                                                                                                                                                                 Thermoanaerobacter CGTase variant beta-cyclodextrin #2.
                                                                                                                                                                                                     01-JUL-1997
                                                                                                                                                                                                                                             AAW17585 standard;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-485774/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andersen C,
         Modified-site
                                       Madified-site
                                                                                                  Synthetic
                                                                                                                       plastic
                                                                                                                                           transglycosylation;
                                                                                                                                                   thermoanaerobacter;
                                                                                                                                                                                                                         AAW17585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to this sequence. The mutants are created using primer mutagenesis to
                                                                     Modified-site
                                                                                                                                                                                                                                                                                               97
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                 24
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                                                                                                                                                                                                                                                                                            syxg
                                                                                                                                                                                                                                                                                                                  syxg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Page -; 161pp; English
                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                        684 AA;
                                                                                                                               removal;
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dijkhuizen
                                                                                                                                                                                                     (first entry)
        /note=
87
                                        /note=
47
                                                                      Location/Qualifiers
/label= L87H
                            'label=
                                                           'label=
                                                                                                                      al; food stabiliser; vi
biodegradable plastic;
                                                                                                                                                                                                                                            protein;
                                                                                                                                cyclic glucose oligomer; glucose oligosaccharide; food stabiliser; vitamin stabiliser; fungicide;
                                                                                                                                                   starch; cyclomaltodextrin; cyclodextrin; pesticide;
                                                                                                                                                                                                                                                                                                                                              37.5%;
                                               " X=
                   " X ==
                                               . V21X
"X= Phe,
                            K47X
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                   Gln,
                                                                                                                                                                                                                                                                                                                                     Score 3; DB 1; Pred. No. 2.5
0; Mismatches
                                                                                                                                                                                                                                              684
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                   Leu,
                                                 Tyr"
                                                                                                                                                                                                                                              AA
                    Ala,
                                                                                                                                                               CGTase; enzyme; Bacillus circulans;
                                                                                                                                                                                                                                                                                                                                               DB 17; L.
2.5e+03;
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                    His,
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                                                                                                                                                                                                                                                                                                                                                          /note= "possible insertion of Pro, 148
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147
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/note= "X= Gly,
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/note= "X= Gln,
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 /label= R192K
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AAW17580-W17591, and AAW17606-W17652 represent mutant versions of the cyclomaltodextrin glucanotransferase (CGTase) of Thermonnaerobacter thermosulphurigenes sp. ATCC 53627. (see AAW06772 for wild type sequence). CGTase catalyses the conversion of starch and similar substrates into cyclomaltodextrins (also known as cyclodextrins) via an intramolecular transglycosylation reaction. Cyclodextrins (CD) are cyclic glucose oligomers with a hydrophobic internal cavity that form inclusion
                                                                                                                                                                                                  16-NOV-1995;
21-APR-1995;
17-OCT-1995;
                                                                                                                                               WPI;
                                                                                                        New variants of cyclo:malto:dextrin glucanotransferase (CGTase) have altered substrate binding, useful for prodn. of cyclodextrin(s) or linear oligosaccharide(s), opt. formed in situ in e.g. baked
                                                                                  Claim
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complexes
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95DK-0000477.
95DK-0001173.
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CGTase mutants
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AAW17:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 main CD types (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides, optionally in situ, e.g. during production of baked goods, to stabilise chemicals during their manufacture and in detergents. CD are known for their usefulness in foods, e.g. as a bread-improving agent, to encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals, pesticides or fungicides, to bind/remove lipophilic compounds such as cholesterol (e.g. in egg yolk or butter), j plastic laminates, films etc. and to make biodegradable plastics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       have a modified substrate binding and/or product selectivity, compared to this sequence. The mutants are created using primer mutagenesis to modify the gene encoding this sequence. These sequences have greater product selectivity and/or reduced product inhibition (better yields) than wild-type CGTase. These mutant sequences are used to manufacture
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                                                                                                                                                                                                                                                                                                                                                                                      thermoanaerobacter; starch; cyclomaltodextrin; cyclodextrin; pesticide; transglycosylation; cyclic glucose oligomer; glucose oligosaccharide; cholesterol removal; food stabiliser; vitamin stabiliser; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclomaltodextrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoanaerobacter CGTase variant beta-cyclodextrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW17589 standard;
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/note= "X= Ala,
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'note= "X= Ala,
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                        /label= K232X
                                                               'label= L197X
                                                                                                       /label= D196X
                                                                                                                                                                                                              'label= R192K
                                                                                                                                                                                                                                                     'label= S185X
                                                                                                                                                                                                                                                                                                                                                                                                                              'label= T168S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 abel= D135L
                                                                                                                                                                                                                                                                                                                                                           = G179X
"X= Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  = E146X
"X= Pro,
                                                                                                                                                                    "X= Gly,
             "X= Gln, Leu"
                                                   "X= Asp, Glu"
                                                                                                                                                                                                                                        "X= Pro,
                                                                                                                                                                                                                                                                               "X= Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "X= Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "X= Ala, Leu, or absent"
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                                                                                          "X= Ala,
                                                                                                                                "X= Leu,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asp, Asn,
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sn, or
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               modify the gene encoding this sequence. Incomposition (better yields) product selectivity and/or reduced product inhibition (better yields) product selectivity and/or reduced product inhibition (better yields) product selectivity and/or reduced product inhibition (better yields) than wild-type CGTase. These mutant sequences are used to manufacture the 6 main CD types (comprising 6-11 glucose units), or linear 2-12 glucose oligosaccharides, optionally in situ, e.g. during production of baked goods, to stabilise chemicals during their manufacture and in detergents. CD are known for their usefulness in foods, e.g. as a bread-improving agent, to encapsulate/stabilise/solubilise vitamins, dyes, pharmaceuticals, pesticides or fungicides, to bind/remove lipophilic compounds such as cholesterol (e.g. in egg yolk or butter), in plastic laminates, films etc. and to make biodegradable plastics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-1995;
21-APR-1995;
17-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                         have altered
or linear oli
                                                                                                                                                            complexes with many small hydrophobic molecules. These CGTase mutants have a modified substrate binding and/or product selectivity, compared to this sequence. The mutants are created using primer mutagenesis to modify the gene encoding this sequence. These sequences have greater product selectivity and/or reduced product inhibition (better yields)
                                                                                                                                                                                                                             substrates into cyclomaltodextrins (also known as cyclodextrins) via an intramolecular transglycosylation reaction. Cyclodextrins (CD) are cycliglucose oligomers with a hydrophobic internal cavity that form inclusion
                                                                                                                                                                                                                                                                               AAW17580-W17591, and AAW17606-W17652 represent mutant versions of the cyclomaltodextrin glucanotransferase (CGTase) of Thermoanaerobacter thermosulphurigenes sp. ATCC 53627. (see AAW06772 for wild type
                                                                                                                                                                                                                                                                                                                                                                        New variants of cyclo:malto:dextrin glucanotransferase (CGTase) have altered substrate binding, useful for prodn. of cyclodextrin(s) or linear oligosaccharide(s), opt. formed in situ in e.g. baked
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               Sequence
                                                                                                                                                                                                                                                                    sequence). CGTase catalyses the conversion of starch and similar
                                                                                                                                                                                                                                                                                                                                    Claim 40;
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               684 AA;
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95DK-0000477.
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/note= "X= Thr,
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/note= "X= Phe,
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'note= "X= Ala,
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